

NCBI Description (AC003114) Contains similarity to dihydrofolate reductase (dfr1) gb\_L13703 from Schizosaccharomyces pombe. ESTs gb\_N37567 and gb\_T43002 come from this gene. [Arabidopsis thaliana]

Seq. No. 25438

Contig ID 127191\_1.R1040 5'-most EST vwf700677441.h1

Seq. No. 25439

Contig ID 127207\_1.R1040 5'-most EST vwf700677467.h1

Method BLASTX
NCBI GI g2114473
BLAST score 273
E value 5.0e-24
Match length 155
% identity 34

NCBI Description (U96963) p140mDia [Mus musculus]

Seq. No. 25440

Contig ID 127225\_1.R1040 5'-most EST vwf700677496.h1

Seq. No. 25441

Contig ID 127232\_1.R1040 5'-most EST zsg701117482.h1

Method BLASTX
NCBI GI g2435511
BLAST score 217
E value 2.0e-17
Match length 69
% identity 58

NCBI Description (AF024504) contains similarity to prolyl 4-hydroxylase

alpha subunit [Arabidopsis thaliana]

Seq. No. 25442

Contig ID 127334\_1.R1040

5'-most EST uC-gmrominsoy122g04b1

Seq. No. 25443

Contig ID 127356\_1.R1040 5'-most EST leu701147136.h1

Method BLASTX
NCBI GI g3641252
BLAST score 344
E value 2.0e-32
Match length 116
% identity 58

NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus

domestica]

Seq. No. 25444

Contig ID 127372\_1.R1040 5'-most EST pcp700991873.h1

Seq. No. 25445

3997



127377 1.R1040 Contig ID vwf700677792.hl 5'-most EST 25446 Seq. No. 127404 1.R1040 Contig ID crh700851307.h15'-most EST BLASTX Method g3152568 NCBI GI 391 BLAST score 4.0e-53 E value 155 Match length 66 % identity (AC002986) Similar to hypothetical protein product NCBI Description gb\_Z97337 from A. thaliana. EST gb\_H76597 comes from this gene. [Arabidopsis thaliana] 25447 Seq. No. 127410 1.R1040 Contig ID epx701104689.hl 5'-most EST BLASTX Method NCBI GI g1653444 227 BLAST score 3.0e-18 E value 169 Match length % identity (D90913) hypothetical protein [Synechocystis sp.] NCBI Description 25448 Seq. No. 127422 1.R1040 Contig ID  $epx701\overline{1}06527.h1$ 5'-most EST 25449 Seq. No. 127433 1.R1040 Contiq ID vwf700677878.h1 5'-most EST 25450 Seq. No. 127450 1.R1040 Contig ID g5677663 5'-most EST 25451 Seq. No. Contig ID 127461 1.R1040 fC-gmse7000758287f1 5'-most EST BLASTN Method g1381672 NCBI GI 193 BLAST score 1.0e-104 E value 525

Match length 84 % identity

NCBI Description Pisum sativum gibberellin 20-oxidase mRNA, complete cds

25452 Seq. No.

127472 1.R1040 Contig ID bth700849456.h1 5'-most EST

BLASTX Method q4415917 NCBI GI BLAST score 238 6.0e-37 E value



Match length % identity 46 (AC006282) putative protein containing zinc finger domain NCBI Description [Arabidopsis thaliana] 25453 Seq. No. 127476\_1.R1040 Contig ID 5'-most EST vwf700677948.h1 Method BLASTX g22380 NCBI GI BLAST score 253 2.0e-22 E value Match length 74 77 % identity (X59714) CAAT-box DNA binding protein subunit B (NF-YB) NCBI Description [Zea mays]

25454 Seq. No. 127478 1.R1040 Contig ID 5'-most EST vwf700677950.h1 Method BLASTX NCBI GI g1695882 BLAST score 405

E value 2.0e-39 154 Match length % identity 58

(U63743) mitotic centromere-associated kinesin [Homo NCBI Description

sapiens]

Seq. No. 25455

127512 1.R1040 Contig ID 5'-most EST  $jex700\overline{9}05903.h1$ 

Method BLASTX NCBI GI q3287695 BLAST score 271 6.0e-24 E value Match length 82 % identity 62

(AC003979) Similar to hypothetical protein C34B7.2 NCBI Description

gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis

thaliana]

Seq. No. 25456

Contig ID 127539 1.R1040 5'-most EST txt700735922.h1

Method BLASTX NCBI GI q4218005 BLAST score 191 E value 1.0e-14 Match length 64 56 % identity

NCBI Description (AC006135) putative vicilin storage protein (globulin-like)

[Arabidopsis thaliana]

Seq. No. 25457

127548 1.R1040 Contig ID 5'-most EST vwf700678069.h1

3999



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BLASTX
Method
NCBI GI
                  q3850582
BLAST score
                  352
                  2.0e-33
E value
Match length
                  112
                  62
% identity
NCBI Description (AC005278) F15K9.14 [Arabidopsis thaliana]
                  25458
Seq. No.
                  127560 1.R1040
Contig ID
                  kl1701213535.h1
5'-most EST
Seq. No.
                  25459
                  127576 1.R1040
Contig ID
5'-most EST
                  kl1701208016.hl
Seq. No.
                   25460
                   127595 1.R1040
Contig ID
5'-most EST
                  vwf700678159.hl
                   25461
Seq. No.
                   127619 1.R1040
Contig ID
5'-most EST
                  rca701000604.hl
                   25462
Seq. No.
                   127650 1.R1040
Contig ID
                   kl1701215475.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1903034
                   233
BLAST score
                   4.0e-19
E value
                   91
Match length
% identity
NCBI Description (X94625) amp-binding protein [Brassica napus]
                   25463
Seq. No.
                   127657 1.R1040
Contig ID
                   vwf700678849.hl
5'-most EST
                   BLASTN
Method
NCBI GI
                   q4206101
BLAST score
                   147
                   3.0e-77
E value
Match length
                   246
                   87
% identity
NCBI Description Glycine max retroelement diaspora gag-pol polyprotein
                   (gag-pol) pseudogene, partial sequence
Seq. No.
                   25464
                   127704 1.R1040
Contig ID
5'-most EST
                   zzp700832927.h1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g4220512
BLAST score 796
E value 2.0e-87
Match length 175
% identity 80

NCBI Description (AL035356) putative pectate lyase [Arabidopsis thaliana]

4000



127705 1.R1040 Contig ID vwf700678483.hl 5'-most EST

Seq. No. 25466

127735 1.R1040 Contig ID vwf700678536.h1 5'-most EST

Seq. No. 25467

Contig ID 127745 1.R1040 5'-most EST vwf700678556.h1

25468 Seq. No.

Contig ID 127760 1.R1040 5'-most EST vwf700678582.h1

Method BLASTX g913445 NCBI GI BLAST score 628 2.0e-65 E value Match length 173 % identity 65

(S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase NCBI Description homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv.

red cherry, Peptide, 389 aa] [Lycopersicon esculentum]

Seq. No. 25469

127817 1.R1040 Contig ID 5'-most EST zsg701118027.h2

Method BLASTX NCBI GI g3122671 BLAST score 311 E value 2.0e-28 Match length 78 76

% identity

NCBI Description HYPOTHETICAL RAE1-LIKE PROTEIN >gi\_2129676\_pir\_\_S71241 probable export protein - Arabidopsis thaliana >gi 1297188

(U53501) Theoretical protein with similarity to Swiss-Prot

Accession Number P41838 poly A+ RNA export protein

[Arabidopsis thaliana]

Seq. No. 25470

127824 1.R1040 Contig ID 5'-most EST epx701107761.h1

Method BLASTX NCBI GI q1769897 BLAST score 141 5.0e-14 E value 97 Match length % identity

NCBI Description (Y08010) lectin receptor kinase [Arabidopsis thaliana]

25471 Seq. No.

127872 1.R1040 Contig ID 5'-most EST zhf700960611.h1

Method BLASTX NCBI GI g2462781

```
BLAST score
                  3.0e-53
E value
                  156
Match length
% identity
                   69
                  (U73175) carbamoyl phosphate synthetase small subunit
NCBI Description
                   [Arabidopsis thaliana]
                   25472
Seq. No.
                   127898 1.R1040
Contig ID
                   asj700967385.hl
5'-most EST
                  BLASTX
Method
                   g4539351
NCBI GI
                   180
BLAST score
                   1.0e-13
E value
Match length
                   60
% identity
                   60
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   25473
Seq. No.
                   127901 1.R1040
Contia ID
                   rlr700900909.hl
5'-most EST
                   BLASTX
Method
                   g130997
NCBI GI
                   269
BLAST score
                   2.0e-23
E value
Match length
                   156
% identity
                   REPETITIVE PROLINE-RICH CELL WALL PROTEIN 1 PRECURSOR
NCBI Description
                   >gi 81809_pir_A29324 proline-rich protein precursor -
                   soybean >gi_170049 (J02746) proline-rich protein [Glycine
                   max]
                   25474
Seq. No.
                   127933 1.R1040
Contig ID
                   vwf700678874.hl
5'-most EST
                   25475
 Seq. No.
                   127959 1.R1040
 Contig ID
                   vwf700678918.h1
 5'-most EST
                   BLASTX
 Method
                   q3132477
 NCBI GI
                   321
 BLAST score
                   6.0e-30
 E value
                   89
 Match length
                   20
 % identity
                   (AC003096) unknown protein [Arabidopsis thaliana]
 NCBI Description
```

Contig ID 127966\_1.R1040 5'-most EST vwf700678951.h1

Seq. No. 25477

Contig ID 127990\_1.R1040 5'-most EST vwf700678986.h1

Seq. No. 25478

Contig ID 128005\_1.R1040

% identity

```
jC-gmf102220094h09a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3935185
BLAST score
                  316
E value
                  4.0e-29
Match length
                  84
% identity
NCBI Description (AC004557) F17L21.28 [Arabidopsis thaliana]
                  25479
Seq. No.
Contig ID
                  128010 1.R1040
5'-most EST
                  kl1701213537.h1
Method
                  BLASTX
NCBI GI
                  g283004
BLAST score
                  155
E value
                  1.0e-10
Match length
                  58
                  27
% identity
NCBI Description DNA-binding protein Gt-2 - rice >gi 20249 emb CAA48328
                  (X68261) gt-2 [Oryza sativa]
                  25480
Seq. No.
Contig ID
                  128069 1.R1040
5'-most EST
                  vwf700679222.h1
Seq. No.
                  25481
                  128074 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220108h01a1
Seq. No.
                  25482
                  128078 1.R1040
Contig ID
5'-most EST
                  vwf700679232.h1
Seq. No.
                  25483
                  128079 1.R1040
Contig ID
5'-most EST
                  vwf700679234.h1
Seq. No.
                  25484
                  128089 1.R1040
Contig ID
5'-most EST
                  vwf700679249.h1
Seq. No.
                  25485
                  128167 1.R1040
Contig ID
5'-most EST
                  vwf700679515.h1
                  25486
Seq. No.
                  128178 1.R1040
Contig ID
5'-most EST
                  asn701139643.hl
Method
                  BLASTX
NCBI GI
                  g2583120
BLAST score
                  670
E value
                  3.0e-70
Match length
                  202
```

NCBI Description (AC002387) putative receptor-like protein kinase

[Arabidopsis thaliana]



Contig ID 128187\_1.R1040 5'-most EST fde700874394.h1

Seq. No. 25488

Contig ID 128199\_1.R1040 5'-most EST pxt700943649.h1

Seq. No. 25489

Contig ID 128210\_1.R1040 5'-most EST epx701106740.h1

Method BLASTX
NCBI GI g4165510
BLAST score 287
E value 1.0e-25
Match length 143
% identity 39

NCBI Description (AL034356) predicted using hexExon; L7610.8, DNAJ-like

protein, len:232 aa; Similarity to prokaryotic DNAJ

proteins and eukarytic DNAJ-like chaperones. E.coli DNAJ (SW:DNAJ\_ECOLI) BLAST score: 405 P: 5.3e-38, 37% identity

in

Seq. No. 25490

Contig ID 128213\_1.R1040 5'-most EST fC-gmro700849489g1

Method BLASTN
NCBI GI 9458339
BLAST score 163
E value 2.0e-86
Match length 336
% identity 90

NCBI Description Vigna radiata clone pVR-ACO2

1-aminocyclopropane-1-carboxylate oxidase homolog mRNA,

partial cds

Seq. No. 25491

Contig ID 128221\_1.R1040 5'-most EST kl1701203893.h1

Seq. No. 25492

Contig ID 128225 1.R1040 5'-most EST gsv701054146.h1

Seq. No. 25493

Contig ID 128238 1.R1040 5'-most EST asn701142726.h1

Method BLASTX
NCBI GI g3329294
BLAST score 593
E value 5.0e-61
Match length 282
% identity 44

NCBI Description (AE001355) Zinc Metalloprotease (insulinase family)

[Chlamydia trachomatis]

Seq. No. 25494



Contig ID 128273\_1.R1040 5'-most EST vwf700679727.h1

Seq. No. 25495

Contig ID 128280\_1.R1040 5'-most EST wvk700685126.h1

Method BLASTN
NCBI GI g2244991
BLAST score 39
E value 3.0e-12
Match length 119
% identity 83

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 25496

Contig ID 128283\_1.R1040 5'-most EST zhf700959967.h1

Method BLASTX
NCBI GI 94038034
BLAST score 434
E value 1.0e-42
Match length 90
% identity 90

NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]

Seq. No. 25497

Contig ID 128283\_2.R1040 5'-most EST dpv701102859.h1

Method BLASTX
NCBI GI 94038034
BLAST score 99
E value 7.0e-09
Match length 37
% identity 89

NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]

Seq. No. 25498

Contig ID 128331\_1.R1040 5'-most EST gsv701049493.h1

Seq. No. 25499

Contig ID 128341 1.R1040

5'-most EST g5342381
Method BLASTX
NCBI GI g4512687
BLAST score 497
E value 4.0e-50
Match length 114
% identity 82

NCBI Description (AC006931) floral homeotic protein AGL5 [Arabidopsis

thaliana]

Seq. No. 25500

Contig ID 128341\_2.R1040 5'-most EST leu701147365.h1

Method BLASTN



NCBI GI g861080
BLAST score 64
E value 1.0e-27
Match length 144
% identity 86

NCBI Description P.ginseng gag2 mRNA for agamous

Seq. No. 25501

Contig ID 128350\_1.R1040 5'-most EST vwf700679892.h1

Seq. No. 25502

Contig ID 128354\_1.R1040 5'-most EST awf700836485.h1

Seq. No. 25503

Contig ID 128362\_1.R1040 5'-most EST ejt700606111.h2

Seq. No. 25504

Contig ID 128385\_1.R1040

5'-most EST jC-gmst02400055a10d1

Seq. No. 25505

Contig ID 128390\_1.R1040 5'-most EST rca701000392.h1

Seq. No. 25506

Contig ID 128396\_1.R1040 5'-most EST ejt700606153.h2

Method BLASTX
NCBI GI g2702284
BLAST score 142
E value 1.0e-12
Match length 86
% identity 66

NCBI Description (AC003033) Argonaute (AG01)-like protein [Arabidopsis

thaliana]

Seq. No. 25507

Contig ID 128432\_1.R1040 5'-most EST ejt700606210.h1

Seq. No. 25508

Contig ID 128443\_1.R1040 5'-most EST pcp700992841.h1

Seq. No. 25509

Contig ID 128445 1.R1040 5'-most EST ejt700606227.h1

Seq. No. 25510

Contig ID 128449\_1.R1040 5'-most EST sat701004913.h1

Seq. No. 25511

Contig ID 128450\_1.R1040



5'-most EST kl1701208990.h1

Seq. No. 25512

Contig ID 128453\_1.R1040 5'-most EST pcp700995447.h1

Seq. No. 25513

Contig ID 128454\_1.R1040 5'-most EST uC-gmropic097a08b1

Seq. No. 25514

Contig ID 128456\_1.R1040 5'-most EST jC-gmle01810059c11a1

Seq. No. 25515

Contig ID 128463\_1.R1040 5'-most EST ejt700606252.h1

Seq. No. 25516

Contig ID 128475\_1.R1040 5'-most EST ejt700606267.h1

Method BLASTX
NCBI GI g3282505
BLAST score 169
E value 2.0e-14
Match length 72
% identity 60

NCBI Description (AF020786) polyphenol oxidase precursor [Prunus armeniaca]

Seq. No. 25517

Contig ID 128476\_1.R1040 5'-most EST ejt700606268.h1

Seq. No. 25518

Contig ID 128478\_1.R1040 5'-most EST bth700847819.h1

Seq. No. 25519

Contig ID 128491\_1.R1040 5'-most EST uC-gmropic064a08b1

Seq. No. 25520

Contig ID 128504 1.R1040 5'-most EST wvk700679904.h2

Seq. No. 25521

Contig ID 128508\_1.R1040

5'-most EST jC-gmle01810046c12a1

Seq. No. 25522

Contig ID 128510\_1.R1040 5'-most EST wvk700682713.h1

Seq. No. 25523

Contig ID 128515\_1.R1040 5'-most EST wvk700679920.h2



Contig ID 128524\_1.R1040 5'-most EST wvk700679931.h2

Seq. No. 25525

Contig ID 128525\_1.R1040 5'-most EST wvk700679932.h2

Seq. No. 25526

Contig ID 128549\_1.R1040 5'-most EST leu701145743.h1

Seq. No. 25527

Contig ID 128554\_1.R1040 5'-most EST jsh701070353.h1

Seq. No. 25528

Contig ID 128568\_1.R1040 5'-most EST wvk700679992.h2

Method BLASTX
NCBI GI g1477468
BLAST score 190
E value 1.0e-14
Match length 90
% identity 44

NCBI Description (U35244) vacuolar protein sorting homolog r-vps33a [Rattus

norvegicus]

Seq. No. 25529

Contig ID 128579 1.R1040

5'-most EST uC-gmflminsoy002d09b1

Method BLASTX
NCBI GI g1477565
BLAST score 220
E value 1.0e-17
Match length 139
% identity 4

NCBI Description (U50078) p532 [Homo sapiens]

>gi\_4557026\_ref\_NP\_003913.1\_pHERC1\_ hect (homologous to the

E6-AP (UBE3A) carboxyl terminus) domain and RCC1

(CHC1)-like domain (RLD)

Seq. No. 25530

Contig ID 128596\_1.R1040

5'-most EST uC-gmrominsoy053c11b1

Seq. No. 25531

Contig ID 128606\_1.R1040 5'-most EST wvk700680061.h2

Seq. No. 25532

Contig ID 128618\_1.R1040

5'-most EST jC-gmro02910073b05d1

Seq. No. 25533

Contig ID 128623\_1.R1040 5'-most EST wvk700680134.h2



Contig ID 128629\_1.R1040 5'-most EST wvk700680115.h2

Method BLASTX
NCBI GI g1854386
BLAST score 508
E value 2.0e-51
Match length 193
% identity 53

NCBI Description (AB001375) similar to soluble NSF attachment protein [Vitis

vinifera]

Seq. No. 25535

Contig ID 128631\_1.R1040 5'-most EST wrg700789621.h2

Method BLASTX
NCBI GI g1707015
BLAST score 493
E value 1.0e-49
Match length 185
% identity 52

NCBI Description (U78721) protein phosphatase 2C isolog [Arabidopsis

thaliana]

Seq. No. 25536

Contig ID 128643\_1.R1040 5'-most EST hyd700728339.h1

Seq. No. 25537

Contig ID 128665\_1.R1040 5'-most EST wvk700680174.h2

Seq. No. 25538

Contig ID 128676\_1.R1040 5'-most EST wvk700680190.h2

Seq. No. 25539

Contig ID 128690\_1.R1040 5'-most EST kmv700741503.h1

Method BLASTX
NCBI GI g2245005
BLAST score 321
E value 1.0e-29
Match length 127
% identity 61

NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 25540

Contig ID 128700\_1.R1040 5'-most EST zhf700951964.h1

Method BLASTX
NCBI GI g3540182
BLAST score 198
E value 2.0e-15
Match length 83
% identity 54

```
(AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
```

128701 1.R1040 Contig ID wvk700680231.h2 5'-most EST

25542 Seq. No.

128711 1.R1040 Contig ID wvk700680252.h2 5'-most EST

BLASTX Method g730692 NCBI GI 160 BLAST score 6.0e-11 E value 84 Match length % identity 44

RUBISCO-ASSOCIATED PROTEIN >gi\_454179 (L28804) putative [Glycine max] >gi\_1090839\_prf\_\_2019481A RuBisCO complex NCBI Description

protein [Glycine max]

25543 Seq. No.

128723 1.R1040 Contig ID  $hrw701\overline{0}63519.h1$ 5'-most EST

BLASTX Method g2317901 NCBI GI BLAST score 247 4.0e-28 E value 132 Match length % identity 51

(U89959) Similar to vesicle transport protein, PIR NCBI Description

Accession Number A55931 [Arabidopsis thaliana]

25544 Seq. No.

128724 1.R1040 Contig ID uC-gmropic032e03b1 5'-most EST

BLASTX Method g2507281 NCBI GI BLAST score 716 5.0e-76 E value 137 Match length 93 % identity

GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi 1668706 emb\_CAA66048\_ NCBI Description

(X97380) atran2 [Arabidopsis thaliana]

25545 Seq. No.

128725 1.R1040 Contig ID hrw701062822.h1 5'-most EST

BLASTX Method g3549660 NCBI GI 228 BLAST score 2.0e-18 E value 94 Match length % identity 63

(AL031394) carbonate dehydratase - like protein NCBI Description

[Arabidopsis thaliana]

25546 Seq. No.

128743\_1.R1040 Contig ID



5'-most EST wvk700680314.h1

Method BLASTX
NCBI GI g2827637
BLAST score 155
E value 3.0e-10
Match length 49
% identity 55

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 25547

Contig ID 128760\_1.R1040 5'-most EST uC-gmropic014e01b1

Seq. No. 25548

Contig ID 128780\_1.R1040 5'-most EST zsg701130245.h1

Seq. No. 25549

Contig ID 128781\_1.R1040 5'-most EST wvk700681073.h1

Seq. No. 25550

Contig ID 128783\_1.R1040 5'-most EST wrg700788805.h2

Seq. No. 25551

Contig ID 128784\_1.R1040 5'-most EST wvk700680430.h1

Seq. No. 25552

Contig ID 128785\_1.R1040 5'-most EST wvk700680439.h1

Seq. No. 25553

Contig ID 128795\_1.R1040 5'-most EST wvk700680464.h1

Method BLASTX
NCBI GI g4539455
BLAST score 291
E value 2.0e-30
Match length 164
% identity 47

NCBI Description (AL049500) T5C23.70 [Arabidopsis thaliana]

Seq. No. 25554

Contig ID 128797\_1.R1040 5'-most EST sat701011752.h1

Seq. No. 25555

Contig ID 128799 1.R1040 5'-most EST wvk700681024.h1

Seq. No. 25556

Contig ID 128805\_1.R1040

5'-most EST jC-gmle01810045e03d1

Seq. No. 25557



Contig ID 128806\_1.R1040 5'-most EST wvk700680496.h1

Seq. No. 25558

Contig ID 128817\_1.R1040 5'-most EST wvk700680524.h1

Seq. No. 25559

Contig ID 128821\_1.R1040 5'-most EST wvk700680533.h1

Seq. No. 25560

Contig ID 128856\_1.R1040 5'-most EST wvk700680658.h1

Seq. No. 25561

Contig ID 128913\_1.R1040 5'-most EST uC-gmropic0001h08b1

Method BLASTX
NCBI GI g3776011
BLAST score 375
E value 4.0e-36
Match length 99
% identity 71

NCBI Description (AJ010469) RNA helicase [Arabidopsis thaliana]

Seq. No. 25562

Contig ID 128917\_1.R1040 5'-most EST wvk700680828.h1

Seq. No. 25563

Contig ID 128921\_1.R1040 5'-most EST wvk700680838.h1

Method BLASTX
NCBI GI g3695389
BLAST score 204
E value 2.0e-16
Match length 89
% identity 22

NCBI Description (AF096371) contains similarity to D-isomer specific

2-hydroxyacid dehydrogenases (Pfam: 2-Hacid\_DH.hmm, score:

19.11) [Arabidopsis thaliana]

Seq. No. 25564

Contig ID 128951\_1.R1040 5'-most EST kmv700744076.h1

Method BLASTX
NCBI GI g3928150
BLAST score 827
E value 1.0e-88
Match length 273
% identity 63

NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 25565

Contig ID 128955\_1.R1040 5'-most EST wvk700680921.h1



```
25566
Seq. No.
                  128961 1.R1040
Contig ID
                  hyd700725028.h1
5'-most EST
                  25567
Seq. No.
                  128962 1.R1040
Contig ID
5'-most EST
                  wvk700680933.h1
                   25568
Seq. No.
                   128965 1.R1040
Contig ID
                   zsg701126127.h1
5'-most EST
                   BLASTX
Method
                   g3859659
NCBI GI
BLAST score
                   349
                   2.0e-49
E value
                   162
Match length
                   72
% identity
                  (AL031394) putative potassium transporter AtKT5p (AtKT5)
NCBI Description
                   [Arabidopsis thaliana]
                   25569
Seq. No.
                   128972 1.R1040
Contig ID
                   wvk700680949.hl
5'-most EST
                   BLASTX
Method
                   g2495724
NCBI GI
BLAST score
                   188
                   4.0e-14
E value
                   100
Match length
                   41
% identity
                   HYPOTHETICAL PROTEIN KIAA0249 >gi_1665767_dbj_BAA13380
NCBI Description
                   (D87436) Similar to Human KIAA0188 protein [Homo sapiens]
                   25570
Seq. No.
                   128980_1.R1040
Contig ID
                   zpv700761263.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3643607
BLAST score
                   881
                   4.0e-95
E value
Match length
                   183
% identity
                   53
                  (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
                   25571
Seq. No.
                   128981 1.R1040
Contig ID
                   wvk700680961.h1
5'-most EST
                   BLASTX
Method
```

NCBI GI q3367534 818 BLAST score E value 9.0e-88 189 Match length % identity 82

NCBI Description

(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis

thaliana]

Contig ID 128987\_1.R1040 5'-most EST jsh701066484.h1

Method BLASTX
NCBI GI g4512668
BLAST score 222
E value 7.0e-18
Match length 87
% identity 49

NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]

Seq. No. 25573

Contig ID 129031\_1.R1040 5'-most EST rca701000407.h1

Method BLASTX
NCBI GI g4512625
BLAST score 291
E value 8.0e-26
Match length 246
% identity 32

NCBI Description (AC004793) ESTs gb\_T20423, gb\_AA712864, gb\_H76323 and

gb Z25560 come from this gene. [Arabidopsis thaliana]

Seq. No. 25574

Contig ID 129052\_1.R1040 5'-most EST jex700904681.h1

Seq. No. 25575

Contig ID 129057\_1.R1040 5'-most EST asn701134235.h1

Method BLASTX
NCBI GI g4432814
BLAST score 386
E value 1.0e-37
Match length 101
% identity 72

NCBI Description (AC006593) unknown protein [Arabidopsis thaliana]

Seq. No. 25576

Contig ID 129066\_1.R1040

5'-most EST jC-gmle01810012a05d1

Method BLASTX
NCBI GI g1750190
BLAST score 319
E value 3.0e-29
Match length 77
% identity 77

NCBI Description (U79744) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 25577

Contig ID 129075\_1.R1040 5'-most EST wvk700681138.h2

Method BLASTX
NCBI GI g3021281
BLAST score 189
E value 2.0e-14



Match length 93 % identity 44

NCBI Description (AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq. No. 25578

Contig ID 129080\_1.R1040 5'-most EST zhf700961334.h1

Seq. No. 25579

Contig ID 129101\_1.R1040 5'-most EST wvk700681184.h2

Seq. No. 25580

Contig ID 129124\_1.R1040 5'-most EST wvk700681229.h1

Seq. No. 25581

Contig ID 129125\_1.R1040 5'-most EST kmv700743615.h1

Seq. No. 25582

Contig ID 129129\_1.R1040 5'-most EST zsg701129676.h1

Seq. No. 25583

Contig ID 129141\_1.R1040 5'-most EST jC-gmst02400056e01d1

Method BLASTX
NCBI GI g4490323
BLAST score 177
E value 9.0e-13
Match length 76

Match length 76 % identity 47

NCBI Description (AJ131464) nitrate transporter [Arabidopsis thaliana]

Seq. No. 25584

Contig ID 129163\_1.R1040 5'-most EST wvk700681317.h2

Seq. No. 25585

Contig ID 129179\_1.R1040 5'-most EST rca701001131.h1

Method BLASTX
NCBI GI g4220514
BLAST score 315
E value 1.0e-29
Match length 85
% identity 79

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 25586

Contig ID 129191\_1.R1040 5'-most EST rca700998186.h1

Method BLASTX
NCBI GI g3738327
BLAST score 1214

1.0e-133 445

% identity 54
NCBI Description (AC005170) putative serine ca

(AC005170) putative serine carboxypeptidase [Arabidopsis

thaliana]

Seq. No. 25587

E value

Match length

Contig ID 129191\_2.R1040 5'-most EST fC-gmle700871950f3

Method BLASTX
NCBI GI g2443888
BLAST score 220
E value 1.0e-23
Match length 98
% identity 58

NCBI Description (AC002294) similar to serine carboxypeptidases [Arabidopsis

thaliana]

Seq. No. 25588

Contig ID 129195 1.R1040 5'-most EST wvk700681364.h2

Seq. No. 25589

Contig ID 129212 1.R1040 5'-most EST wvk700681386.h2

Seq. No. 25590

Contig ID 129226 1.R1040

5'-most EST jC-gmle01810036d12a2

Method BLASTX
NCBI GI g3063469
BLAST score 333
E value 6.0e-31
Match length 158
% identity 47

NCBI Description (AC003981) F22013.31 [Arabidopsis thaliana]

Seq. No. 25591

Contig ID 129233 1.R1040

5'-most EST jC-gmle01810085d08d1

Method BLASTX
NCBI GI g3269291
BLAST score 314
E value 9.0e-29
Match length 117
% identity 54

NCBI Description (AL030978) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 25592

Contig ID 129259 1.R1040 5'-most EST wvk700681471.h2

Seq. No. 25593

Contig ID 129268\_1.R1040 5'-most EST smc700746085.h1

Method BLASTX

```
q2342690
NCBI GI
BLAST score
                    265
                    1.0e-23
E value
Match length
                    74
                    69
% identity
                   (AC000106) Similar to Homo copine I (gb_U83246).
NCBI Description
                    [Arabidopsis thaliana]
                    25594
Seq. No.
                    129303 1.R1040
Contig ID
                    uC-gmflminsoy007h11b1
5'-most EST
                    BLASTX
Method
                    g126409
NCBI GI
                    327
BLAST score
                    2.0e-30
E value
                    108
Match length
                    59
% identity
                   LIPOXYGENASE 1 >gi_100005_pir__S22153 lipoxygenase (EC 1.13.11.12) - kidney bean >gi_21017_emb_CAA45088_ (X63525)
NCBI Description
                    lipoxygenase [Phaseolus vulgaris]
                    25595
Seq. No.
                    129308 1.R1040
Contig ID
                    jC-gmf102220113h03d1
5'-most EST
                    25596
Seq. No.
                    129313 1.R1040
Contig ID
                    g4396199
5'-most EST
                    BLASTX
Method
                    q2462834
NCBI GI
                    132
BLAST score
                    9.0e-13
E value
                    102
Match length
                    41
% identity
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]
                    25597
Seq. No.
                    129333 1.R1040
Contig ID
                    wvk700682529.h2
5'-most EST
                    BLASTX
Method
                    a2501460
NCBI GI
                    314
BLAST score
E value
                    3.0e-29
```

87 Match length 72 % identity

NCBI Description PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC

PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP)

(HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE)

>qi 1545952 emb CAA96580 (Z72499) herpesvirus associated

ubiquitin-specific protease (HAUSP) [Homo sapiens]

>qi 4507857 ref NP 003461.1 pUSP7 Herpes virus-associated

ubiquitin-specific protease

25598 Seq. No.

129338 1.R1040 Contig ID asn701137047.h1 5'-most EST



Contig ID 129354\_1.R1040 5'-most EST zhf700952848.h1

Seq. No. 25600

Contig ID 129369 1.R1040 5'-most EST wvk700681663.h1

Seq. No. 25601

Contig ID 129380\_1.R1040 5'-most EST fC-gmse700853357a1

Method BLASTX
NCBI GI g541825
BLAST score 923
E value 1.0e-168
Match length 403
% identity 75

NCBI Description protein kinase - spinach >gi\_457711\_emb\_CAA82993\_ (Z30332)

protein kinase [Spinacia oleracea]

Seq. No. 25602

Contig ID 129383\_1.R1040

5'-most EST jC-gmf102220086b10a1

Seq. No. 25603

Contig ID 129384\_1.R1040 5'-most EST ncj700986288.h1

Method BLASTX
NCBI GI g3451075
BLAST score 316
E value 4.0e-29
Match length 86
% identity 70

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 25604

Contig ID 129410\_1.R1040 5'-most EST rca701000232.h1

Method BLASTX
NCBI GI g3687652
BLAST score 375
E value 2.0e-36
Match length 90
% identity 80

NCBI Description (AF047352) rubisco activase precursor [Datisca glomerata]

Seq. No. 25605

Contig ID 129415\_1.R1040 5'-most EST zzp700833878.h1

Seq. No. 25606

Contig ID 129429 1.R1040 5'-most EST sat701011274.h1

Method BLASTX
NCBI GI g3249065
BLAST score 904



E value 9.0e-98
Match length 239
% identity 71

NCBI Description (AC0044)

(AC004473) Similar to HAK1 gb\_U22945 high affinity potassium transporter from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 25607

Contig ID 129462\_1.R1040 5'-most EST pmv700894546.h1

Seq. No. 25608

Contig ID 129479\_1.R1040 5'-most EST wvk700686236.h1

Seq. No. 25609

Contig ID 129481\_1.R1040 5'-most EST wvk700681867.h1

Seq. No. 25610

Contig ID 129490\_1.R1040 5'-most EST rca700997233.h1

Seq. No. 25611

Contig ID 129491\_1.R1040 5'-most EST wvk700681885.h1

Method BLASTX
NCBI GI g3659909
BLAST score 179
E value 4.0e-13
Match length 46
% identity 78

NCBI Description (AF020715) histidyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 25612

Contig ID 129535\_1.R1040 5'-most EST wvk700682268.h1

Seq. No. 25613

Contig ID 129537\_1.R1040 5'-most EST wvk700681974.h1

Method BLASTN
NCBI GI g4097568
BLAST score 66
E value 1.0e-28
Match length 126
% identity 88

NCBI Description Glycine max farnesylated protein GMFP4 mRNA, partial cds

Seq. No. 25614

Contig ID 129556\_1.R1040 5'-most EST wvk700682012.h1

Seq. No. 25615

Contig ID 129576\_2.R1040 5'-most EST pmv700894164.h1

Method BLASTX

```
q2829902
NCBI GI
                   538
BLAST score
                   3.0e-55
E value
                   126
Match length
% identity
                   (AC002311) Putative sulphate transporter protein#protein
NCBI Description
                   [Arabidopsis thaliana]
                   25616
Seq. No.
                   129613 1.R1040
Contig ID
                   zhf700964751.h1
5'-most EST
                   BLASTX
Method
                   g4467115
NCBI GI
BLAST score
                   148
                   1.0e-09
E value
                   41
Match length
                   76
% identity
                   (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                   25617
Seq. No.
                   129643 1.R1040
Contig ID
                   jC-gmf102220102b09a1
5'-most EST
                   BLASTX
Method
                   g2104529
NCBI GI
                   462
BLAST score
                   6.0e-46
E value
                   113
Match length
                   76
% identity
                   (AF001308) putative hexose transporter [Arabidopsis
NCBI Description
                   thaliana]
                   25618
Seq. No.
                   129655 1.R1040
Contig ID
                   jsh701\overline{0}66637.h1
5'-most EST
                   25619
Seq. No.
                   129660 1.R1040
Contig ID
                   pxt700945311.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3033400
                   251
BLAST score
                   2.0e-21
E value
                    68
Match length
                    63
% identity
                    (AC004238) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                    thaliana]
                    25620
 Seq. No.
                    129675 1.R1040
 Contig ID
                    g56070\overline{3}2
 5'-most EST
                    BLASTX
 Method
                    q2342686
 NCBI GI
                    181
 BLAST score
                    4.0e-13
 E value
 Match length
                    69
                    49
 % identity
 NCBI Description (AC000106) Similar to Saccharomyces hypothetical protein
```

```
R051c (gb_Z49209). ESTs gb_T44436,
```

YDR051c (gb\_Z49209). ESTs gb\_T44436,gb\_42252 come from this gene. [Arabidopsis thaliana]

 Seq. No.
 25621

 Contig ID
 129712\_1.R1040

 5'-most EST
 jC-gmro02910005f04a1

 Method
 BLASTX

 NCBI GI
 q2894611

NCBI GI g2894611 BLAST score 417 E value 1.0e-40 Match length 198 % identity 54

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 25622

Contig ID 129717\_1.R1040 5'-most EST wvk700682301.h2

Method BLASTN
NCBI GI g3850561
BLAST score 253
E value 1.0e-140
Match length 274
% identity 97

NCBI Description Homo sapiens chromosome 19, cosmid F23613, complete

sequence [Homo sapiens]

Seq. No. 25623

Contig ID 129751\_1.R1040

5'-most EST uC-gmflminsoy064a05b1

Method BLASTX
NCBI GI g3096930
BLAST score 267
E value 2.0e-23
Match length 86
% identity 65

NCBI Description (AL023094) Homeodomain - like protein [Arabidopsis

thaliana]

Seq. No. 25624

Contig ID 129759\_1.R1040 5'-most EST jC-gmro02910004e05d1

5'-most EST jC-gmro029100 Method BLASTX NCBI GI g2129613

NCBI GI g2129613 BLAST score 159 E value 1.0e-10 Match length 64 % identity 62

NCBI Description homeotic protein BEL1 - Arabidopsis thaliana >gi\_1122533

(U39944) BELL1 [Arabidopsis thaliana]

Seq. No. 25625

Contig ID 129764\_1.R1040 5'-most EST pcp700993852.h1

Seq. No. 25626

Contig ID 129768\_1.R1040 5'-most EST fde700872939.h1



```
25627
Seq. No.
                   129841 1.R1040
Contig ID
                   wvk700682496.h2
5'-most EST
                   BLASTN
Method
                   q3283923
NCBI GI
BLAST score
                   248
                   1.0e-137
E value
Match length
                   256
                   99
% identity
NCBI Description Homo sapiens clone 24452 mRNA sequence
                   25628
Seq. No.
                   129858 1.R1040
Contig ID
                   wvk700682530.h2
5'-most EST
                   BLASTX
Method
                   q3176076
NCBI GI
BLAST score
                   265
                   3.0e-23
E value
                   68
Match length
% identity
                   (AJ002487) protein phosphatase 1 catalitic subunit
NCBI Description
                   [Medicago sativa]
Seq. No.
                   25629
                   129860 1.R1040
Contig ID
                   jC-gmle01810022a04a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2244910
                   379
BLAST score
E value
                   1.0e-36
                   121
Match length
% identity
                   (Z97339) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                   25630
Seq. No.
                   129867 1.R1040
Contig ID
                   leu701\overline{1}52970.h1
5'-most EST
                   BLASTX
Method
                   g3402722
NCBI GI
BLAST score
                    421
                   1.0e-41
E value
Match length
                   105
                    69
 % identity
                   (AC004261) CPDK-related protein [Arabidopsis thaliana]
NCBI Description
                    25631
 Seq. No.
                    129884 1.R1040
 Contig ID
                    hyd700729914.h1
 5'-most EST
                    BLASTX
 Method
                    q3875246
 NCBI GI
                    206
 BLAST score
                    2.0e-16
 E value
                    78
 Match length
```

(Z81490) similar to WD domain, G-beta repeats (2 domains);

cDNA EST EMBL: T00482 comes from this gene; cDNA EST

45

% identity

NCBI Description

EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gene;

 Seq. No.
 25632

 Contig ID
 129886\_1.R1040

 5'-most EST
 rca700997554.h1

Method BLASTX
NCBI GI g3367578
BLAST score 435
E value 4.0e-43
Match length 142
% identity 61

NCBI Description (AL031135) protein kinase - like protein [Arabidopsis

thaliana]

Seq. No. 25633

Contig ID 129930\_1.R1040 5'-most EST fua701040551.h1

Method BLASTX
NCBI GI g1706102
BLAST score 325
E value 4.0e-30
Match length 158
% identity 42

NCBI Description CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 160 KD

SUBUNIT (CPSF 160 KD SUBUNIT) >gi\_1045574 (U37012) cleavage

and polyadenylation specificity factor [Homo sapiens]

Seq. No. 25634

Contig ID 129934\_1.R1040

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 25635

Contig ID 129944\_1.R1040 5'-most EST fde700876378.h1

Seq. No. 25636

Contig ID 129948\_1.R1040 5'-most EST wvk700682711.h1

Method BLASTX
NCBI GI g3413703
BLAST score 164
E value 3.0e-11
Match length 51
% identity 65

NCBI Description (AC004747) unknown protein [Arabidopsis thaliana]

Seq. No. 25637

Contig ID 129953\_1.R1040 5'-most EST leu701147955.h1



129954 1.R1040 Contig ID fC-gmle700685171a1 5'-most EST

BLASTX Method g2465923 NCBI GI 914 BLAST score 1.0e-98 E value 359 Match length 53 % identity

(AF024648) receptor-like serine/threonine kinase NCBI Description

[Arabidopsis thaliana]

25639 Seq. No.

129956 1.R1040 Contig ID wvk700682726.hl 5'-most EST

Method BLASTX g2245004 NCBI GI BLAST score 153 7.0e-10 E value 60 Match length % identity 55

(Z97341) similarity to membrane transport protein NCBI Description

[Arabidopsis thaliana]

25640 Seq. No.

129988 1.R1040 Contiq ID jC-gmle01810000e06d1 5'-most EST

25641 Seq. No.

129999 1.R1040 Contig ID 5'-most EST jC-gmle01810065g04a1

25642 Seq. No.

130008 1.R1040 Contig ID fde700871610.hl 5'-most EST

BLASTX Method q3450842 NCBI GI BLAST score 202 4.0e-16 E value 65 Match length 60 % identity

(AF080436) mitogen activated protein kinase kinase [Oryza NCBI Description

sativa]

25643 Seq. No.

130011 1.R1040 Contig ID wvk700683001.h1 5'-most EST

BLASTN Method q2739003 NCBI GI BLAST score 65 E value 3.0e-28 144 Match length 87 % identity

Glycine max cytochrome P450 monooxygenase CYP82C1p NCBI Description

(CYP82C1) mRNA, complete cds

```
. .
Seq. No.
                  130013 1.R1040
Contig ID
5'-most EST
                  wvk700682836.hl
Seq. No.
                  25645
                  130029 1.R1040
Contig ID
                  g5509621
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3341687
BLAST score
                  146
                  4.0e-09
E value
Match length
                  64
% identity
                  52
NCBI Description (AC003672) putative ras protein [Arabidopsis thaliana]
                  25646
Seq. No.
                  130049 1.R1040
Contig ID
                  rca700996474.hl
5'-most EST
                  25647
Seq. No.
                  130054 1.R1040
Contig ID
5'-most EST
                  rca701001964.hl
Seq. No.
                  25648
                  130059 1.R1040
Contig ID
5'-most EST
                  fde700870532.h1
Method
                  BLASTX
NCBI GI
                  q4049353
BLAST score
                  325
                  2.0e-30
E value
Match length
                  85
                  72
% identity
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
                  25649
Seq. No.
                  130066 1.R1040
Contig ID
                  wvk700682952.hl
5'-most EST
                  BLASTX
Method
                  q1881585
NCBI GI
BLAST score
                   361
                   5.0e-34
E value
Match length
                  156
% identity
                   49
NCBI Description (U72489) remorin [Solanum tuberosum]
                   25650
Seq. No.
Contig ID
                  130067 1.R1040
5'-most EST
                  wvk700682953.h1
                  BLASTX
Method
NCBI GI
                   g2494266
BLAST score
                   269
                   5.0e-24
E value
                   87
Match length
                   56
% identity
                  GTP-BINDING PROTEIN LEPA >gi 1653961 dbj BAA18871 (D90917)
NCBI Description
                   LepA [Synechocystis sp.]
```

```
Seq. No.
                  130081 1.R1040
Contig ID
                  fC-gmle700682990f1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2578033
BLAST score
                  190
                  1.0e-14
E value
Match length
                  88
                  50
% identity
NCBI Description (X97016) omega-6 desaturase [Gossypium hirsutum]
Seq. No.
                  25652
                  130116 1.R1040
Contig ID
5'-most EST
                  ncj700979430.hl
                  25653
Seq. No.
                  130122 1.R1040
Contig ID
5'-most EST
                  wvk700683088.hl
                  25654
Seq. No.
                  130155 1.R1040
Contig ID
                  qsv701051819.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2494266
                   274
BLAST score
                   2.0e-29
E value
                   96
Match length
                   70
% identity
                  GTP-BINDING PROTEIN LEPA >gi_1653961_dbj_BAA18871_ (D90917)
NCBI Description
                  LepA [Synechocystis sp.]
                   25655
Seq. No.
                   130158 1.R1040
Contig ID
                   wvk700683121.h1
5'-most EST
                   25656
Seq. No.
                   130160 1.R1040
Contig ID
                   uC-gmropic075e05b1
5'-most EST
Method
                   BLASTX
                   g107350
NCBI GI
                   207
BLAST score
                   5.0e-16
E value
                   163
Match length
                   33
% identity
                  Pm5 protein - human >gi_1335273_emb_CAA40655_ (X57398) pm5
NCBI Description
                   protein [Homo sapiens]
                   25657
Seq. No.
                   130188 1.R1040
Contig ID
                   fC-gmle700683156a1
5'-most EST
                   BLASTX
Method
                   g4512616
NCBI GI
                   374
BLAST score
                   7.0e-36
E value
                   157
Match length
                   66
% identity
NCBI Description (AC004793) Contains similarity to gi_1653332 extragenic
```



suppressor (SuhB) from Synechocystis sp. gb\_D90912 and is a member of the Inositol monophophatase family PF\_00459. gb AA597395 comes from this gene. [Arabidopsis tha

25658 Seq. No. 130189 1.R1040 Contig ID 5'-most EST g43960<u>2</u>2

25659 Seq. No.

Contig ID 130191 1.R1040 5'-most EST wvk700683161.h1

Method BLASTX NCBI GI q4512678 BLAST score 360 1.0e-34 E value Match length 89 % identity 80

NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]

Seq. No. 25660

130219 1.R1040 Contig ID 5'-most EST gsv701053976.h1

Seq. No. 25661

130237 1.R1040 Contig ID 5'-most EST wvk700683241.h1

Seq. No. 25662

130244 1.R1040 Contig ID 5'-most EST wvk700683251.h1

Method BLASTX NCBI GI g2244910 BLAST score 392 7.0e-45 E value Match length 158 % identity 68

NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No. 25663

Contig ID 130249 1.R1040 5'-most EST wvk700683262.h1

Method BLASTX NCBI GI g2505876 BLAST score 275 2.0e-24 E value Match length 66 % identity 82

NCBI Description (Y12776) MYB-related protein [Arabidopsis thaliana]

Seq. No. 25664

130272 2.R1040 Contig ID wvk700684493.h1 5'-most EST

Method BLASTX NCBI GI q2832661 BLAST score 625 E value 9.0e-71Match length 262



% identity 57
NCBI Description (AL021710) pherophorin - like protein [Arabidopsis thaliana]

Seq. No. 25665

Contig ID 130283\_1.R1040 5'-most EST leu701156006.h1

Seq. No. 25666

Contig ID 130295\_1.R1040 5'-most EST wvk700683345.h1

Method BLASTX
NCBI GI g3402685
BLAST score 268
E value 7.0e-31
Match length 107
% identity 66

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 25667

Contig ID 130296\_1.R1040 5'-most EST wvk700683347.h1

Seq. No. 25668

Contig ID 130297\_1.R1040 5'-most EST ncj700975366.h1

Method BLASTX
NCBI GI g4512705
BLAST score 695
E value 2.0e-73
Match length 174
% identity 78

NCBI Description (AC006569) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 25669

Contig ID 130329\_1.R1040 5'-most EST bth700845688.h1

Method BLASTX
NCBI GI g4262162
BLAST score 210
E value 1.0e-16
Match length 64
% identity 69

NCBI Description (AC005275) putative glycosylation enzyme [Arabidopsis

thaliana]

Seq. No. 25670

Contig ID 130335\_1.R1040 5'-most EST wvk700683422.h1

Seq. No. 25671

Contig ID 130335\_2.R1040 5'-most EST bth700843517.h1

Seq. No. 25672

Contig ID 130359\_1.R1040

```
5'-most EST
                  wvk700683463.hl
                  25673
Seq. No.
                  130367 1.R1040
Contig ID
                  wvk700683477.hl
5'-most EST
                  25674
Seq. No.
                  130371 1.R1040
Contig ID
                  dpv701100843.h1
5'-most EST
                  BLASTX
Method
                   q1694711
NCBI GI
BLAST score
                   357
E value
                   7.0e-34
Match length
                   153
                   44
% identity
NCBI Description (Y09581) FRO1 [Arabidopsis thaliana]
                   25675
Seq. No.
                   130411 1.R1040
Contig ID
                   jC-gmle01810026h11a1
5'-most EST
                   25676
Seq. No.
                   130414 1.R1040
Contig ID
5'-most EST
                   pmv700893194.hl
                   25677
Seq. No.
                   130440 1.R1040
Contig ID
                   wvk700683587.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4336610
                   166
BLAST score
E value
                   6.0e-12
                   49
Match length
% identity
                   59
NCBI Description (AF099112) sigma factor; Sig3 [Zea mays]
                   25678
Seq. No.
                   130452 1.R1040
Contig ID
5'-most EST
                   wvk700683611.h1
Method
                   BLASTX
                   q3269292
NCBI GI
BLAST score
                   279
                   7.0e-25
E value
Match length
                   97
% identity
                   57
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
```

Contig ID 130459 1.R1040

5'-most EST jC-gmst02400076c05a1

Method BLASTX
NCBI GI g4262142
BLAST score 978
E value 1.0e-106
Match length 268
% identity 70

NCBI Description (AC005275) putative alcohol dehydrogenase [Arabidopsis



130461 1.R1040 Contig ID 5'-most EST wvk700683622.h1

Seq. No. 25681

130465 1.R1040 Contig ID 5'-most EST wvk700683629.h1

Seq. No. 25682

Contig ID 130503 1.R1040 5'-most EST wvk700683889.hl

25683 Seq. No.

130509 1.R1040 Contig ID

5'-most EST jC-gmro02910004d02d1

25684 Seq. No.

130510 1.R1040 Contig ID 5'-most EST zhf700961103.h1

25685 Seq. No.

130511 1.R1040 Contig ID 5'-most EST wvk700683709.h1

25686 Seq. No.

130540 1.R1040 Contig ID 5'-most EST wvk700683752.h1

BLASTX Method q3834314 NCBI GI 255 BLAST score 4.0e-22 E value Match length 57 84 % identity

(AC005679) Similar to gene pi010 glycosyltransferase NCBI Description gi\_2257490 from S. pombe clone 1750 gb\_AB004534. ESTs

gb T46079 and gb AA394466 come from this gene. [Arabidopsis

thaliana]

25687 Seq. No.

130560 1.R1040 Contig ID 5'-most EST rca700995993.hl

25688 Seq. No.

130582 1.R1040 Contig ID bth700844767.h1 5'-most EST

25689 Seq. No.

130601 1.R1040 Contig ID

jC-gmle01810062e12d1 5'-most EST

25690 Seq. No.

130623 1.R1040 Contig ID wvk700683909.h1 5'-most EST

Seq. No. 25691

```
Contig ID 130658_1.R1040
5'-most EST wrg700789817.h2
Method BLASTX
NCBI GI g3540208
BLAST score 418
E value 4.0e-41
Match length 122
```

% identity 74 NCBI Description (AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 25692

Contig ID 130679\_1.R1040 5'-most EST jC-gmro02910067a04a1

Method BLASTX
NCBI GI g4210330
BLAST score 988
E value 1.0e-107
Match length 245
% identity 79

NCBI Description (AJ223802) 2-oxoglutarate dehydrogenase, El subunit

[Arabidopsis thaliana]

Seq. No. 25693

Contig ID 130719\_1.R1040 5'-most EST jC-gmro02910054e03d1

Seq. No. 25694

Contig ID 130732\_1.R1040 5'-most EST rca700998726.h1

Method BLASTN
NCBI GI g2739003
BLAST score 60
E value 3.0e-25
Match length 132
% identity 86

NCBI Description Glycine max cytochrome P450 monooxygenase CYP82C1p

(CYP82C1) mRNA, complete cds

Seq. No. 25695

Contig ID 130734 2.R1040 5'-most EST sat701006057.h2

Seq. No. 25696

Contig ID 130764\_1.R1040 5'-most EST kmv700740196.h1

Seq. No. 25697

Contig ID 130765\_1.R1040

5'-most EST uC-gmrominsoy169c07b1

Method BLASTX
NCBI GI g4263696
BLAST score 647
E value 1.0e-67
Match length 224
% identity 55

NCBI Description (AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No. 130766 1.R1040 Contig ID rca700998607.hl 5'-most EST

25699 Seq. No.

130766 2.R1040 Contig ID 5'-most EST wvk700684142.hl

25700 Seq. No.

130771 1.R1040 Contig ID

5'-most EST jC-gmf102220065f12a1

Seq. No. 25701

130833 1.R1040 Contig ID wvk700684236.hl 5'-most EST

BLASTX Method q3193316 NCBI GI BLAST score 599 3.0e-62 E value Match length 141 % identity

(AF069299) contains similarity to nucleotide sugar NCBI Description

epimerases [Arabidopsis thaliana]

25702 Seq. No.

130834 1.R1040 Contig ID yz1700967069.h1 5'-most EST

BLASTX Method q2398523 NCBI GI 368 BLAST score E value 9.0e-35 179 Match length % identity

(Y13721) Transcription factor [Arabidopsis thaliana] NCBI Description

25703 Seq. No.

130834 2.R1040 Contiq ID jC-gmle01810026d12a1 5'-most EST

25704 Seq. No.

130834 4.R1040 Contig ID

uC-gmrominsoy177b04b1 5'-most EST

25705 Seq. No.

130846 1.R1040 Contig ID wvk700684255.h1 5'-most EST

25706 Seq. No.

130866 1.R1040 Contig ID eep700865972.h15'-most EST

BLASTX Method q3341699 NCBI GI BLAST score 146 3.0e-09 E value 60 Match length 45 % identity

NCBI Description (AC003672) putative giberellin beta-hydroxylase



## [Arabidopsis thaliana]

 Seq. No.
 25707

 Contig ID
 130880\_1.R1040

 5'-most EST
 ncj700987812.h1

Seq. No. 25708

Contig ID 130881\_1.R1040 5'-most EST wvk700684312.h1

Method BLASTX
NCBI GI g3928097
BLAST score 180
E value 2.0e-13
Match length 83
% identity 46

NCBI Description (AC005770) unknown protein, 5' partial [Arabidopsis

thaliana]

Seq. No. 25709

Contig ID 130884\_1.R1040 5'-most EST wvk700684315.h1

Seq. No. 25710

Contig ID 130897\_1.R1040 5'-most EST wvk700684332.h1

Seq. No. 25711

Contig ID 130899\_1.R1040 5'-most EST wvk700684334.h1

Seq. No. 25712

Contig ID 130908\_1.R1040 5'-most EST wvk700684350.h1

Method BLASTX
NCBI GI g4049353
BLAST score 127
E value 2.0e-13
Match length 69
% identity 51

NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

. . .

 Seq. No.
 25713

 Contig ID
 130909\_1.R1040

 5'-most EST
 uC-gmropic020h05b1

Seq. No. 25714

Contig ID 130909 2.R1040 5'-most EST jsh701069001.h1

Seq. No. 25715

Contig ID 130916\_1.R1040 5'-most EST wvk700686045.h1

Seq. No. 25716

Contig ID 130919 1.R1040 5'-most EST awf700839342.h1



Seq. No. 2571

Contig ID 130952\_1.R1040

5'-most EST jC-gmle01810053f07a1

Method BLASTX
NCBI GI g3024871
BLAST score 312
E value 1.0e-28
Match length 153
% identity 43

NCBI Description HYPOTHETICAL 77.3 KD PROTEIN SLL0005

>gi\_1001579\_dbj\_BAA10206\_ (D64000) ABC1-like [Synechocystis

sp.]

Seq. No. 25718

Contig ID 130957\_1.R1040 5'-most EST wvk700685061.h1

Seq. No. 25719

Contig ID 130959\_1.R1040 5'-most EST fC-gmle700684428f1

Method BLASTN
NCBI GI g3168616
BLAST score 83
E value 8.0e-39
Match length 159
% identity 88

NCBI Description Drosophila melanogaster DNA sequence (P1 DS07982 (D185)),

complete sequence [Drosophila melanogaster]

Seq. No. 25720

Contig ID 130967\_1.R1040 5'-most EST wvk700684442.h1

Method BLASTX
NCBI GI g3402692
BLAST score 372
E value 2.0e-35
Match length 106
% identity 71

NCBI Description (AC004697) putative

CDP-diacylglycerol--glycerol-3-phosphate

3-phosphatidyltransferase [Arabidopsis thaliana]

Seq. No. 25721

Contig ID 130981\_1.R1040 5'-most EST epx701106843.h1

Seq. No. 25722

Contig ID 130993\_1.R1040 5'-most EST zhf700959682.h1

Seq. No. 25723

Contig ID 131026\_1.R1040 5'-most EST zhf700957356.h1

Method BLASTX
NCBI GI g1899175
BLAST score 864
E value 5.0e-93

```
Match length
% identity
                  73
                   (U90262) calcium-dependent calmodulin-independent protein
NCBI Description
                  kinase CDPK [Cucurbita pepo]
                  25724
Seq. No.
                  131031 1.R1040
Contig ID
                  ncj700978609.hl
5'-most EST
                  BLASTX
Method
                   q3122818
NCBI GI
BLAST score
                   186
                   6.0e-14
E value
Match length
                   86
                   36
% identity
                   30S RIBOSOMAL PROTEIN S6 >gi 2196757 (AF003196) ribosomal
NCBI Description
                   protein S6 [Neisseria gonorrhoeae]
                   25725
Seq. No.
                   131044 1.R1040
Contig ID
                   uC-gmrominsoy105e05b1
5'-most EST
Method
                   BLASTX
                   q4455233
NCBI GI
BLAST score
                   363
E value
                   1.0e-34
                   103
Match length
                   63
% identity
                   (AL035523) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   25726
Seq. No.
                   131047 1.R1040
Contig ID
                   wvk700684575.hl
5'-most EST
Method
                   BLASTX
                   q3080740
NCBI GI
BLAST score
                   383
                   6.0e-37
E value
Match length
                   117
% identity
                   (U77366) pasticcino 1-D [Arabidopsis thaliana]
NCBI Description
                   25727
Seq. No.
                   131053 1.R1040
Contig ID
                   uC-gmflminsoy059e06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2462745
BLAST score
                   374
                   1.0e-35
E value
Match length
                   131
                   49
% identity
                   (AC002292) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   25728
Seq. No.
                   131059 2.R1040
Contig ID
5'-most EST
                   kl1701212104.hl
                   25729
Seq. No.
                   131065 1.R1040
Contig ID
```

wvk700684604.hl

5'-most EST



```
25730
Seq. No.
                  131076 1.R1040
Contig ID
                  bth700847411.hl
5'-most EST
                  25731
Seq. No.
                  131089 1.R1040
Contig ID
                  wvk700684646.h1
5'-most EST
                  BLASTX
Method
                  g3776569
NCBI GI
                  150
BLAST score
                  8.0e-10
E value
Match length
                  96
% identity
                  38
                  (AC005388) ESTs gb_R65549 and gb_AA651123 come from this
NCBI Description
                  gene. [Arabidopsis thaliana]
                   25732
Seq. No.
                   131091 1.R1040
Contig ID
                   wvk700684649.h1
5'-most EST
                   BLASTX
Method
                   g3290022
NCBI GI
                   286
BLAST score
                   7.0e-26
E value
Match length
                   79
                   66
% identity
                   (AF044173) cysteine synthase; CS-B; O-acetylserine (thiol)
NCBI Description
                   lyase; plastidic isoform [Solanum tuberosum]
                   25733
Seq. No.
                   131097 1.R1040
Contig ID
                   uC-gmropic050h10b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4539322
                   483
BLAST score
                   9.0e-49
E value
Match length
                   132
% identity
                   (AL035679) putative protein [Arabidopsis thaliana]
NCBI Description
                   25734
Seq. No.
                   131111 1.R1040
Contig ID
                   jC-gmle01810071b04a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4102727
                   153
BLAST score
                   5.0e-10
E value
                   106
Match length
 % identity
                   (AF015782) blight-associated protein pl2 precursor [Citrus
NCBI Description
                   jambhiri]
                   25735
 Seq. No.
```

131122 1.R1040 Contig ID wvk700684701.hl 5'-most EST

25736

Seq. No.

4036



```
131135 1.R1040
Contig ID
                  wvk700\overline{6}85349.h1
5'-most EST
                   25737
Seq. No.
                  131136 1.R1040
Contig ID
5'-most EST
                  wvk700684721.hl
Method
                  BLASTX
                   g4335764
NCBI GI
                   228
BLAST score
E value
                   1.0e-18
Match length
                   57
% identity
                   55
                   (AC006284) putative WRKY DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   25738
Seq. No.
                   131138 1.R1040
Contig ID
                   wvk700684723.h1
5'-most EST
Seq. No.
                   25739
                   131168 1.R1040
Contig ID
                   jC-gmst02400057c10a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3287270
BLAST score
                   1014
                   1.0e-110
E value
Match length
                   240
                   81
% identity
NCBI Description (Y09533) involved in starch metabalism [Solanum tuberosum]
                   25740
Seq. No.
                   131169 1.R1040
Contig ID
5'-most EST
                   wrg700789831.h2
Seq. No.
                   25741
                   131183 1.R1040
Contig ID
                   wvk700684787.h1
5'-most EST
                   BLASTX
Method
                   q4262181
NCBI GI
                   205
BLAST score
                   8.0e-16
E value
                   140
Match length
% identity
                   41
                   (AC005508) 37496 [Arabidopsis thaliana]
NCBI Description
                   25742
Seq. No.
                   131187 1.R1040
Contig ID
5'-most EST
                   zzp700836025.h1
                   25743
Seq. No.
                   131187 2.R1040
Contig ID
                   uC-gmflminsoy056d09b1
5'-most EST
```

BLASTX Method g1350795 NCBI GI 169 BLAST score 7.0e-12 E value Match length 75



% identity NCBI Description

MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L24 PRECURSOR (YML24) >gi\_1078342\_pir\_\_S50921 ribosomal protein YmL24,
mitochondrial - yeast (Saccharomyces cerevisiae)

>gi 642285\_emb\_CAA87814\_ (Z47815) ribosomal protein

[Saccharomyces cerevisiae]

25744 Seq. No.

131200 1.R1040 Contig ID wvk700684815.hl 5'-most EST

Seq. No. 25745

131207 1.R1040 Contig ID wvk700684822.hl 5'-most EST

Seq. No. 25746

131214 1.R1040 Contig ID hyd700731144.h1 5'-most EST

Seq. No. 25747

131217 1.R1040 Contig ID dpv701101582.h1 5'-most EST

Seq. No. 25748

131241 1.R1040 Contig ID hyd700730220.h1 5'-most EST BLASTX

Method q3874228 NCBI GI BLAST score 140 1.0e-08 E value 78 Match length

27 % identity

(Z49909) cDNA EST CEMSF21F comes from this gene; cDNA EST NCBI Description

EMBL:D73546 comes from this gene; cDNA EST EMBL:D73669 comes from this gene; cDNA EST EMBL: D70979 comes from this gene; cDNA EST EMBL:D71075 comes from this gene; cDNA E

25749 Seq. No.

131248 1.R1040 Contig ID fua701042655.h1 5'-most EST

BLASTX Method g2506139 NCBI GI 659 BLAST score 5.0e-69 E value 210 Match length 61 % identity

COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) NCBI Description

(ARCHAIN) >gi\_1314049\_emb\_CAA91901\_ (Z67962)

archain/delta-COP [Oryza sativa]

25750 Seq. No.

131273 1.R1040 Contig ID wvk700684921.hl 5'-most EST

BLASTX Method q3831455 NCBI GI 433 BLAST score E value 5.0e-43



Match length 102 % identity 76 NCBI Description (AC

(AC005700) putative ubiquitin activating enzyme [Arabidopsis thaliana]

Seq. No. 25751

Contig ID 131284\_1.R1040 5'-most EST wvk700684943.h1

Seq. No. 25752

Contig ID 131295\_1.R1040 5'-most EST rca700998264.h1

Seq. No. 25753

Contig ID 131300\_1.R1040 5'-most EST rlr700895636.h1

Seq. No. 25754

Contig ID 131318\_1.R1040 5'-most EST wvk700686586.h1 Method BLASTX

Method BLASTX
NCBI GI g3513747
BLAST score 188
E value 2.0e-14
Match length 62
% identity 60

NCBI Description (AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]

Seq. No. 25755

Contig ID 131322\_1.R1040 5'-most EST wvk700685010.h1

Method BLASTX
NCBI GI g541825
BLAST score 578
E value 1.0e-59
Match length 125
% identity 84

NCBI Description protein kinase - spinach >gi\_457711\_emb\_CAA82993\_ (Z30332)

protein kinase [Spinacia oleracea]

Seq. No. 25756

Contig ID 131362\_1.R1040 5'-most EST sat701006671.h1

Method BLASTX
NCBI GI g2129473
BLAST score 323
E value 1.0e-29
Match length 142
% identity 49

NCBI Description arabinogalactan-like protein - loblolly pine >gi\_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No. 25757

Contig ID 131366\_1.R1040 5'-most EST zzp700835704.h1



 Seq. No.
 25758

 Contig ID
 131386\_1.R1040

 5'-most EST
 zhf700961336.h1

Method BLASTX
NCBI GI g3582341
BLAST score 366
E value 4.0e-35
Match length 112
% identity 63

NCBI Description (AC005496) putative flavonol 3-o-glucosyltransferase

[Arabidopsis thaliana]

Seq. No. 25759

Contig ID 131387\_1.R1040 5'-most EST wvk700685101.h1

Method BLASTN
NCBI GI g3033512
BLAST score 66
E value 7.0e-29
Match length 181
% identity 84

NCBI Description Phaseolus vulgaris rubisco activase (Rcal) mRNA, complete

cds

Seq. No. 25760

Contig ID 131390\_1.R1040

5'-most EST jC-gmle01810078d02a1

Seq. No. 25761

Contig ID 131393\_1.R1040 5'-most EST wvk700685109.h1

Seq. No. 25762

Contig ID 131398\_1.R1040 5'-most EST ncj700975439.h1

Seq. No. 25763

Contig ID 131401\_1.R1040 5'-most EST wvk700685119.h1

Seq. No. 25764

Contig ID 131435\_1.R1040 5'-most EST wvk700685171.h1

Method BLASTX
NCBI GI g585748
BLAST score 642
E value 2.0e-70
Match length 155
% identity 86

NCBI Description PHYTOENE SYNTHASE PRECURSOR >gi\_413732 (L25812) phytoene

synthase [Arabidopsis thaliana]

Seq. No. 25765

Contig ID 131448\_1.R1040 5'-most EST hyd700725932.h1

Seq. No. 25766



131456 1.R1040 Contig ID

uC-gmflminsoy008b01b1 5'-most EST

25767 Seq. No.

131457 1.R1040 Contig ID

jC-gmro02910063a05a1 5'-most EST

25768 Seq. No.

131466 1.R1040 Contig ID 5'-most EST wvk700685214.h1

25769 Seq. No.

131484 1.R1040 Contig ID fde700876531.hl 5'-most EST

BLASTX Method q1084374 NCBI GI 535 BLAST score E value 7.0e-55 127 Match length

80 % identity

histone-lysine N-methyltransferase (EC 2.1.1.43) large NCBI Description

chain N-methyltransferase - garden pea >gi 508551 (L34291)

ribulose-1,5 bisphosphate carboxylase large subunit

N-methyltransferase [Pisum sativum]

25770 Seq. No.

131492 1.R1040 Contig ID 5'-most EST tku700646415.hl

25771 Seq. No.

131502\_1.R1040 Contig ID

jC-gmle01810047c08a1 5'-most EST

25772 Seq. No.

131520 1.R1040 Contig ID kl1701204808.h1 5'-most EST

BLASTX Method q4539335 NCBI GI BLAST score 512 8.0e-52 E value 218 Match length 48 % identity

(AL035539) putative protein [Arabidopsis thaliana] NCBI Description

25773 Seq. No.

131533 1.R1040 Contig ID wvk700685302.h1 5'-most EST

25774 Seq. No.

131574 1.R1040 Contig ID zsg701117850.h2 5'-most EST

25775 Seq. No.

131584 1.R1040 Contig ID jC-gmro02800039b02a1 5'-most EST

BLASTX Method NCBI GI g2244855



BLAST score 222 E value 5.0e-18 Match length 106 % identity 47

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 25776

Contig ID 131591\_1.R1040 5'-most EST wvk700685375.h1

Seq. No. 25777

Contig ID 131633\_1.R1040 5'-most EST wvk700685427.h1

Method BLASTX
NCBI GI g1708462
BLAST score 511
E value 8.0e-52
Match length 148
% identity 66

NCBI Description IAA-AMINO ACID HYDROLASE HOMOLOG 2 PRECURSOR >gi\_902791

(U23796) ILL2 [Arabidopsis thaliana]

Seq. No. 25778

Contig ID 131656\_1.R1040 5'-most EST bth700846728.h1

Method BLASTX
NCBI GI g3935141
BLAST score 156
E value 1.0e-18
Match length 90
% identity 53

NCBI Description (AC005106) T25N20.5 [Arabidopsis thaliana]

Seq. No. 25779

Contig ID 131658\_1.R1040 5'-most EST wvk700685689.h1

Seq. No. 25780

Contig ID 131663\_1.R1040 5'-most EST xpa700793558.h1

Seq. No. 25781

Contig ID 131681\_1.R1040

5'-most EST jC-gmle01810087f02d1

Seq. No. 25782

Contig ID 131681\_2.R1040 5'-most EST wvk700685504.h1

Seq. No. 25783

Contig ID 131688 1.R1040

5'-most EST jC-gms\overline{T}02400008a01a1

Seq. No. 25784

Contig ID 131694\_1.R1040 5'-most EST wvk700685522.h1

Method BLASTX

```
g2500959
```

NCBI GI g2500959 BLAST score 242 E value 1.0e-20 Match length 68 % identity 68

NCBI Description ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS) >gi\_1653611\_dbj\_BAA18523\_ (D90915) alanyl-tRNA synthetase

[Synechocystis sp.]

Seq. No. 25785

Contig ID 131700\_1.R1040 5'-most EST leu701157716.h1

Seq. No. 25786

Contig ID 131704\_1.R1040 5'-most EST rca700997286.h1

Method BLASTX
NCBI GI g4220486
BLAST score 175
E value 6.0e-13
Match length 81
% identity 44

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 25787

Contig ID 131720\_1.R1040 5'-most EST jC-gmro02800038a05a1

Method BLASTX
NCBI GI g2583120
BLAST score 407
E value 1.0e-39
Match length 166
% identity 38

NCBI Description (AC002387) putative receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 25788

Contig ID 131739\_1.R1040 5'-most EST fC-gmle700685575f1

Method BLASTX
NCBI GI g4220514
BLAST score 295
E value 2.0e-38
Match length 156
% identity 58

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 25789

Contig ID 131757\_1.R1040 5'-most EST wvk700685602.h1

Method BLASTX
NCBI GI g584998
BLAST score 98
E value 4.0e-09
Match length 65
% identity 51

NCBI Description FLAVONOID 3',5'-HYDROXYLASE (F3'5'H) (CYTOCHROME P450





LXXVA2) (P-450EG1) >gi\_629713\_pir\_\_S43342 flavonoid hydroxylase cytochrome P450 - eggplant >gi\_395261\_emb\_CAA50155\_ (X70824) flavonoid hydroxylase (P450) [Solanum melongena]

Seq. No. 25790

Contig ID 131763\_1.R1040 5'-most EST wvk700685611.h1

Seq. No. 25791

Contig ID 131771\_1.R1040

5'-most EST jC-gmro02910040b11d1

Seq. No. 25792

Contig ID 131778\_1.R1040 5'-most EST fde700870859.h1

Seq. No. 25793

Contig ID 131780\_1.R1040 5'-most EST wvk700685628.h1 Method BLASTX

NCBI GI g3367522 BLAST score 375 E value 8.0e-36 Match length 122

Match length 122 % identity 53

NCBI Description (AC004392) EST gb\_T04691 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 25794

Contig ID 131796\_1.R1040 5'-most EST epx701104168.h1

Seq. No. 25795

Contig ID 131806\_1.R1040 5'-most EST wvk700685659.h1

Seq. No. 25796

Contig ID 131814 1.R1040

5'-most EST jC-gmf102220078a08a1

Seq. No. 25797

Contig ID 131851\_1.R1040 5'-most EST wvk700685718.h1

Seq. No. 25798

Contig ID 131887\_1.R1040 5'-most EST kl1701212956.h1

Seq. No. 25799

Contig ID 131887\_2.R1040 5'-most EST jC-gmro02910074c11a1

Seq. No. 25800

Contig ID 131893\_1.R1040

5'-most EST jC-gmle01810070a09a1

2580

Seq. No. 25801 Contig ID 131896\_1.R1040

5'-most EST jC-gmle01810090e08d1

Seq. No. 25802

Contig ID 131898\_1.R1040 5'-most EST wvk700685775.h1

Seq. No. 25803

Contig ID 131907\_1.R1040

5'-most EST jC-gmst02400053e06a1

Method BLASTX
NCBI GI g4455335
BLAST score 459
E value 7.0e-46
Match length 137
% identity 61

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 25804

Contig ID 131913\_1.R1040

5'-most EST jC-gmro02910073g11a1

Method BLASTX
NCBI GI g961450
BLAST score 262
E value 1.0e-22
Match length 140
% identity 39

NCBI Description (D63879) KIAA0156 gene product is related to Xenopus

nucleolin. [Homo sapiens]

Seq. No. 25805

Contig ID 131933\_1.R1040 5'-most EST bth700845467.h1

Seq. No. 25806

Contig ID 131941\_1.R1040 5'-most EST fC-gmle700685831f1

Method BLASTX
NCBI GI g1345882
BLAST score 249
E value 5.0e-21
Match length 83
% identity 55

NCBI Description CYTOCHROME B5

Seq. No. 25807

Contig ID 131956\_1.R1040 5'-most EST zzp700830844.h1

Seq. No. 25808

Contig ID 132015\_1.R1040 5'-most EST wvk700685935.h1

Seq. No. 25809

Contig ID 132025\_1.R1040 5'-most EST fde700875380.h1



 Seq. No.
 25810

 Contig ID
 132038\_1.R1040

 5'-most EST
 jC-gmst02400060d05a1

 Seq. No.
 25811

Contig ID 132038 2.R1040 5'-most EST wvk700685966.h1

 Seq. No.
 25814

 Contig ID
 132057\_1.R1040

 5'-most EST
 wvk700685991.h1

Method BLASTX
NCBI GI g3367570
BLAST score 308
E value 7.0e-33
Match length 90
% identity 83

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

 Seq. No.
 25815

 Contig ID
 132099 1.R1040

 5'-most EST
 ncj700988583.h1

Seq. No. 25816

Contig ID 132112\_1.R1040 5'-most EST hyd700725489.h1

Seq. No. 25817 Contig ID 132112\_2.R1040

5'-most EST gsv701049903.h1

 Seq. No.
 25818

 Contig ID
 132122\_1.R1040

 5'-most EST
 jex700908111.h1

Method BLASTX
NCBI GI g4539301
BLAST score 239
E value 1.0e-19
Match length 188
% identity 33

NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis

thaliana]

Seq. No. 25819

Contig ID 132126\_1.R1040 5'-most EST uC-gmropic111g04b1

Method BLASTX NCBI GI g2244813



```
BLAST score 184
E value 1.0e-13
Match length 85
% identity 47
```

NCBI Description (Z97336) acylaminoacyl-peptidase homolog [Arabidopsis

thaliana]

Seq. No. 25820

Contig ID 132137\_1.R1040 5'-most EST wvk700686110.h1

Seq. No. 25821

Contig ID 132140\_1.R1040
5'-most EST vzy700753224.h1
Method BLASTN

NCBI GI g1877523 BLAST score 70 E value 4.0e-31 Match length 146 % identity 87

NCBI Description Arabidopsis thaliana BAC T7I23, complete sequence

[Arabidopsis thaliana]

Seq. No. 25822

Contig ID 132141\_1.R1040 5'-most EST wvk700686114.h1

Seq. No. 25823

Contig ID 132154\_1.R1040 5'-most EST pcp700992239.h1

Method BLASTX
NCBI GI g3183285
BLAST score 255
E value 2.0e-21
Match length 204
% identity 32

NCBI Description HYPOTHETICAL 54.4 KD PROTEIN IN AROH-NLPC INTERGENIC REGION

>gi\_1742787\_dbj\_BAA15475\_ (D90813) ORF\_ID:o322#7; similar
to [SwissProt Accession Number Q06373] [Escherichia coli]

>gi\_1787999 (AE000266) orf, hypothetical protein

[Escherichia coli]

Seq. No. 25824

Contig ID 132179\_1.R1040 5'-most EST asn701139089.h1

Seq. No. 25825

Contig ID 132183\_1.R1040 5'-most EST fC-gmle700686166f1

Method BLASTX
NCBI GI g3873408
BLAST score 196
E value 9.0e-15
Match length 71
% identity 54

NCBI Description (L76926) putative zinc finger protein [Arabidopsis

thaliana]

5'-most EST

Method NCBI GI



```
25826
Seq. No.
                   132189 1.R1040
Contig ID
                   jC-gmle01810053e04a1
5'-most EST
Seq. No.
                   25827
                   132191 1.R1040
Contig ID
                   jC-gmle01810082g11a1
5'-most EST
Seq. No.
                   25828
                   132210 2.R1040
Contig ID
5'-most EST
                   wvk700686205.hl
Method
                   BLASTX
                   q2465925
NCBI GI
BLAST score
                   184
E value
                   1.0e-13
Match length
                   108
                   70
% identity
                   (AF024649) receptor-like serine/threonine kinase
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                   25829
                   132214 1.R1040
Contig ID
                   wvk700686209.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4204303
BLAST score
                   444
E value
                   2.0e-44
                   104
Match length
% identity
                   74
                    (AC003027) lcl_prt_seq No definition line found
NCBI Description
                    [Arabidopsis thaliana]
                    25830
Seq. No.
                   132215 1.R1040
Contig ID
                   wvk700\overline{6}86544.h1
5'-most EST
                    25831
Seq. No.
                    132226 1.R1040
 Contig ID
                   pcp700993733.hl
 5'-most EST
                    25832
Seq. No.
                    132247 1.R1040
 Contig ID
                    uC-gmflminsoy010f07b1
 5'-most EST
                    BLASTX
Method
                    g2062175
 NCBI GI
                    425
 BLAST score
                    1.0e-41
 E value
                    96
Match length
                    88
 % identity
                   (AC001645) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    25833
 Seq. No.
                    132256 1.R1040
 Contig ID
```

eep700869103.h1

BLASTX

g2342682



BLAST score 1.0e-53 E value Match length 181 65 % identity

(AC000106) Contains similarity to Rattus AMP-activated NCBI Description protein kinase (gb\_X95577). [Arabidopsis thaliana]

25834 Seq. No.

132269 1.R1040 Contig ID pmv700891180.h1 5'-most EST

Method BLASTX NCBI GI q2114104 BLAST score 755 4.0e-80 E value 253 Match length 59 % identity

(AB003590) sulfate transporter [Arabidopsis thaliana] NCBI Description

>qi 2114106 dbj BAA20085\_ (AB003591) sulfate transporter

[Arabidopsis thaliana]

25835 Seq. No.

132293 1.R1040 Contig ID 5'-most EST wvk700686314.h1

25836 Seq. No.

132331 1.R1040 Contig ID txt700734795.h1 5'-most EST

BLASTX Method NCBI GI g1888357 BLAST score 247 3.0e-21 E value Match length 97 48 % identity

(X98130) alpha-mannosidase [Arabidopsis thaliana] NCBI Description

>gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

25837 Seq. No.

132334 1.R1040 Contig ID wvk700686362.hl 5'-most EST

25838 Seq. No.

132335 1.R1040 Contig ID wvk700686364.h1 5'-most EST

BLASTX Method g2398523 NCBI GI 367 BLAST score 6.0e-35 E value 191 Match length 49 % identity

(Y13721) Transcription factor [Arabidopsis thaliana] NCBI Description

25839 Seq. No.

132359 1.R1040 Contig ID

5'-most EST jC-gmf102220061e10a1

25840 Seq. No.



```
132384 1.R1040
Contia ID
                  wvk700686429.hl
5'-most EST
                  25841
Seq. No.
                  132419 1.R1040
Contig ID
5'-most EST
                  wvk700686474.hl
                  25842
Seq. No.
                  132425 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810002f06a1
                  BLASTX
Method
NCBI GI
                  g3738306
BLAST score
                   365
                   1.0e-34
E value
                   115
Match length
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                   25843
                   132432 1.R1040
Contig ID
                   xzm700763741.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1651689
BLAST score
                   206
                   1.0e-15
E value
                   222
Match length
% identity
                  (D90899) hypothetical protein [Synechocystis sp.]
NCBI Description
                   25844
Seq. No.
                   132447 1.R1040
Contig ID
                   uC-gmropic113a09b1
5'-most EST
                   25845
Seq. No.
                   132462 1.R1040
Contig ID
                   bth700847866.hl
5'-most EST
                   25846
Seq. No.
                   132478 1.R1040
Contig ID
                   fde700\overline{8}72781.h1
5'-most EST
                   25847
Seq. No.
                   132480 1.R1040
Contig ID
                   wvk700686555.hl
5'-most EST
                   BLASTX
Method
                   g1513144
NCBI GI
                   426
BLAST score
                   1.0e-41
E value
                   236
Match length
                   36
% identity
                   (U65391) PRF [Lycopersicon esculentum]
NCBI Description
```

Seq. No. 132484 1.R1040 Contig ID 5'-most EST wvk700686560.h1

25848

Seq. No.

25849



Contig ID 132503\_1.R1040 5'-most EST wvk700686583.h1

Seq. No. 25850

Contig ID 132507\_1.R1040 5'-most EST jC-gmro02910046g08a1

Seq. No. 25851

Contig ID 132507\_2.R1040 5'-most EST gsv701051478.h1

Seq. No. 25852

Contig ID 132514 1.R1040 5'-most EST wvk700686596.h1

Seq. No. 25853

Contig ID 132525\_1.R1040 5'-most EST zsg701124687.h1

Seq. No. 25854

Contig ID 132526\_1.R1040 5'-most EST wvk700686615.h1

Seq. No. 25855

Contig ID 132536\_1.R1040 5'-most EST wvk700686627.h1

Seq. No. 25856

Contig ID 132546\_1.R1040 5'-most EST wvk700686637.h1

Seq. No. 25857

Contig ID 132564\_1.R1040 5'-most EST wvk700686663.h1

Method BLASTX
NCBI GI g2829902
BLAST score 264
E value 4.0e-23
Match length 67
% identity 72

NCBI Description (AC002311) Putative sulphate transporter protein#protein

[Arabidopsis thaliana]

Seq. No. 25858

Contig ID 132571\_1.R1040 5'-most EST wvk700686679.h1

Seq. No. 25859

Contig ID 132588\_1.R1040 5'-most EST hyd700724918.h1

Method BLASTX
NCBI GI g2832661
BLAST score 714
E value 1.0e-75
Match length 212
% identity 70

NCBI Description (AL021710) pherophorin - like protein [Arabidopsis



## thaliana]

Seq. No. 25861

Contig ID 132598\_1.R1040 5'-most EST hyd700724931.h1

Seq. No. 25862

Contig ID 132640\_1.R1040 5'-most EST fC-gmle700559531a1

Method BLASTX
NCBI GI g2827637
BLAST score 208
E value 2.0e-16
Match length 104
% identity 40

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 25863

Contig ID 132649 1.R1040 5'-most EST hyd700724993.h1

Seq. No. 25864

Contig ID 132686\_1.R1040 5'-most EST ncj700986206.h1

Seq. No. 25865

Contig ID 132691\_1.R1040 5'-most EST fC-gmse700676135d3

Seq. No. 25866

Contig ID 132692\_1.R1040 5'-most EST jC-gmro02910047a11a1

Method BLASTX
NCBI GI g285741
BLAST score 173
E value 2.0e-12
Match length 60
% identity 50

NCBI Description (D14550) EDGP precursor [Daucus carota]

Seq. No. 25867

Contig ID 132694\_1.R1040

5'-most EST g5057675
Method BLASTX
NCBI GI g2435517
BLAST score 159
E value 2.0e-10
Match length 181
% identity 27

NCBI Description (AF024504) contains similarity to peptidase family A1

[Arabidopsis thaliana]

Seq. No. 25868



```
132703 1.R1040
Contig ID
                   hyd700725073.h1
5'-most EST
                   25869
Seq. No.
                   132735 1.R1040
Contig ID
                   jC-gmro02910062f03a1
5'-most EST
                   BLASTX
Method
                   g4204287
NCBI GI
                   375
BLAST score
E value
                   4.0e-36
                   76
Match length
% identity
                   89
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   25870
Seq. No.
                   132756 1.R1040
Contig ID
                   jex700905848.hl
5'-most EST
Method
                   BLASTX
                   g4006915
NCBI GI
                   449
BLAST score
E value
                   1.0e-44
Match length
                   172
% identity
                   52
                   (Z99708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   25871
                   132760_1.R1040
Contig ID
                   943141\overline{5}3
5'-most EST
                   BLASTX
Method
                   g285741
NCBI GI
BLAST score
                   303
                   1.0e-27
E value
                   141
Match length
                   48
% identity
                   (D14550) EDGP precursor [Daucus carota]
NCBI Description
                   25872
Seq. No.
                   132784 1.R1040
Contig ID
                   k11701206261.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2492792
                   758
BLAST score
                   1.0e-80
E value
Match length
                   204
                   70
% identity
                   LATE NODULIN 56 (N-56) >gi 532290 dbj BAA07212 (D38015)
NCBI Description
                   soybean late nodulin [Glycine max]
                   25873
Seq. No.
                   132791 1.R1040
Contig ID
5'-most EST
                   hyd700725194.h1
```

Method BLASTN
NCBI GI g296444
BLAST score 129
E value 2.0e-66
Match length 173



% identity 9

NCBI Description G.max ADR6 mRNA

Seq. No. 25874

Contig ID 132810\_1.R1040 5'-most EST jex700909628.h1

Method BLASTX
NCBI GI g3885340
BLAST score 403
E value 3.0e-39
Match length 145
% identity 60

NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

Seq. No. 25875

Contig ID 132816\_1.R1040 5'-most EST ncj700978827.h1

Seq. No. 25876

Contig ID 132829\_1.R1040 5'-most EST hyd700726742.h1

Seq. No. 25877

Contig ID 132839\_1.R1040 5'-most EST ncj700977830.h1

Seq. No. 25878

Contig ID 132867\_1.R1040 5'-most EST vzy700753550.h1

Method BLASTX
NCBI GI 94325339
BLAST score 592
E value 2.0e-61
Match length 131
% identity 75

NCBI Description (AF128392) No definition line found [Arabidopsis thaliana]

Seq. No. 25879

Contig ID 132869 1.R1040 5'-most EST hyd700725305.h1

Seq. No. 25880

Contig ID 132874\_1.R1040 5'-most EST fC-gmse700725312f1

Method BLASTX
NCBI GI g3355465
BLAST score 708
E value 6.0e-75
Match length 179
% identity 74

NCBI Description (AC004218) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 25881

Contig ID 132902\_1.R1040 5'-most EST hyd700728976.h1



```
Seq. No.
                  132916 1.R1040
Contig ID
                  hyd700726058.hl
5'-most EST
Seq. No.
                  25883
                  132919 1.R1040
Contig ID
                  hyd700726515.hl
5'-most EST
Seq. No.
                  25884
                  132945 1.R1040
Contig ID
5'-most EST
                  q5057762
Method
                  BLASTX
NCBI GI
                  g2191167
                   156
BLAST score
                   2.0e-10
E value
                   69
Match length
% identity
                   (AF007270) A_IG002P16.18 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   25885
Seq. No.
                   132949 1.R1040
Contig ID
5'-most EST
                   hyd700730232.hl
Method
                   BLASTX
                   g2708744
NCBI GI
                   231
BLAST score
                   2.0e-19
E value
                   87
Match length
                   52
% identity
                   (AC003952) putative Bop-like zinc finger protein
NCBI Description
                   [Arabidopsis thaliana]
                   25886
Seq. No.
                   132960 1.R1040
Contig ID
5'-most EST
                   ncj700981193.hl
Method
                   BLASTN
                   g2760172
NCBI GI
BLAST score
                   33
                   5.0e-09
E value
Match length
                   41
                   95
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUB3, complete sequence [Arabidopsis thaliana]
                   25887
Seq. No.
                   132966 1.R1040
Contig ID
                   uC-gmflminsoy044d09b1
5'-most EST
                   BLASTX
Method
                   q3461835
NCBI GI
                   925
BLAST score
                   1.0e-100
E value
```

246 Match length

70 % identity NCBI Description

(AC005315) putative protein kinase [Arabidopsis thaliana] >gi 3927840 (AC005727) putative protein kinase [Arabidopsis

thaliana]



Seq. No. 2588

Contig ID 132981\_1.R1040 5'-most EST jC-gmst02400031c09a1

Seq. No. 25889

Contig ID 132984 1.R1040 5'-most EST txt700734711.h1

Seq. No. 25890

Contig ID 132990\_1.R1040 5'-most EST epx701109845.h1

Method BLASTX
NCBI GI g2462834
BLAST score 142
E value 5.0e-09
Match length 40
% identity 57

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 25891

Contig ID 132993\_1.R1040 5'-most EST hyd700729996.h1

Method BLASTX
NCBI GI g122087
BLAST score 566
E value 2.0e-58
Match length 136
% identity 85

NCBI Description HISTONE H3 >gi\_81849\_pir\_\_S04520 histone H3 (clone pH3c-1)

- alfalfa >gi\_82609\_pir\_A26014 histone H3 - wheat >gi\_19607\_emb\_CAA31964 (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi\_19609\_emb\_CAA31965 (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi\_21797\_emb\_CAA25451\_(X00937) H3 histone [Triticum aestivum] >gi\_488565 (U09459) histone H3.1 [Medicago sativa] >gi\_2565419 (AF026803)

histone H3 [Onobrychis viciifolia]

Seq. No. 25892

Contig ID 132999\_1.R1040 5'-most EST hyd700725529.h1

Seq. No. 25893

Contig ID 133000\_1.R1040 5'-most EST gsv701054148.h1

Method BLASTX
NCBI GI 94337196
BLAST score 143
E value 9.0e-09
Match length 89
% identity 38

NCBI Description (AC006403) putative serine/threonine receptor kinase

[Arabidopsis thaliana]

Seq. No. 25894

Contig ID 133041\_1.R1040 5'-most EST pmv700892548.h1

Method BLASTX



NCBI GI g4454012 BLAST score 307 E value 3.0e-28 Match length 96 % identity 57

NCBI Description (AL035396) Pollen-specific protein precursor like

[Arabidopsis thaliana]

Seq. No. 25895

Contig ID 133053\_1.R1040 5'-most EST dpv701099963.h1

Method BLASTX
NCBI GI g3128170
BLAST score 789
E value 4.0e-84
Match length 303
% identity 52

NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 25896

Contig ID 133053\_2.R1040

5'-most EST uC-gmrominsoy177a04b1

Seq. No. 25897

Contig ID 133077\_1.R1040 5'-most EST hyd700725652.h1

Seq. No. 25898

Contig ID 133080\_1.R1040 5'-most EST uC-gmronoir019c09b1

Method BLASTX
NCBI GI g2829912
BLAST score 352
E value 1.0e-33
Match length 104
% identity 64

NCBI Description (AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis

thaliana]

Seq. No. 25899

Contig ID 133091\_1.R1040 5'-most EST zhf700959395.h1

Method BLASTX
NCBI GI g3176680
BLAST score 855
E value 7.0e-92
Match length 298
% identity 55

NCBI Description (AC003671) Identical to polygalacuronase isoenzyme 1 beta subunit homolog mRNA gb U63373. EST gb AA404878 comes from

this gene. [Arabidopsis thaliana]

Seq. No. 25900

Contig ID 133129\_1.R1040

5'-most EST uC-gmflminsoy053g01b1

Method BLASTX NCBI GI g1532169



BLAST score 360 E value 3.0e-34 Match length 108 % identity 61

NCBI Description (U63815) similar to a E. coli hypothetical protein F402 encoded by GenBank Accession Number S47768 [Arabidopsis

thaliana]

Seq. No. 25901

Contig ID 133130\_1.R1040 5'-most EST hyd700726911.h1

Seq. No. 25902

Contig ID 133137 1.R1040 5'-most EST hyd700725744.h1

Method BLASTX
NCBI GI g2129636
BLAST score 189
E value 3.0e-14
Match length 114
% identity 41

NCBI Description lipase - Arabidopsis thaliana >gi\_1145627 (U38916) lipase

[Arabidopsis thaliana]

Seq. No. 25903

Contig ID 133138 1.R1040 5'-most EST zhf700959276.h1

Seq. No. 25904

Contig ID 133142 1.R1040 5'-most EST bth700846204.h1

Seq. No. 25905

Contig ID 133142 2.R1040 5'-most EST vzy700755455.h1

Seq. No. 25906

Contig ID 133143 1.R1040 5'-most EST hrw701061304.h1

Seq. No. 25907

Contig ID 133166\_1.R1040 5'-most EST epx701104982.h1

Seq. No. 25908

Contig ID 133170\_1.R1040 5'-most EST smw700646165.h1

Seq. No. 25909

Contig ID 133177 1.R1040 5'-most EST hyd700725813.h1

Method BLASTX
NCBI GI g3859570
BLAST score 165
E value 1.0e-11
Match length 39
% identity 72

4058



## NCBI Description (AF098753) unknown [Oryza sativa]

```
25910
Seq. No.
                  133211 1.R1040
Contig ID
                  q5752743
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3738319
                  512
BLAST score
                  9.0e-52
E value
                  139
Match length
% identity
                  (AC005170) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  25911
Seq. No.
                  133241 1.R1040
Contig ID
                  hyd700725948.h1
5'-most EST
                  25912
Seq. No.
                  133242 1.R1040
Contig ID
                  hyd700725959.hl
5'-most EST
                   25913
Seq. No.
                  133243 1.R1040
Contig ID
5'-most EST
                  hyd700725953.h1
                   25914
Seq. No.
                   133250 1.R1040
Contig ID
                   pcp700993564.hl
5'-most EST
Method
                   BLASTX
                   g2323344
NCBI GI
BLAST score
                   520
                   1.0e-76
E value
Match length
                   204
% identity
                   71
                  (AF014806) alpha-glucosidase 1 [Arabidopsis thaliana]
NCBI Description
                   25915
Seq. No.
                   133260 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910016b12d1
                   25916
Seq. No.
                   133262 1.R1040
Contig ID
                   hyd700725990.h1
5'-most EST
                   25917
Seq. No.
                   133269 1.R1040
Contig ID
                   ncj700985354.h1
5'-most EST
Method
                   BLASTX
                   q4220485
NCBI GI
BLAST score
                   1688
                   0.0e + 00
E value
                   420
Match length
                   73
% identity
                   (AC006069) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
```

Seq. No. 25918

thaliana]



```
133273 1.R1040
Contig ID
                   hyd700726008.h1
5'-most EST
                   25919
Seq. No.
                   133291 1.R1040
Contig ID
5'-most EST
                   g4289592
                    25920
Seq. No.
                    133296 1.R1040
Contig ID
                    jC-qmro02910025f03a1
5'-most EST
Method
                    BLASTX
NCBI GI
                    q1345933
BLAST score
                    230
                    4.0e-19
E value
                    57
Match length
                    74
% identity
                   CITRATE SYNTHASE, GLYOXYSOMAL PRECURSOR (GCS)
NCBI Description
                    >gi_1084323_pir__S53007 citrate synthase - cucurbit
>gi_975633_dbj_BAA07328_ (D38132) glyoxysomal citrate
                    synthase [Cucurbita sp.]
Seq. No.
                    25921
                    133345 1.R1040
Contig ID
5'-most EST
                    epx701109327.hl
                    BLASTX
Method
NCBI GI
                    q4580394
BLAST score
                    184
                    8.0e-14
E value
Match length
                    74
                    47
% identity
                    (AC007171) putative fatty acid elongase [Arabidopsis
NCBI Description
                    thaliana]
                    25922
Seq. No.
                    133390 1.R1040
Contig ID
                    hrw701062525.hl
5'-most EST
Method
                    BLASTX
                    q3360289
NCBI GI
BLAST score
                    144
                    1.0e-18
E value
                    129
Match length
                    50
% identity
                    (AF023164) leucine-rich repeat transmembrane protein kinase
NCBI Description
                    1 [Zea mays]
                    25923
Seq. No.
                    133392 1.R1040
Contig ID
5'-most EST
                    hyd700726181.h1
                    BLASTX
Method
                    g3668088
NCBI GI
                    236
BLAST score
                    2.0e-19
E value
                    129
Match length
                    47
```

% identity NCBI Description

25924

(AC004667) G9a-like protein [Arabidopsis thaliana]

Seq. No.

4060



Contig ID 133397\_1.R1040 5'-most EST fde700872396.h1

Seq. No. 25925

Contig ID 133437\_1.R1040 5'-most EST hyd700726257.h1

Seq. No. 25926

Contig ID 133445 1.R1040

5'-most EST uC-gmrominsoy103c11b1

Seq. No. 25927

Contig ID 133463\_1.R1040 5'-most EST zzp700829722.h1

Method BLASTX
NCBI GI g3850111
BLAST score 337
E value 1.0e-31
Match length 101
% identity 55

NCBI Description (AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]

Seq. No. 25928

Contig ID 133477\_1.R1040 5'-most EST leu701157351.h1

Method BLASTX
NCBI GI g1172586
BLAST score 438
E value 1.0e-43
Match length 113
% identity 70

NCBI Description POLYPHENOL OXIDASE A1 PRECURSOR (PPO) (CATECHOL OXIDASE) >gi 22029 emb CAA77764 (Z11702) polyphenol oxidase [Vicia

faba]

Seq. No. 25929

Contig ID 133489\_1.R1040

5'-most EST g5605687
Method BLASTX
NCBI GI g731690
BLAST score 160
E value 8.0e-11
Match length 118
% identity 36

NCBI Description HYPOTHETICAL 20.9 KD PROTEIN IN HXT5-NRK1 INTERGENIC REGION

>gi\_630117\_pir\_\_S48943 hypothetical protein YHR100c - yeast
(Saccharomyces cerevisiae) >gi 529129 (U00059) Yhr100cp

[Saccharomyces cerevisiae]

Seq. No. 25930

Contig ID 133491 1.R1040

5'-most EST jC-gmro02800044h03a1

Method BLASTX
NCBI GI g3763926
BLAST score 193
E value 2.0e-14



Match length 109 % identity 46

NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

Seq. No. 25931

Contig ID 133498\_1.R1040

5'-most EST uC-gmrominsoy145f11b1

Method BLASTX
NCBI GI g2146731
BLAST score 108
E value 8.0e-09
Match length 70
% identity 36

NCBI Description FK506-binding protein - Arabidopsis thaliana >gi\_1354207

(U49453) rof1 [Arabidopsis thaliana]

Seq. No. 25932

Contig ID 133512\_1.R1040 5'-most EST sat701007834.h1

Method BLASTX
NCBI GI g2736075
BLAST score 522
E value 8.0e-80
Match length 324
% identity 51

NCBI Description (AF016644) PAP-specific phosphatase; HAL2-like protein

[Arabidopsis thaliana]

Seq. No. 25933

Contig ID 133526\_1.R1040 5'-most EST hrw701058310.h1

Seq. No. 25934

Contig ID 133533\_1.R1040 5'-most EST uC-gmropic010e10b1

Method BLASTX
NCBI GI g3688191
BLAST score 155
E value 3.0e-10
Match length 115
% identity 40

NCBI Description (AJ010090) MAP3K alpha protein kinase [Arabidopsis

thaliana]

Seq. No. 25935

Contig ID 133543 1.R1040 5'-most EST pcp700989456.h1

Method BLASTX
NCBI GI g2832661
BLAST score 317
E value 8.0e-32
Match length 121
% identity 64

NCBI Description (AL021710) pherophorin - like protein [Arabidopsis

thaliana]

Seq. No. 25936

```
133553_1.R1040
hyd700726438.h1
```

Contig ID 133553\_1.R1040 5'-most EST hyd700726438.h: Method BLASTX NCBI GI g2829886

BLAST score 169 E value 3.0e-12 Match length 39

% identity 43

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 25937

Contig ID 133562\_1.R1040 5'-most EST hyd700726451.h1

Seq. No. 25938

Contig ID 133586\_1.R1040 5'-most EST hyd700726481.h1

Method BLASTX
NCBI GI g3915020
BLAST score 447
E value 1.0e-44
Match length 87
% identity 95

NCBI Description SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE

GLUCOSYLTRANSFERASE) >gi\_1022365\_emb\_CAA91217\_ (Z56278)

sucrose phosphate synthase [Vicia faba]

Seq. No. 25939

Contig ID 133588\_1.R1040 5'-most EST hyd700726483.h1

Seq. No. 25940

Contig ID 133598\_1.R1040 5'-most EST ncj700978225.h1

Method BLASTX
NCBI GI g3355476
BLAST score 244
E value 2.0e-20
Match length 138
% identity 40

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 25941

Contig ID 133598\_2.R1040 5'-most EST epx701104843.h1

Seq. No. 25942

Contig ID 133616\_1.R1040 5'-most EST hyd700728679.h1

Seq. No. 25943

Contig ID 133620\_1.R1040 5'-most EST gsv701045620.h1

Method BLASTX
NCBI GI g3928083
BLAST score 563
E value 4.0e-58



Match length 145 % identity 72

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 25944

Contig ID 133621\_1.R1040 5'-most EST gsv701051960.h1

Seq. No. 25945

Contig ID 133622\_1.R1040 5'-most EST hyd700726531.h1

Method BLASTX
NCBI GI g3885336
BLAST score 276
E value 2.0e-27
Match length 100
% identity 62

NCBI Description (AC005623) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 25946

Contig ID 133626\_1.R1040 5'-most EST ncj700984019.h1

Method BLASTX
NCBI GI g2623297
BLAST score 238
E value 3.0e-20
Match length 71
% identity 69

NCBI Description (AC002409) unknown protein [Arabidopsis thaliana]

>gi\_3790583 (AF079180) RING-H2 finger protein RHCla

[Arabidopsis thaliana]

Seq. No. 25947

Contig ID 133627\_1.R1040 5'-most EST pcp700990344.h1

Method BLASTX
NCBI GI g417148
BLAST score 294
E value 6.0e-27
Match length 82
% identity 70

NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A)

(G2-4) >gi\_99912\_pir\_ A33654 heat shock protein 26A -

soybean >gi 169981 (M20363) Gmhsp26-A [Glycine max]

Seq. No. 25948

Contig ID 133628\_1.R1040 5'-most EST kll701211868.h1

Seq. No. 25949

Contig ID 133643\_1.R1040

5'-most EST jC-gmst02400055a08a1

Method BLASTX
NCBI GI g3319353
BLAST score 443
E value 1.0e-43

4064



Match length 114 % identity 63

NCBI Description (AF077407) contains similarity to copper-binding proteins [Arabidopsis thaliana]

Seq. No. 25950

Contig ID 133648\_1.R1040 5'-most EST hyd700730850.h1

Method BLASTN
NCBI.GI g3116019
BLAST score 145
E value 5.0e-76
Match length 244
% identity 90

NCBI Description Pisum sativum mRNA for ftsZ gene

Seq. No. 25951

Contig ID 133652\_1.R1040

5'-most EST jC-gmf102220093b05a1

Method BLASTX
NCBI GI g3892709
BLAST score 304
E value 1.0e-27
Match length 89
% identity 74

NCBI Description (AL033545) putative protein [Arabidopsis thaliana]

Seq. No. 25952

Contig ID 133659\_1.R1040 5'-most EST jC-gmfI02220070e03a1

Method BLASTX
NCBI GI g1842158
BLAST score 588
E value 1.0e-60
Match length 191
% identity 58

NCBI Description (D83260) HXC-26 [Homo sapiens] >gi\_1842163\_dbj\_BAA11907\_

(D83389) HXC-26 [Homo sapiens]

Seq. No. 25953

Contig ID 133659\_3.R1040 5'-most EST eep700868425.h1

Seq. No. 25954

Contig ID 133667\_1.R1040 5'-most EST hyd700726606.h1

Method BLASTX
NCBI GI g2342683
BLAST score 159
E value 1.0e-10
Match length 63
% identity 68

NCBI Description (AC000106) Contains similarity to Bos beta-mannosidase

(gb\_U46067). [Arabidopsis thaliana]

Seq. No. 25955

Contig ID 133673 1.R1040



5'-most EST hyd700726614.h1

Seq. No. 25956

Contig ID 133678\_1.R1040 5'-most EST hyd700726621.h1

Seq. No. 25957

Contig ID 133686 2.R1040 5'-most EST hyd700726635.h1

Seq. No. 25958

Contig ID 133687\_1.R1040 5'-most EST kl1701215026.h1

Seq. No. 25959

Contig ID 133709\_1.R1040

5'-most EST jC-gmle01810056g08a1

Seq. No. 25960

Contig ID 133715\_1.R1040 5'-most EST epx701108745.h1

Method BLASTX
NCBI GI g3327394
BLAST score 241
E value 1.0e-20
Match length 58
% identity 71

NCBI Description (AC004483) putative RNA helicase [Arabidopsis thaliana]

Seq. No. 25961

Contig ID 133717\_1.R1040 5'-most EST hyd700726677.h1

Seq. No. 25962

Contig ID 133724\_1.R1040 5'-most EST uC-gmronoir028d04b1

Method BLASTX
NCBI GI g4490327
BLAST score 345
E value 1.0e-32
Match length 106
% identity 56

NCBI Description (AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No. 25963

Contig ID 133770\_1.R1040 5'-most EST hyd700727631.h1

Seq. No. 25964

Contig ID 133775\_1.R1040 5'-most EST hyd700726778.h1

Method BLASTX
NCBI GI g4467151
BLAST score 340
E value 4.0e-32
Match length 83
% identity 73

4066



NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 25965

Contig ID 133803\_1.R1040 5'-most EST ncj700987390.h1

Method BLASTX
NCBI GI g2511715
BLAST score 573
E value 2.0e-59
Match length 124
% identity 83

NCBI Description (AF019380) putative phosphatidylinositol-4-phosphate

5-kinase [Arabidopsis thaliana]

Seq. No. 25966

Contig ID 133805\_1.R1040 5'-most EST hyd700730139.h1

Method BLASTX
NCBI GI g2895510
BLAST score 151
E value 3.0e-10
Match length 74
% identity 47

NCBI Description (AF033204) putative pectin methylesterase [Arabidopsis

thaliana]

Seq. No. 25967

Contig ID 133821\_1.R1040

5'-most EST uC-gmflminsoy036d09b1

Method BLASTX
NCBI GI 94490753
BLAST score 155
E value 3.0e-10
Match length 130
% identity 35

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 25968

Contig ID 133827 1.R1040

5'-most EST uC-gmrominsoy131f04b1

Method BLASTX
NCBI GI g3249070
BLAST score 248
E value 3.0e-21
Match length 63
% identity 76

NCBI Description (AC004473) Contains similarity to siah binding protein 1 (SiahBP1) qb U51586 from Homo sapiens. ESTs qb T43314,

gb T43315 and gb\_R90521, gb\_T75905 [Arabidopsis thaliana]

Seq. No. 25969

Contig ID 133832\_1.R1040 5'-most EST hyd700726974.h1

Method BLASTX
NCBI GI g3914468
BLAST score 346
E value 6.0e-33

4067



Match length 78 % identity 86

NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)

>gi\_478411\_pir\_\_JQ2257 nuclear antigen 21D7 - carrot
>gi\_217911\_dbj\_BAA02696\_ (D13434) 21D7 antigen [Daucus

carota]

Seq. No. 25970

Contig ID 133852\_1.R1040 5'-most EST hyd700727010.h1

Method BLASTX
NCBI GI g2760839
BLAST score 551
E value 1.0e-56
Match length 129
% identity 81

NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 25971

Contig ID 133862\_1.R1040 5'-most EST hyd700727229.h1

Seq. No. 25972

Contig ID 133866\_1.R1040 5'-most EST zhf700964958.h1

Seq. No. 25973

Contig ID 133868\_1.R1040 5'-most EST ncj700979106.h1

Method BLASTX
NCBI GI g3176660
BLAST score 154
E value 6.0e-10
Match length 104
% identity 39

NCBI Description (AC004393) Similar to ERECTA receptor protein kinase

gb\_U47029 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 25974

Contig ID 133884\_1.R1040 5'-most EST xpa700792867.h1

Seq. No. 25975

Contig ID 133889 1.R1040 5'-most EST hyd700727075.h1 Method BLASTN

NCBI GI g4580454
BLAST score 37
E value 2.0e-11
Match length 81
% identity 86

NCBI Description Arabidopsis thaliana chromosome II BAC T2G17 genomic

sequence, complete sequence

Seq. No. 25976

Contig ID 133892\_1.R1040 5'-most EST hyd700727080.h1



BLASTX Method NCBI GI g4239675 BLAST score 279 4.0e-25 E value 90 Match length 62 % identity

(AL031546) heavy metal tolerance protein precursor NCBI Description

[Schizosaccharomyces pombe]

25977 Seq. No. 133952 1.R1040 Contig ID hyd700727183.h1 5'-most EST

BLASTX Method g1170659 NCBI GI 263 BLAST score 7.0e-23 E value 139 Match length

40 % identity

KINESIN-LIKE PROTEIN KIF4 >gi\_1083417\_pir\_\_A54803 NCBI Description

microtubule-associated motor KIF4 - mouse

>gi\_563773\_dbj\_BAA02167\_ (D12646) KIF4 [Mus musculus]

25978 Seq. No.

133956 1.R1040 Contig ID kl1701203118.hl 5'-most EST

BLASTX Method q4006888 NCBI GI Ž75 BLAST score 7.0e-45E value 154 Match length 53 % identity

(Z99708) putative protein [Arabidopsis thaliana] NCBI Description

25979 Seq. No.

133964 1.R1040 Contig ID ncj700985202.hl 5'-most EST

BLASTX Method NCBI GI q4544436 BLAST score 220 4.0e-18 E value 81 Match length 53 % identity

(AC006592) anthocyanidin-3-glucoside rhamnosyltransferase, NCBI Description

3' partial [Arabidopsis thaliana]

25980 Seq. No.

133985 1.R1040 Contig ID hyd700727228.h1 5'-most EST

25981 Seq. No.

133994 1.R1040 Contig ID 5'-most EST hyd700727745.h1

25982 Seq. No.

Contig ID 133996 1.R1040 5'-most EST hyd700727692.h1



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25983
Seq. No.
                  133997 1.R1040
Contig ID
5'-most EST
                  bth700845047.h1
Method
                  BLASTX
                  g1653395
NCBI GI
                  306
BLAST score
                  3.0e-33
E value
                  120
Match length
                  66
% identity
                  (D90913) PET112 [Synechocystis sp.]
NCBI Description
                  25984
Seq. No.
                  134010 1.R1040
Contig ID
                  leu701155671.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1708971
                  174
BLAST score
                  2.0e-12
E value
                  61
Match length
                  56
% identity
NCBI Description
                  (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
                   (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
                  >gi_421871_pir__S32156 mandelonitrile lyase (EC 4.1.2.10) -
                  black cherry >gi 288116_emb_CAA51194_ (X72617)
                  mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814)
                   (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus
                  serotina] >qi 1090776 prf 2019441A mandelonitrile lyase
                   [Prunus serotina]
                  25985
Seq. No.
                  134010 3.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy040h12b1
                  25986
Seq. No.
                  134014 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy122h02b1
                  25987
Seq. No.
                  134019 1.R1040
Contig ID
                  zhf700964050.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2462750
BLAST score
                  267
                   2.0e-23
E value
                  100
Match length
                   50
% identity
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
```

25988 Seq. No.

Contig ID 134031 1.R1040 5'-most EST leu701146461.h1

Method BLASTX NCBI GI g4538905 BLAST score 395 1.0e-38 E value Match length 88



% identity 81

NCBI Description (AL049482) putative protein [Arabidopsis thaliana]

Seq. No. 25989

Contig ID 134048\_1.R1040 5'-most EST hyd700727328.h1

Method BLASTX
NCBI GI g2290532
BLAST score 310
E value 1.0e-28
Match length 83
% identity 72

NCBI Description (U94748) AN11 [Petunia x hybrida]

Seq. No. 25990

Contig ID 134054\_1.R1040 5'-most EST ncj700984713.h1

Method BLASTX
NCBI GI g3128213
BLAST score 167
E value 6.0e-12
Match length 76
% identity 53

NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No. 25991

Contig ID 134071\_1.R1040 5'-most EST gsv701052826.h1

Method BLASTX
NCBI GI g2262114
BLAST score 319
E value 3.0e-29
Match length 195
% identity 35

NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No. 25992

Contig ID 134078\_1.R1040 5'-most EST gsv701045403.h1

Method BLASTX
NCBI GI g3608154
BLAST score 146
E value 2.0e-09
Match length 77
% identity 48

NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 25993

Contig ID 134123\_1.R1040 5'-most EST bth700844265.h1

Seq. No. 25994

Contig ID 134136\_1.R1040 5'-most EST zhf700953454.h1

Seq. No. 25995

Contig ID 134152\_1.R1040

NCBI Description

```
5'-most EST
                    gsv701046909.h1
Method
                    BLASTX
NCBI GI
                   g4538967
BLAST score
                    160
E value
                    4.0e-11
Match length
                    51
% identity
NCBI Description
                   (AL049488) major intrinsic protein (MIP)-like [Arabidopsis
                   thaliana]
Seq. No.
                   25996
                   134161 1.R1040
Contig ID
5'-most EST
                   fC-gmf\overline{1}700903761d2
Seq. No.
                   25997
                   134166 1.R1040
Contig ID
5'-most EST
                   hyd700727506.h1
Method
                   BLASTX
NCBI GI
                   g4006876
BLAST score
                   173
                   8.0e-13
E value
Match length
                   80
% identity
                   54
NCBI Description
                   (299707) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   25998
                   134186 1.R1040
Contig ID
5'-most EST
                   hyd700727529.h1
Seq. No.
                   25999
Contig ID
                   134223 1.R1040
5'-most EST
                   jC-gmle01810080h09a1
Method
                   BLASTX
NCBI GI
                   q3212870
BLAST score
                   631
E value
                   6.0e-66
Match length
                   179
% identity
                   67
NCBI Description
                   (AC004005) putative N-myristoyltransferase [Arabidopsis
                   thaliana]
Seq. No.
                   26000
Contig ID
                   134232 1.R1040
5'-most EST
                   hyd700727593.h1
Seq. No.
                   26001
Contig ID
                   134273 1.R1040
5'-most EST
                   pmv700893164.h1
Method
                   BLASTX
NCBI GI
                   g4151321
BLAST score
                   528
E value
                   4.0e-54
Match length
                   111
% identity
                   91
```

[Arabidopsis thaliana]

(AF089085) putative auxin efflux carrier protein; AtPIN1



Seq. No. 134279 1.R1040 Contig ID 5'-most EST ncj700988327.hl BLASTX Method

q3738310 NCBI GI BLAST score 500 1.0e-50 E value Match length 116

% identity

(AC005309) putative nuclear protein [Arabidopsis thaliana] NCBI Description

Seq. No. 26003

134296 1.R1040 Contig ID hyd700727675.h1 5'-most EST

26004 Seq. No.

134299 1.R1040 Contig ID hyd700727684.h1 5'-most EST

26005 Seq. No.

134300 1.R1040 Contig ID 5'-most EST hyd700727685.h1

Seq. No. 26006

134305 1.R1040 Contig ID hyd700727691.h1 5'-most EST

26007 Seq. No.

134308 1.R1040 Contig ID hyd700727703.h1 5'-most EST

26008 Seq. No.

134323 1.R1040 Contig ID hyd700727722.h1 5'-most EST

Method BLASTX q3176664 NCBI GI 134 BLAST score 6.0e-11 E value 137 Match length 35 % identity

(AC004393) Contains similarity to beta scruin gb\_Z47541 NCBI Description from Limulus polyphemus. ESTs gb\_T04493 and gb\_ $\overline{A}A585955$ 

come from this gene. [Arabidopsis thaliana]

26009 Seq. No.

134323 2.R1040 Contig ID dpv701097311.hl 5'-most EST

26010 Seq. No.

134325 1.R1040 Contig ID zzp700833044.h1 5'-most EST

Seq. No. 26011

134333 1.R1040 Contig ID hyd700727733.h1 5'-most EST

BLASTX Method q4204313 NCBI GI



BLAST score 186 E value 7.0e-14 Match length 77

% identity 55

NCBI Description (AC003027) lcl\_prt\_seq No definition line found [Arabidopsis thaliana]

Seq. No. 26012

Contig ID 134343\_1.R1040 5'-most EST zsg701117682.h1

Method BLASTX
NCBI GI g2809246
BLAST score 658
E value 4.0e-69
Match length 151
% identity 83

NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]

Seq. No. 26013

Contig ID 134351\_1.R1040 5'-most EST hyd700727758.h1

Seq. No. 26014

Contig ID 134361\_1.R1040 5'-most EST fde700876873.h1

Method BLASTX
NCBI GI g3213227
BLAST score 229
E value 1.0e-18
Match length 166
% identity 31

NCBI Description (AF035209) putative v-SNARE Vtila [Mus musculus]

>qi 3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]

Seq. No. 26015

Contig ID 134367 1.R1040 5'-most EST fde700873113.h1

Seq. No. 26016

Contig ID 134372\_1.R1040 5'-most EST fde700871842.h1

Seq. No. 26017

Contig ID 134392\_1.R1040 5'-most EST hyd700727808.h1

Seq. No. 26018

Contig ID 134395\_1.R1040 5'-most EST hyd700727812.h1

Seq. No. 26019

Contig ID 134439\_1.R1040 5'-most EST hyd700730260.h1

Seq. No. 26020

Contig ID 134443\_1.R1040 5'-most EST hyd700727908.h1

```
BLASTX
Method
                  g3269290
NCBI GI
BLAST score
                   161
                   5.0e-11
E value
                   50
Match length
% identity
                   68
                   (AL030978) putative receptor like kinase [Arabidopsis
NCBI Description
                   thaliana]
                   26021
Seq. No.
                   134455 1.R1040
Contig ID
                   hyd700727929.h1
5'-most EST
                   26022
Seq. No.
                   134457 1.R1040
Contig ID
                   hyd700727931.h1
5'-most EST
                   26023
Seq. No.
                   134467_1.R1040
Contig ID
                   hyd700727947.h1
5'-most EST
Seq. No.
                   26024
                   134470 1.R1040
Contig ID
                   uC-qmflminsoy080h01b1
5'-most EST
                   BLASTN
Method
                   g2739043
NCBI GI
                   123
BLAST score
                   2.0e-62
E value
                   255
Match length
                   87
% identity
                   Glycine max polyphosphoinositide binding protein Ssh1p
NCBI Description
                   (SSH1) mRNA, complete cds
                   26025
Seq. No.
                   134518 1.R1040
Contig ID
                   pcp700994803.h1
5'-most EST
                   BLASTX
Method
                   q4006882
NCBI GI
                   199
BLAST score
                   4.0e-15
E value
                   141
Match length
                   44
% identity
```

(Z99707) UDP-glucuronyltransferase-like protein NCBI Description

[Arabidopsis thaliana]

26026 Seq. No.

134557 1.R1040 Contig ID hyd700728088.h1 5'-most EST

BLASTN Method g169360 NCBI GI BLAST score 138 8.0e-72E value 260 Match length 88 % identity

P.vulgaris PVPK-1 protein, complete cds NCBI Description

26027 Seq. No.

```
134560 1.R1040
Contig ID
                   awf700\overline{8}40236.h1
5'-most EST
                   BLASTX
Method
                   g3242659
NCBI GI
                   376
BLAST score
                   2.0e-42
E value
                   117
Match length
                   62
NCBI Description (AB015599) spermidine synthase [Coffea arabica]
Seq. No.
                   134589 1.R1040
Contig ID
                   smc700744363.hl
5'-most EST
                   26029
Seq. No.
                   134597 1.R1040
Contig ID
                   jC-gmf102220055b06a1
5'-most EST
                    26030
Seq. No.
                    134597 2.R1040
Contig ID
                   hyd700728194.hl
5'-most EST
                    26031
 Seq. No.
                    134678 1.R1040
 Contig ID
                    hyd700728614.hl
 5'-most EST
                    BLASTX
 Method
                    q2244792
 NCBI GI
                    431
 BLAST score
                    7.0e-43
 E value
                    97
 Match length
                    43
 NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]
                    26032
 Seq. No.
                    134682 1.R1040
 Contig ID
                    jC-gmf\overline{1}02220061c10a1
 5'-most EST
                    BLASTX
 Method
                    q2495155
 NCBI GI
                     421
 BLAST score
                     3.0e-41
 E value
                     129
 Match length
                     67
  % identity
                    GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR)
 NCBI Description
                     >gi_1694926_dbj_BAA08910_ (D50407) glutamyl-tRNA reductase
                     [Cucumis sativus]
                     26033
  Seq. No.
                     134721 1.R1040
  Contig ID
                     jC-gmle01810053d05a1
  5'-most EST
                     26034
  Seq. No.
                     134733 1.R1040
```

Contig ID 134733\_1.R1040 5'-most EST hyd700728523.h1

Method BLASTX
NCBI GI g4544423
BLAST score 265
E value 1.0e-23



Match length 84 % identity

NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No.

26035

Contig ID 5'-most EST 134751 1,R1040 hyd700728548.h1

Method NCBI GI BLAST score BLASTX q2499609

E value Match length 236 7.0e-20 57

% identity

74

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 5 (MAP KINASE 5) (ATMPK5) >gi\_629546\_pir\_\_S40471 mitogen-activated protein

kinase 5 (EC 2.7.1.-) - Arabidopsis thaliana

>gi 457402 dbj\_BAA04868 (D21841) MAP kinase [Arabidopsis

thaliana]

Seq. No.

26036

Contig ID 5'-most EST

134760 1.R1040 hyd700728564.h1

Seq. No.

26037

Contig ID

134761 1.R1040

5'-most EST

jC-gmst02400067h03d1

Seq. No.

26038

Contig ID 5'-most EST 134771\_1.R1040 fde700873290.h1

Method

BLASTN

NCBI GI

q3128143

BLAST score

38

E value

1.0e-11

Match length

94

% identity

85 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.

26039

Contiq ID

134787 1.R1040

5'-most EST

 $k11701\overline{2}13449.h1$ 

Seq. No.

26040

Contig ID

134795 1.R1040

5'-most EST

zsg701122196.hl

Seq. No.

26041

Contig ID

134798 1.R1040 fC-qmf1700909108a1

5'-most EST Method

BLASTN

NCBI GI

g2213533

BLAST score

E value

167

7.0e-89

Match length

383 86

% identity

NCBI Description P.sativum mRNA encoding DNA-binding PD1-like protein



 Seq. No.
 26042

 Contig ID
 134808\_1.R1040

 5'-most EST
 zzp700833135.h1

 Method
 BLASTX

 NCBI GI
 g2213602

NCBI GI g2213602 BLAST score 368 E value 9.0e-35 Match length 162 % identity 52

NCBI Description (AC000348) T7N9.22 [Arabidopsis thaliana]

Seq. No. 26043

Contig ID 134810\_1.R1040 5'-most EST hyd700728631.h1

Seq. No. 26044

Contig ID 134814\_1.R1040 5'-most EST dpv701097007.h1

Method BLASTX
NCBI GI g1346261
BLAST score 356
E value 6.0e-34
Match length 114
% identity 65

NCBI Description GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR)

>gi 1015319 dbj BAA11091 (D67088) glutamyl-tRNA reductase

[Cucumis sativus]

Seq. No. 26045

Contig ID 134818\_1.R1040 5'-most EST hyd700729833.h1

Seq. No. 26046

Contig ID 134820\_1.R1040 5'-most EST gsv701056004.h1

Method BLASTX
NCBI GI g1652678
BLAST score 389
E value 1.0e-40
Match length 196
% identity 47

NCBI Description (D90907) amidase [Synechocystis sp.]

Seq. No. 26047

Contig ID 134821\_1.R1040

5'-most EST jC-gmro02910004c03d1

Seq. No. 26048

Contig ID 134826 1.R1040

5'-most EST uC-qmflminsoy021f06b1

Method BLASTX
NCBI GI g2262143
BLAST score 237
E value 1.0e-19
Match length 112
% identity 52

4078



NCBI Description (AC002330) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 26049

Contig ID 134850\_1.R1040 5'-most EST hyd700729423.h1

Method BLASTX
NCBI GI g2583108
BLAST score 327
E value 7.0e-31
Match length 87
% identity 72

NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No. 26050

Contig ID 134856 1.R1040 5'-most EST ncj700986123.h1

Method BLASTN
NCBI GI g2304954
BLAST score 115
E value 5.0e-58
Match length 276
% identity 89

NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No. 26051

Contig ID 134860\_1.R1040 5'-most EST eep700866321.h1

Seq. No. 26052

Contig ID 134874\_1.R1040 5'-most EST hyd700730111.h1

Seq. No. 26053

Contig ID 134882\_1.R1040

5'-most EST  $g42971\overline{4}5$  Method BLASTX NCBI GI g477819 BLAST score 511 E value 5.0e-52 Match length 131 % identity 76

NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) beta

chain precursor - potato >gi\_410634\_bbs\_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,

530 aa]

Seq. No. 26054

Contig ID 134888\_1.R1040 5'-most EST uC-gmronoir037f06b1

Method BLASTX
NCBI GI g3420052
BLAST score 304
E value 8.0e-28
Match length 66
% identity 83



NCBI Description (AC004680) putative ubiqinone reductase [Arabidopsis thaliana]

Seq. No. 26055

134889 1.R1040 Contig ID 5'-most EST fua701042019.h1

26056 Seq. No.

Contig ID 134890 1.R1040 5'-most EST hyd700728755.h1

Seq. No. 26057

134893 1.R1040 Contig ID

5'-most EST q4284766 Method BLASTX NCBI GI g2244946 BLAST score 613 E value 7.0e-64 Match length 152

% identity 80

NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]

>gi 2326344 emb CAA72072 (Y11187) G14587-6 [Arabidopsis

thaliana]

26058

Seq. No.

134894 1.R1040 Contig ID 5'-most EST sat701008814.h1

26059 Seq. No.

134900 1.R1040 Contig ID 5'-most EST hyd700728773.h1 Method BLASTX

NCBI GI q3080420 BLAST score 238 E value 2.0e-22 70 Match length

% identity 79

NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis

thaliana]

26060 Seq. No.

Contig ID 134914 1.R1040 5'-most EST uC-gmropic029f09b1

Seq. No. 26061

134935 1.R1040 Contig ID 5'-most EST kl1701204606.h1

Method BLASTX NCBI GI q1778093 BLAST score 321 E value 5.0e-30 Match length 88 % identity 69

NCBI Description (U64902) putative sugar transporter; member of major

facilitative superfamily; integral membrane protein [Beta

vulgaris]



Seq. No. 260

Contig ID 134937\_1.R1040 5'-most EST hyd700728833.h1

Seq. No. 26063

Contig ID 134947 1.R1040 5'-most EST hyd700730565.h1

Method BLASTX
NCBI GI g2191136
BLAST score 193
E value 5.0e-15
Match length 88
% identity 49

NCBI Description (AF007269) Similar to UTP-Glucose Glucosyltransferase;

coded for by A. thaliana cDNA T46230; coded for by A.

thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidopsis thaliana]

Seq. No. 26064

Contig ID 134952 1.R1040 5'-most EST hyd700728860.h1 Method BLASTX

NCBI GI g2244831
BLAST score 357
E value 5.0e-34
Match length 107
% identity 64

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26065

Contig ID 134958\_1.R1040 5'-most EST pmv700890114.h1

Seq. No. 26066

Contig ID 134959\_1.R1040

5'-most EST jC-gmle01810035a02d1

Seq. No. 26067

Contig ID 134967 1.R1040 5'-most EST hrw701063159.h1

Seq. No. 26068

Contig ID 134968 1.R1040 5'-most EST xpa700796826.h1

Method BLASTX
NCBI GI g2145356
BLAST score 848
E value 3.0e-91
Match length 208
% identity 75

NCBI Description (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi\_3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No. 26069

Contig ID 134979 1.R1040 5'-most EST wrg700791340.h1

Method BLASTX



```
NCBI GI g4063744
BLAST score 219
E value 1.0e-17
Match length 84
% identity 54
```

NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26070

Contig ID 134980 1.R1040 5'-most EST gsv701043982.h1

Method BLASTX
NCBI GI g3176691
BLAST score 150
E value 2.0e-09
Match length 116
% identity 38

NCBI Description (AC003671) Contains homology to serine/threonine protein

kinase gb X99618 from Mycobacterium tuberculosis. ESTs gb F14403, gb F14404, and gb N96730 come from this gene.

[Arabidopsis thaliana]

Seq. No. 26071

Contig ID 134983\_1.R1040 5'-most EST txt700734791.h1

Method BLASTX
NCBI GI g3643606
BLAST score 345
E value 2.0e-32
Match length 131
% identity 47

NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26072

Contig ID 134991 1.R1040

5'-most EST g4396464

Seq. No. 26073

Contig ID 135004\_1.R1040 5'-most EST sat701004706.h1

Seq. No. 26074

Contig ID 135005\_1.R1040 5'-most EST rca701001644.h1

Seq. No. 26075

Contig ID 135009\_1.R1040 5'-most EST zhf700958906.h1

Method BLASTX
NCBI GI g1402878
BLAST score 501
E value 2.0e-50
Match length 198
% identity 47

NCBI Description (X98130) unknown [Arabidopsis thaliana]

Seq. No. 26076

Contig ID 135040 1.R1040



5'-most EST hyd700729004.h1

Method BLASTX
NCBI GI g2618691
BLAST score 158
E value 2.0e-16
Match length 80
% identity 54

NCBI Description (AC002510) putative chloroplast envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 26077

Contig ID 135046\_1.R1040 5'-most EST sat701013987.h1

Seq. No. 26078

Contig ID 135049 1.R1040 5'-most EST hyd700729014.h1

Method BLASTX
NCBI GI g882341
BLAST score 338
E value 2.0e-31
Match length 115
% identity 61

NCBI Description (U24702) LRP1 [Arabidopsis thaliana]

Seq. No. 26079

Contig ID 135064 1.R1040 5'-most EST hyd700729035.h1

Method BLASTX
NCBI GI 94567312
BLAST score 356
E value 9.0e-34
Match length 137
% identity 55

% identity 55

NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26080

Contig ID 135067\_1.R1040 5'-most EST ncj700980427.h1

Seq. No. 26081

Contig ID 135068 1.R1040 5'-most EST hyd700729040.h1

Seq. No. 26082

Contig ID 135070 1.R1040

5'-most EST jC-gmle01810018b03a2

Seq. No. 26083

Contig ID 135095\_1.R1040 5'-most EST pxt700944052.h1

Method BLASTX
NCBI GI g2500543
BLAST score 494
E value 9.0e-50
Match length 211
% identity 47



NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE EEED8.5 >gi\_733602 (U23484) similar to S. cerevisiae pre-mRNA splicing factor RNA helicase PRP22 (SP:PR22\_YEAST, P24384) and other DEAH subfamily members of the DEAD box family helicases [Caenorhabditis elegans]

Seq. No. 26084

Contig ID 135098\_1.R1040 5'-most EST hyd700729106.h1

Method BLASTX
NCBI GI g2655098
BLAST score 212
E value 9.0e-27
Match length 135
% identity 53

NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

Seq. No. 26085

Contig ID 135106 1.R1040 5'-most EST hyd700729118.h1

Seq. No. 26086

Contig ID 135109\_1.R1040 5'-most EST hyd700729124.h1

Method BLASTX
NCBI GI g3212848
BLAST score 550
E value 7.0e-73
Match length 217
% identity 66

NCBI Description (AC004005) putative inositol polyphosphate-5-phosphatase

[Arabidopsis thaliana]

Seq. No. 26087

Contig ID 135113 1.R1040

5'-most EST jC-gmst02400061a06a1

Method BLASTX
NCBI GI g3327389
BLAST score 1129
E value 1.0e-124
Match length 262
% identity 85

NCBI Description (AC004483) putative DNA replication licensing factor, mcm5

[Arabidopsis thaliana]

Seq. No. 26088

Contig ID 135117\_1.R1040 5'-most EST hyd700729134.h1

Seq. No. 26089

Contig ID 135133\_1.R1040 5'-most EST jC-gmro02910073h01d1

Seq. No. 26090

Contig ID 135163\_1.R1040 5'-most EST hyd700729210.h1



```
Seq. No.
                   135189 1.R1040
Contig ID
                   jC-gmr\overline{o}02910014a01a1
5'-most EST
                   BLASTX
Method
                   g1585128
NCBI GI
BLAST score
                   279
                   9.0e-25
E value
                   147
Match length
                   30
% identity
NCBI Description isopeptidase T [Homo sapiens]
```

Seq. No. 26092

135206 1.R1040 Contig ID hyd700729271.h1 5'-most EST

BLASTX Method q4115383 NCBI GI 343 BLAST score E value 1.0e-32 97 Match length 70 % identity

(AC005967) receptor-like protein kinase [Arabidopsis NCBI Description

thaliana]

Seq. No. 26093

135207 1.R1040 Contig ID ncj700976544.hl 5'-most EST

26094 Seq. No.

135250 1.R1040 Contig ID hyd700729366.h1 5'-most EST

26095 Seq. No.

135256\_1.R1040 Contig ID wrg700788111.hl 5'-most EST

26096 Seq. No.

135281 1.R1040 Contig ID

q5752508 5'-most EST Method BLASTX q1705594 NCBI GI 227 BLAST score 1.0e-18 E value 107 Match length 42 % identity

PEROXISOME ASSEMBLY PROTEIN CAR1 (PEROXIN-2) NCBI Description

>gi\_2133320\_pir\_\_A56730 carl protein - Podospora anserina >gi\_1360119\_emb\_CAA60739\_ (X87329) peroxisome assembly

factor [Podospora anserina]

26097 Seq. No.

135285 1.R1040 Contig ID hyd700729453.h15'-most EST

26098 Seq. No.

135297 1.R1040 Contig ID jC-gmro02910062h10d1 5'-most EST

BLASTX Method



```
g3004551
NCBI GI
                  217
BLAST score
                  2.0e-17
E value
                   74
Match length
                   50
% identity
                   (AC003673) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   26099
Seq. No.
                   135304 1.R1040
Contig ID
                   jC-gmst02400066e12a2
5'-most EST
                   26100
Seq. No.
                   135309 1.R1040
Contig ID
                   ncj700983374.h1
5'-most EST
                   BLASTN
Method
                   q19496
NCBI GI
                   93
BLAST score
                   1.0e-44
E value
                   165
Match length
                   89
% identity
NCBI Description L.polyphyllus pPLB02 mRNA
                   26101
Seq. No.
                   135328 1.R1040
Contig ID
                   txt700735342.h1
5'-most EST
                   26102
Seq. No.
                   135333 1.R1040
Contig ID
                   gsv701054416.hl
5'-most EST
                   BLASTN
Method
                   g1370173
NCBI GI
                   118
BLAST score
                   1.0e-59
E value
Match length
                   250
                   87
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB1Y
                   26103
Seq. No.
                   135333 2.R1040
Contig ID
                   hrw701059593.hl
5'-most EST
                   BLASTN
Method
                   g1370173
NCBI GI
BLAST score
                   109
                   2.0e-54
E value
                   209
Match length
                   88
 % identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB1Y
                    26104
 Seq. No.
                    135335 1.R1040
 Contig ID
                    jex700904520.h1
 5'-most EST
```

26105 Seq. No.

135361 1.R1040 Contig ID hyd700730246.h1 5'-most EST

BLASTX Method g2462756 NCBI GI



BLAST score 172 E value 7.0e-13 Match length 65 % identity 35

NCBI Description (AC002292) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 26106

Contig ID 135385\_1.R1040 5'-most EST bth700844330.h1

Seq. No. 26107

Contig ID 135419 1.R1040 5'-most EST gsv701046154.h1

Method BLASTX
NCBI GI 94454031
BLAST score 214
E value 5.0e-17
Match length 138
% identity 36

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 26108

Contig ID 135425\_1.R1040 5'-most EST hyd700729837.h1

Seq. No. 26109

Contig ID 135434 1.R1040 5'-most EST hyd700729854.h1

Method BLASTX
NCBI GI g4559329
BLAST score 271
E value 3.0e-24
Match length 73
% identity 63

NCBI Description (AC007087) putative protein kinase MAP3K [Arabidopsis

thaliana]

Seq. No. 26110

Contig ID 135443 1.R1040 5'-most EST crh700853910.h1

Method BLASTX
NCBI GI g1711382
BLAST score 257
E value 3.0e-22
Match length 114
% identity 51

NCBI Description SET PROTEIN >gi 940889 (U30470) SET [Drosophila

melanogaster]

Seq. No. 26111

Contig ID 135463\_1.R1040 5'-most EST gsv701052328.h1

Method BLASTX
NCBI GI g3337361
BLAST score 597
E value 5.0e-62
Match length 160



% identity 64
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 26112

Contig ID 135473\_1.R1040 5'-most EST hrw701062888.h1

Method BLASTX
NCBI GI g3695059
BLAST score 648
E value 6.0e-68
Match length 165
% identity 77

NCBI Description (AF064787) rac GTPase activating protein 1 [Lotus

japonicus]

Seq. No. 26113

Contig ID 135488\_1.R1040 5'-most EST vzy700753081.h1

Method BLASTX
NCBI GI g3096944
BLAST score 145
E value 2.0e-09
Match length 55
% identity 55

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 26114

Contig ID 135532 1.R1040 5'-most EST hyd700730018.h1

Method BLASTX
NCBI GI g4544451
BLAST score 185
E value 6.0e-14
Match length 67
% identity 54

NCBI Description (AC006592) unknown protein [Arabidopsis thaliana]

Seq. No. 26115

Contig ID 135549\_1.R1040 5'-most EST hyd700730041.h1

Method BLASTX
NCBI GI g4104931
BLAST score 228
E value 8.0e-19
Match length 49
% identity 88

NCBI Description (AF042196) auxin response factor 8 [Arabidopsis thaliana]

Seq. No. 26116

Contig ID 135573\_1.R1040 5'-most EST hyd700730073.h1

Seq. No. 26117

Contig ID 135579\_1.R1040 5'-most EST jC-gmst02400071a01a1

Seq. No. 26118

135590 1.R1040 Contig ID 5'-most EST  $sat701\overline{0}07611.h1$ 26119 Seq. No. 135670 1.R1040 Contig ID hyd700730214.h1 5'-most EST BLASTX Method g2244766 NCBI GI BLAST score 185 4.0e-14 E value 68 Match length % identity 54 (Z97335) glucosyltransferase [Arabidopsis thaliana] NCBI Description 26120 Seq. No. 135678 1.R1040 Contiq ID 5'-most EST hyd700730225.h1 Method BLASTX NCBI GI g4454465 BLAST score 314 9.0e-29 E value Match length 127 % identity (AC006234) unknown protein [Arabidopsis thaliana] NCBI Description 26121 Seq. No. 135683 1.R1040 Contig ID 5'-most EST hyd700730230.h1 26122 Seq. No. 135703 1.R1040 Contig ID uC-gmflminsoy082c12b1 5'-most EST Method BLASTX g2204096 NCBI GI 508 BLAST score E value 1.0e-51 123 Match length 39 % identity NCBI Description (Z82992) FCA delta [Arabidopsis thaliana] 26123 Seq. No. 135713 1.R1040 Contig ID

5'-most EST fde700876537.h1

BLASTX Method g3878117 NCBI GI BLAST score 212 5.0e-17 E value 122 Match length 19 % identity

(Z49068) mitochondrial carrier protein [Caenorhabditis NCBI Description

elegans]

26124 Seq. No.

135725 1.R1040 Contig ID  $jsh701\overline{0}69540.h1$ 5'-most EST

BLASTX Method NCBI GI g3264830



BLAST score 183
E value 2.0e-13
Match length 124
% identity 34
NCBI Description (AF072405) cotton fiber expressed protein 2 [Gossypium

 Seq. No.
 26125

 Contig ID
 135737\_1.R1040

 5'-most EST
 jC-gmfl02220094g04a1

hirsutum]

Method BLASTX
NCBI GI g4455276
BLAST score 594
E value 1.0e-61
Match length 159
% identity 70

NCBI Description (AL035527) peptide transporter-like protein [Arabidopsis

thaliana]

Seq. No. 26126

Contig ID 135738\_1.R1040 5'-most EST leu701149626.h1

Method BLASTX
NCBI GI g3341417
BLAST score 270
E value 1.0e-23
Match length 120
% identity 46

NCBI Description (AJ009657) Mu3 subunit of clathrin-associated protein

complex AP-3 [Drosophila melanogaster]

Seq. No. 26127

Contig ID 135757\_1.R1040 5'-most EST hyd700730341.h1

Method BLASTX
NCBI GI g4454043
BLAST score 340
E value 6.0e-32
Match length 98

% identity 62

NCBI Description (AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 26128

Contig ID 135771 1.R1040 5'-most EST hyd700730364.h1

Seq. No. 26129

Contig ID 135789 1.R1040 5'-most EST sat701004596.h1

Seq. No. 26130

Contig ID 135791 1.R1040 5'-most EST bth700847492.h1

Seq. No. 26131

Contig ID 135794 1.R1040 5'-most EST hyd700730392.h1



Seq. No. 26132

Contig ID 135796\_1.R1040

5'-most EST uC-gmrominsoy046h07b1

Seq. No. 26133

Contig ID 135814\_1.R1040 5'-most EST hyd700730441.h1

Method BLASTX
NCBI GI g3309583
BLAST score 438
E value 1.0e-43
Match length 98
% identity 82

NCBI Description (AF073830) fructose-6-phosphate

2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum]

Seq. No. 26134

Contig ID 135822 1.R1040 5'-most EST hyd700730501.h1

Seq. No. 26135

Contig ID 135828\_1.R1040 5'-most EST hyd700730515.h1

Seq. No. 26136

Contig ID 135839\_1.R1040

5'-most EST g5057830

Seq. No. 26137

Contig ID 135865\_1.R1040 5'-most EST wrg700790686.h2

Seq. No. 26138

Contig ID 135870 1.R1040 5'-most EST kmv700739491.h1

Method BLASTX
NCBI GI g2618691
BLAST score 254
E value 1.0e-30
Match length 104
% identity 72

NCBI Description (AC002510) putative chloroplast envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 26139

Contig ID 135877\_1.R1040 5'-most EST hyd700730640.h1

Seq. No. 26140

Contig ID 135886\_1.R1040 5'-most EST wrg700789835.h2

Seq. No. 26141

Contig ID 135891\_1.R1040 5'-most EST hyd700730882.h1



Seq. No. 135901 1.R1040 Contig ID  $r1r700\overline{9}00402.h1$ 5'-most EST

Seq. No. Contig ID 5'-most EST 26143 135906 1.R1040 g51266<del>1</del>3

BLASTX Method g3834322 NCBI GI 554 BLAST score 2.0e-56 E value

Match length 205 % identity 58

(AC005679) EST gb\_R30300 comes from this gene. [Arabidopsis NCBI Description

thaliana]

Seq. No.

26144

Contig ID

135917 1.R1040

5'-most EST

uC-gmrominsoy316d06b1

Method BLASTN g2760165 NCBI GI BLAST score 40 E value 6.0e-13 Match length 84 87

% identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MAC9, complete sequence [Arabidopsis thaliana]

Seq. No. 26145

Contig ID 5'-most EST 135917 2.R1040 fde700873034.hl

Seq. No. 26146

135925 1.R1040 Contig ID txt700737685.h1 5'-most EST

26147 Seq. No.

135925 2.R1040 Contig ID 5'-most EST pxt700946004.hl

26148 Seq. No.

135932 1.R1040 Contig ID r1r700898642.h15'-most EST

26149 Seq. No.

135979 1.R1040 Contig ID wrg700790417.h2 5'-most EST

Seq. No.

26150 136000 1.R1040 Contig ID hyd700730924.h1 5'-most EST

Seq. No. 26151

136015 1.R1040 Contig ID 5'-most EST kmv700743630.h1

Method BLASTX q2499535 NCBI GI



BLAST score 551 E value 1.0e-56 Match length 161 % identity 67

NCBI Description 2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi\_595681

(U13238) 2-oxoglutarate/malate translocator [Spinacia

oleracea]

Seq. No. 26152

Contig ID 136017\_1.R1040 5'-most EST kmv700742078.h1

Seq. No. 26153

Contig ID 136027\_1.R1040 5'-most EST ncj700985144.h1

Seq. No. 26154

Contig ID 136049\_1.R1040 5'-most EST hyd700731011.h1

Method BLASTX
NCBI GI g584862
BLAST score 387
E value 2.0e-37
Match length 138
% identity 54

NCBI Description CYTOCHROME P450 71A3 (CYPLXXIA3) (P-450EG3)

>gi\_480397\_pir\_\_S36807 cytochrome P450 71A3 - eggplant

(fragment) >gi\_408142\_emb\_CAA50313\_ (X70982) P450

hydroxylase [Solanum melongena]

Seq. No. 26155

Contig ID 136051\_1.R1040 5'-most EST hyd700731013.h1

Seq. No. 26156

Contig ID 136068\_1.R1040 5'-most EST eep700866603.h1

Method BLASTN
NCBI GI g1354856
BLAST score 241
E value 1.0e-133
Match length 512
% identity 89

NCBI Description Phaseolus vulgaris bZIP transcriptional repressor ROM1

mRNA, complete cds

Seq. No. 26157

Contig ID 136070\_1.R1040 5'-most EST uC-gmronoir036a06b1

Seq. No. 26158

Contig ID 136077\_1.R1040 5'-most EST hyd700731046.h1

Method BLASTX
NCBI GI g4432861
BLAST score 252
E value 2.0e-21



Match length % identity 60

NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.

26159

136081 1.R1040 Contig ID

5'-most EST

g5753061

Seq. No.

26160

Contig ID

136081 2.R1040

5'-most EST

uC-gmronoir059d01b1

Seq. No.

26161

Contig ID 5'-most EST 136111 1.R1040 uC-gmronoir031h08b1

Seq. No.

26162

Contig ID 5'-most EST 136115 1.R1040 hyd700731114.hl

Method NCBI GI BLASTX g4220512

BLAST score E value

659 6.0e-69

Match length % identity

224 54

NCBI Description

(AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No.

26163

Contig ID

136121 1.R1040

5'-most EST

g5175622

Seq. No.

26164

Contig ID

136141\_1.R1040 hyd700731162.h1

5'-most EST

BLASTN

Method NCBI GI

g2304954

BLAST score

94

E value

2.0e-45

Match length

221

% identity

NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No.

26165

Contig ID

136142 1.R1040

5'-most EST

hyd700731165.h1

Seq. No.

26166

Contig ID 5'-most EST 136149 1.R1040

Method

hyd700731178.h1

BLASTX

NCBI GI BLAST score g3033377

E value

171

Match length

4.0e-12

% identity

86 43

NCBI Description

(AC004238) putative berberine bridge enzyme [Arabidopsis

thaliana]



Seq. No. 26167

Contig ID 136152\_1.R1040 5'-most EST pxt700944589.h1

Method BLASTX
NCBI GI 94454484
BLAST score 504
E value 3.0e-51
Match length 135
% identity 73

NCBI Description (AC006234) putative diacylglycerol kinase [Arabidopsis

thaliana]

Seq. No. 26168

Contig ID 136170 1.R1040 5'-most EST rca701000867.h1

Seq. No. 26169

Contig ID 136174\_1.R1040

5'-most EST jC-gmf102220056f09a1

Method BLASTN
NCBI GI g4490324
BLAST score 48
E value 2.0e-17
Match length 185
% identity 85

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14

(ESSA project)

Seq. No. 26170

Contig ID 136176 1.R1040 5'-most EST zhf700952763.h1

Method BLASTX
NCBI GI g119636
BLAST score 264
E value 9.0e-23
Match length 150
% identity 43

NCBI Description ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT PRECURSOR

(ALPHA-ETF) >gi\_87351\_pir\_\_A31998 electron transfer flavoprotein alpha chain precursor - human >gi\_182251 (J04058) electron transport flavoprotein [Homo sapiens] >gi\_4503607\_ref\_NP\_000117.1\_pETFA\_ electron transfer

flavoprotein, alpha polypeptide

Seq. No. 26171

Contig ID 136177\_1.R1040 5'-most EST hyd700731230.h1

Method BLASTX
NCBI GI g2653281
BLAST score 160
E value 4.0e-11
Match length 41
% identity 71

NCBI Description (AJ002173) cyclin-dependent kinase inhibitor protein

[Chenopodium rubrum]

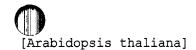


```
Seq. No.
                   136189 1.R1040
Contig ID
                   zhf700962042.hl
5'-most EST
Seq. No.
                   26173
                   136200 1.R1040
Contig ID
                   crh700853301.h1
5'-most EST
                   26174
Seq. No.
                   136200 2.R1040
Contig ID
                   zsg701126146.h1
5'-most EST
                   26175
Seq. No.
                   136206 1.R1040
Contig ID
                   asn701137826.h1
5'-most EST
                   26176
Seq. No.
                   136213 1.R1040
Contig ID
                   jC-gmro02910060e05d1
5'-most EST
Seq. No.
                   26177
                   136246 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220054d08a1
Seq. No.
                   26178
                   136248 1.R1040
Contig ID
                   nsy700645540.h1
5'-most EST
                   BLASTX
Method
                   g3482970
NCBI GI
                   359
BLAST score
                   2.0e-34
E value
                   93
Match length
% identity
                   78
NCBI Description (AL031369) putative protein [Arabidopsis thaliana]
                    26179
Seq. No.
                    136250 1.R1040
Contig ID
                   ncj700983242.hl
5'-most EST
                    26180
Seq. No.
                    136257 1.R1040
Contig ID
                    \mathtt{sat701\overline{0}03116.h1}
5'-most EST
                    26181
Seq. No.
                    136264 1.R1040
Contig ID
                    hrw701\overline{0}61387.h1
5'-most EST
                    26182
Seq. No.
                    136265 1.R1040
Contig ID
```

 $qsv701\overline{0}51472.h1$ 5'-most EST

BLASTX Method g4006914 NCBI GI BLAST score 266 4.0e-23 E value 93 Match length 53 % identity

NCBI Description (Z99708) serine C-palmitoyltransferase like protein



Seq. No. 26183

Contig ID 136265 2.R1040

5'-most EST uC-gmrominsoy028c07b1

Seq. No. 26184

Contig ID 136271\_1.R1040 5'-most EST eep700865594.h1

Method BLASTX
NCBI GI g3885339
BLAST score 516
E value 3.0e-75
Match length 317
% identity 50

NCBI Description (AC005623) putative bzip protein [Arabidopsis thaliana]

Seq. No. 26185

Contig ID 136281\_1.R1040 5'-most EST vzy700755147.h1

Seq. No. 26186

Contig ID 136299\_1.R1040 5'-most EST leu701154347.h1

Method BLASTX
NCBI GI g2231312
BLAST score 496
E value 2.0e-65
Match length 138
% identity 94

NCBI Description (U75603) AtRab18 [Arabidopsis thaliana]

Seq. No. 26187

Contig ID 136299 2.R1040 5'-most EST zhf700954322.h1

Seq. No. 26188

Contig ID 136307\_1.R1040 5'-most EST kl1701213372.h1

Method BLASTX
NCBI GI g1706947
BLAST score 480
E value 3.0e-48
Match length 108
% identity 85

NCBI Description (U43528) RAD51 homolog AtRad51 [Arabidopsis thaliana]

>gi\_1706949 (U43652) AtRAD51 [Arabidopsis thaliana]
>gi\_2388778\_emb\_CAA04529\_ (AJ001100) Rad51-like protein

[Arabidopsis thaliana]

Seq. No. 26189

Contig ID 136307\_2.R1040 5'-most EST sat701010232.h2

Seq. No. 26190

Contig ID 136375\_1.R1040 5'-most EST fua701038576.h1



```
BLASTX
Method
NCBI GI
                   q4006918
                   238
BLAST score
                   8.0e-20
E value
Match length
                   68
                   66
% identity
                   (Z99708) peroxidase like protein [Arabidopsis thaliana]
NCBI Description
                   26191
Seq. No.
                   136379 1.R1040
Contiq ID
5'-most EST
                   ncj700975155.hl
                   26192
Seq. No.
                   136389 1.R1040
Contig ID
5'-most EST
                   ncj700975175.hl
Seq. No.
                   26193
                   136411 1.R1040
Contig ID
                   asn701\overline{1}41964.h1
5'-most EST
                   26194
Seq. No.
                   136439 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220102a12a1
                   BLASTX
Method
                   g2702364
NCBI GI
                   184
BLAST score
E value
                   1.0e-13
Match length
                   59
                   51
% identity
                   (AF036706) No definition line found [Caenorhabditis
NCBI Description
                   elegans]
                   26195
Seq. No.
                   136455 1.R1040
Contig ID
5'-most EST
                   smc700745808.h1
                   BLASTX
Method
NCBI GI
                   g3820531
BLAST score
                   376
                   7.0e-36
E value
                   134
Match length
                   54
% identity
NCBI Description
                  (AF072736) beta-glucosidase [Pinus contorta]
Seq. No.
                   26196
Contig ID
                   136472 1.R1040
5'-most EST
                   hrw701060419.h1
                   26197
Seq. No.
                   136480 1.R1040
Contig ID
                   ncj700975335.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g3873174
BLAST score
                   32
                   1.0e-08
E value
Match length
                   146
% identity
```

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14N23,





## complete sequence [Arabidopsis thaliana]

Seq. No. 26198 136500 1.R1040 Contig ID 5'-most EST ncj700978962.h1 Method BLASTN NCBI GI g4140025 BLAST score 212 1.0e-115 E value Match length 417 90 % identity Vigna mungo UF3GaT mRNA for flavonoid 3-0-galactosyl NCBI Description transferase, complete cds 26199 Seq. No. 136508\_1.R1040 Contig ID uC-gmflminsoy014e02b1 5'-most EST Method BLASTX NCBI GI g2262115 BLAST score 305 E value 2.0e-27 192 Match length % identity 31 (AC002343) cellulose synthase isolog [Arabidopsis thaliana] NCBI Description Seq. No. 26200 136531 1.R1040 Contig ID rca700999611.h1 5'-most EST BLASTX Method g2126855 NCBI GI BLAST score 178 E value 7.0e-13 153 Match length 31 % identity DNA polymerase I - Bacillus stearothermophilus >gi\_806281 NCBI Description (L42111) DNA polymerase I [Bacillus stearothermophilus] Seq. No. 26201 136532 1.R1040 Contig ID 5'-most EST ncj700980605.h126202 Seq. No. 136539 1.R1040 Contig ID  $ncj700\overline{9}75451.h1$ 5'-most EST 26203 Seq. No. Contig ID 136545 1.R1040 uC-gmflminsoy028c08b1 5'-most EST Method BLASTX NCBI GI g4185599 BLAST score 195

BLAST score 195 E value 6.0e-15 Match length 117 % identity 37

NCBI Description (AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana

triflora]



```
Seq. No.
                    136546 1.R1040
Contig ID
5'-most EST
                    jC-gmf102220063d04a1
                    26205
Seq. No.
                    136547 1.R1040
Contig ID
5'-most EST
                    ncj700\overline{9}75465.h1
                    26206
Seq. No.
```

136570 1.R1040 Contig ID  $ncj700\overline{9}75519.h1$ 5'-most EST 26207

Seq. No. 136593 1.R1040 Contig ID 5'-most EST wrg700787273.h2 BLASTX Method g4469027 NCBI GI

262 BLAST score 5.0e-23 E value 66 Match length 71 % identity

(AL035602) forever young gene (FEY) [Arabidopsis thaliana] NCBI Description

26208 Seq. No. 136608 1.R1040 Contig ID ncj700975585.hl 5'-most EST

26209 Seq. No.

136619 1.R1040 Contig ID  $ncj700\overline{9}75602.h1$ 5'-most EST

BLASTX Method NCBI GI g2262171 BLAST score 226 2.0e-18 E value 115 Match length 45 % identity

(AC002329) putative RNA/ssDNA-binding protein [Arabidopsis NCBI Description thaliana]

26210 Seq. No.

136619 2.R1040 Contig ID

5'-most EST uC-gmrominsoy145h06b1

Method BLASTX NCBI GI g2262172 BLAST score 404 5.0e-40 E value 186 Match length 55 % identity

(AC002329) predicted protein of unknown function NCBI Description

[Arabidopsis thaliana]

Seq. No. 26211

136627 1.R1040 Contig ID 5'-most EST  $ncj700\overline{9}75614.h1$ 

Seq. No. 26212

136643 1.R1040 Contig ID



5'-most EST xpa700794387.h1 Method BLASTX

g2529685 NCBI GI BLAST score 644 E value 2.0e-67 Match length 150

% identity NCBI Description (AC002535) putative dimethyladenosine transferase [Arabidopsis thaliana]

Seq. No. 26213

Contig ID 136668 1.R1040

5'-most EST jC-gmf102220063f03d1

Method BLASTX NCBI GI g2880042 BLAST score 273 E value 6.0e-24 Match length 79 % identity 61

(AC002340) putative 3-hydroxyisobutyryl-coenzyme A NCBI Description

hydrolase [Arabidopsis thaliana]

Seq. No. 26214

136670 2.R1040 Contig ID 5'-most EST  $rca700\overline{9}97758.h1$ 

Seq. No. 26215

136688 1.R1040 Contig ID 5'-most EST uC-gmropic087c03b1

Method BLASTX g2129955 NCBI GI BLAST score 199 E value 1.0e-15 Match length 55 % identity 67

NCBI Description

photoassimilate-responsive protein PAR-1b precursor common tobacco >gi\_871487\_emb\_CAA58731\_ (X83851) mRNA

inducible by sucrose and salicylic acid expressed in sugar-accumulating tobacco plants [Nicotiana tabacum]

26216 Seq. No.

Contig ID 136690 1.R1040 5'-most EST  $ncj700\overline{9}75715.h1$ 

Seq. No. 26217

Contig ID 136696 1.R1040 5'-most EST ncj700975723.h1

Seq. No. 26218

Contig ID 136710 1.R1040 5'-most EST kmv700741711.h1

26219 Seq. No.

Contig ID 136716 1.R1040 5'-most EST ncj700975761.h1

Seq. No. 26220

```
136729 1.R1040
Contig ID
5'-most EST
                  zsg701123246.h1
                  26221
Seq. No.
                  136742 1.R1040
Contig ID
                  ncj700975805.hl
5'-most EST
Method
                  BLASTX
                  g2864614
NCBI GI
                  361
BLAST score
                  2.0e-34
E value
Match length
                  116
% identity
                  57
NCBI Description (AL021811) putative protein [Arabidopsis thaliana]
                  26222
Seq. No.
                  136748 1.R1040
Contig ID
5'-most EST
                  g4302457
Method
                  BLASTX
                  g3386609
NCBI GI
BLAST score
                  271
                  2.0e-23
E value
Match length
                  172
% identity
                  47
                  (AC004665) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  26223
                  136758 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy071gl1bl
Method
                  BLASTX
NCBI GI
                  q4567303
                   392
BLAST score
                   9.0e-38
E value
                  81
Match length
% identity
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
                   26224
Seq. No.
                  136777_1.R1040
Contig ID
5'-most EST
                   asn701141013.hl
Method
                  BLASTX
                  g4580395
NCBI GI
                   132
BLAST score
E value
                   3.0e-13
Match length
                   84
                   52
% identity
NCBI Description (AC007171) putative kinesin-related protein [Arabidopsis
                   thaliana]
Seq. No.
                   26225
                   136790 1.R1040
Contig ID
5'-most EST
                  ncj700975914.hl
```

26226

136793 1.R1040

ncj700978696.hl

Seq. No.

Contig ID

5'-most EST



Seq. No. 26227 Contig ID 136793\_2.R1040 5'-most EST ncj700979468.h1

Seq. No. 26228

Contig ID 136808\_1.R1040 5'-most EST zhf700956972.h1

Method BLASTX
NCBI GI g3135273
BLAST score 428
E value 3.0e-42
Match length 127
% identity 61

NCBI Description (AC003058) hypothetical protein [Arabidopsis thaliana]

>gi\_4191773 (AC005917) putative WD-40 repeat protein

[Arabidopsis thaliana]

Seq. No. 26229

Contig ID 136815\_1.R1040 5'-most EST vzy700752479.h1

Method BLASTX
NCBI GI g320585
BLAST score 450
E value 1.0e-44
Match length 138
% identity 58

NCBI Description polygalacturonase (EC 3.2.1.15) 1 beta chain precursor -

tomato >gi\_170480 (M98466) polygalacturonase isoenzyme 1 beta subunit [Lycopersicon esculentum] >gi\_1762586 (U63374) polygalacturonase isoenzyme 1 beta subunit [Lycopersicon

esculentum]

Seq. No. 26230

Contig ID 136821\_1.R1040 5'-most EST ncj700976007.h1

Seq. No. 26231

Contig ID 136852 1.R1040 5'-most EST leu701149191.h1

Seq. No. 26232

Contig ID 136856 1.R1040 5'-most EST ncj700976137.h1

Method BLASTX
NCBI GI g3065835
BLAST score 492
E value 6.0e-50
Match length 108
% identity 84

NCBI Description (AF058800) putative methyltransferase [Arabidopsis

thaliana]

Seq. No. 26233

Contig ID 136866\_1.R1040

5'-most EST uC-gmflminsoy040a02b1

Seq. No. 26234

Contig ID



```
Contig ID
                   136879 1.R1040
5'-most EST
                  bth700846149.hl
                   26235
Seq. No.
                  136884 1.R1040
Contig ID
                  zzp700830287.hl
5'-most EST
Method
                  BLASTX
                  q3063471
NCBI GI
                   357
BLAST score
                   6.0e-34
E value
Match length
                  123
% identity
                   56
NCBI Description (AC003981) F22013.33 [Arabidopsis thaliana]
                   26236
Seq. No.
                   136903 1.R1040
Contig ID
5'-most EST
                  ncj700976415.hl
                   26237
Seq. No.
                  136947_1.R1040
Contig ID
5'-most EST
                   jex700907988.hl
Method
                  BLASTN
NCBI GI
                  q3894098
BLAST score
                   285
E value
                  1.0e-159
Match length
                  809
                   86
% identity
NCBI Description Pisum sativum mRNA for protein encoded by MCM3 gene,
                  partial
Seq. No.
                   26238
Contig ID
                   137008 1.R1040
5'-most EST
                  ncj700976718.hl
Method
                  BLASTX
NCBI GI
                   g2252840
BLAST score
                   155
                   1.0e-10
E value
Match length
                   64
% identity
                   45
NCBI Description (AF013293) contains regions of similarity to Haemophilus
                   influenzae permease (SP:P38767) [Arabidopsis thaliana]
                   26239
Seq. No.
                   137009 1.R1040
Contig ID
5'-most EST
                   dpv701097153.h1
Method
                   BLASTX
NCBI GI
                   q3249066
BLAST score
                   387
E value
                   2.0e-37
Match length
                   130
% identity
                   64
                  (AC004473) Similar to S. cerevisiae SIK1P protein
NCBI Description
                   gb 984964. ESTs gb_F15433 and gb_AA395158 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   26240
```

137019 1.R1040

NCBI GI

E value

BLAST score

g1370143

2.0e-35

77



```
ncj700976735.h1
5'-most EST
Seq. No.
                  26241
Contig ID
                  137024 1.R1040
                  ncj700980607.hl
5'-most EST
                  BLASTX
Method
                  g464365
NCBI GI
BLAST score
                  194
E value
                  4.0e-15
Match length
                  54
% identity
                  63
NCBI Description PEROXIDASE P7 >gi_66306 pir_OPNB7 peroxidase (EC 1.11.1.7)
                  - turnip
                  26242
Seq. No.
Contig ID
                  137027 1.R1040
5'-most EST
                  ncj700976748.hl
Method
                  BLASTX
NCBI GI
                  g4220445
BLAST score
                  166
E value
                  1.0e-11
Match length
                  124
% identity
NCBI Description (AC006216) Similar to gi 3004555 F19F24.14 salt inducible
                  protein homolog from Arabidopsis thaliana BAC gb AC003673.
                  [Arabidopsis thaliana]
Seq. No.
                  26243
                  137035 1.R1040
Contig ID
5'-most EST
                  fua701037758.hl
Method
                  BLASTX
NCBI GI
                  g3242721
BLAST score
                  288
E value
                  7.0e-26
Match length
                  84
% identity
NCBI Description (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
                  thaliana]
Seq. No.
                  26244
                  137082 1.R1040
Contig ID
5'-most EST
                  ncj700980969.hl
Method
                  BLASTX
                  g3402684
NCBI GI
BLAST score
                  237
                  6.0e-20
E value
Match length
                  127
% identity
NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  26245
                  137088 1.R1040
Contig ID
5'-most EST
                  ncj700976860.hl
Method
                  BLASTN
```



Match length 179 % identity 91

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB11B

Seq. No. 26246

Contig ID 137098\_1.R1040 5'-most EST uC-gmropic033g02b1

Method BLASTX
NCBI GI g1669655
BLAST score 263
E value 1.0e-22
Match length 113
% identity 50

NCBI Description (X95962) CER3 [Arabidopsis thaliana]

Seq. No. 26247

Contig ID 137108\_1.R1040 5'-most EST vzy700752796.h1

Seq. No. 26248

Contig ID 137125\_1.R1040 5'-most EST ncj700976924.h1

Seq. No. 26249

Contig ID 137148\_1.R1040 5'-most EST ncj700976970.h1

Method BLASTX
NCBI GI 94454033
BLAST score 284
E value 1.0e-25
Match length 97
% identity 48

NCBI Description (AL035394) putative potassium transport protein

[Arabidopsis thaliana]

Seq. No. 26250

Contig ID 137173\_1.R1040 5'-most EST txt700735556.h1

Method BLASTX
NCBI GI g3157949
BLAST score 302
E value 3.0e-27
Match length 94
% identity 66

NCBI Description (AC002131) Similar to glucan endo-1,3-beta-D-glucosidase precursor gb\_Z28697 from Nicotiana tabacum. ESTs gb\_Z18185

and gb AA605362 come from this gene. [Arabidopsis thaliana]

Seq. No. 26251

Contig ID 137186\_1.R1040 5'-most EST ncj700977123.h1

Seq. No. 26252

Contig ID 137188\_1.R1040 5'-most EST fC-gmf1700903880a1

Method BLASTX NCBI GI g3688600



BLAST score 2672 E value 0.0e+00 Match length 610 % identity 76

NCBI Description (AB009030) beta-Amyrin Synthase [Panax ginseng]

Seq. No. 26253

Contig ID 137192\_1.R1040 5'-most EST jC-gmst02400069g05a1

Method BLASTX
NCBI GI g2499005
BLAST score 202
E value 1.0e-15
Match length 109
% identity 42

NCBI Description 4-METHYL-5(B-HYDROXYETHYL)-THIAZOLE MONOPHOSPHATE

BIOSYNTHESIS ENZYME >gi\_1100872 (U34923) ThiJ [Escherichia

coli] >gi\_1773108 (U82664)

4-methyl- $\overline{5}$  (b-hydroxyethyl)-thiazole monophosphate biosynthesis protein [Escherichia coli] >gi\_1786626 (AE000148) 4-methyl-5 (beta-hydroxyethyl)-thiazole

monophosphate synthesis [Escherichia coli]

Seq. No. 26254

Contig ID 137221\_1.R1040 5'-most EST ncj700977219.h1

Seq. No. 26255

Contig ID 137222\_1.R1040 5'-most EST ncj700977222.h1

Seq. No. 26256

Contig ID 137246\_1.R1040

5'-most EST uC-gmrominsoy220d06b1

Method BLASTX
NCBI GI g3096947
BLAST score 186
E value 8.0e-30
Match length 117
% identity 54

NCBI Description (Y16327) putative cyclic nucleotide-regulated ion channel

[Arabidopsis thaliana]

Seq. No. 26257

Contig ID 137248\_1.R1040 5'-most EST fde700874237.h1

Method BLASTX
NCBI GI g4309731
BLAST score 313
E value 5.0e-29
Match length 97
% identity 62

NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26258

Contig ID 137259\_1.R1040

5'-most EST uC-gmrominsoy194b12b1



BLASTX Method g4432863 NCBI GI 606 BLAST score 2.0e-73 E value 200 Match length 73 % identity

(AC006300) putative phosphate/phosphoenolpyruvate NCBI Description

translocator protein [Arabidopsis thaliana]

26259 Seq. No.

137268 1.R1040 Contig ID ncj700977293.hl 5'-most EST

26260 Seq. No.

137291 1.R1040 Contig ID

jC-gmf\(\overline{1}\)02220073g03a1 5'-most EST

BLASTX Method g2245039 NCBI GI 185 BLAST score 1.0e-13 E value 97 Match length % identity 49

NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

26261 Seq. No.

137291 2.R1040 Contig ID k11701208291.h1 5'-most EST

BLASTX Method g2245039 NCBI GI 160 BLAST score 9.0e-11 E value Match length 73 51

% identity

NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26262

137291 3.R1040 Contig ID fde700873901.h1 5'-most EST

26263 Seq. No.

137314 1.R1040 Contig ID ncj700977374.hl 5'-most EST

26264 Seq. No.

137325 1.R1040 Contig ID ncj700983016.hl 5'-most EST

26265 Seq. No.

137365 1.R1040 Contig ID asn701138469.hl 5'-most EST

Seq. No. 26266

137378 1.R1040 Contig ID kl1701211957.h1 5'-most EST Method BLASTX

NCBI GI q3582436 BLAST score 487



E value 5.0e-49
Match length 145
% identity 61

NCBI Description (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No. 26267

Contig ID 137378\_2.R1040 5'-most EST jC-gmle01810012d02a1

Method BLASTX
NCBI GI g3582436
BLAST score 295
E value 8.0e-45
Match length 145
% identity 61

NCBI Description (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No. 26268

Contig ID 137401\_1.R1040

5'-most EST uC-gmflminsoy030c07b1

Method BLASTX
NCBI GI g3482920
BLAST score 188
E value 4.0e-14
Match length 112
% identity 43

NCBI Description (AC003970) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 26269

Contig ID 137408\_1.R1040 5'-most EST ncj700977523.h1

Seq. No. 26270

Contig ID 137415\_1.R1040 5'-most EST zzp700832246.h1

Method BLASTX
NCBI GI g3168840
BLAST score 147
E value 3.0e-09
Match length 63
% identity 41

NCBI Description (U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No. 26271

Contig ID 137418\_1.R1040 5'-most EST fua701038626.h1

Method BLASTX
NCBI GI g4455300
BLAST score 307
E value 6.0e-53
Match length 156
% identity 64

NCBI Description (AL035528) putative pectate lyase All (fragment)

[Arabidopsis thaliana]

Seq. No. 26272

Contig ID 137418 2.R1040 5'-most EST jex700905217.h1



 Seq. No.
 26273

 Contig ID
 137453\_1.R1040

 5'-most EST
 ncj700977616.h1

Seq. No. 26274

Contig ID 137457\_1.R1040 5'-most EST leu701146856.h1

Method BLASTX
NCBI GI g537317
BLAST score 1219
E value 1.0e-134
Match length 335
% identity 74

NCBI Description (L36157) peroxidase [Medicago sativa]

Seq. No. 26275

Contig ID 137484\_1.R1040 5'-most EST ncj700977666.h1

Seq. No. 26276

Contig ID 137486\_1.R1040 5'-most EST ncj700977668.h1

Method BLASTX
NCBI GI g4240207
BLAST score 231
E value 5.0e-19
Match length 141
% identity 43

NCBI Description (AB020666) KIAA0859 protein [Homo sapiens]

Seq. No. 26277

Contig ID 137517\_1.R1040

5'-most EST jC-gmf102220078h08a1

Seq. No. 26278

Contig ID 137534\_1.R1040 5'-most EST ncj700977745.h1

Method BLASTX
NCBI GI g2827528
BLAST score 200
E value 8.0e-16
Match length 67
% identity 54

NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 26279

Contig ID 137549\_1.R1040

5'-most EST jC-gmf102220079b03d1

Seq. No. 26280

Contig ID 137574\_1.R1040 5'-most EST ncj700977809.h1

Seq. No. 26281

Contig ID 137576\_1.R1040 5'-most EST zzp700830316.h1

Seq. No.

Contig ID

26290

137667 1.R1040



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26282
Seq. No.
                  137581 1.R1040
Contig ID
                  ncj700977821.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1184077
BLAST score
                  215
                  2.0e-17
E value
                  109
Match length
% identity
NCBI Description (U42445) Cf-2.2 [Lycopersicon pimpinellifolium]
Seq. No.
                  26283
                  137593 1.R1040
Contig ID
5'-most EST
                  ncj700977844.hl
Seq. No.
                  26284
                  137610 1.R1040
Contig ID
                  vzy700755310.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4567095
BLAST score
                  290
                  4.0e-26
E value
Match length
                  80
                  64
% identity
NCBI Description (AF129516) fertilization-independent endosperm protein
                  [Arabidopsis thaliana]
Seq. No.
                  26285
Contig ID
                  137621 1.R1040
5'-most EST
                  smc700746759.h1
                  26286
Seq. No.
                  137632 1.R1040
Contig ID
5'-most EST
                  kmv700738119.h1
                  BLASTX
Method
NCBI GI
                  g3451463
BLAST score
                  246
E value
                  9.0e-21
                  128
Match length
% identity
                  41
NCBI Description (AL031349) hypothetical protein [Schizosaccharomyces pombe]
                  26287
Seq. No.
                  137634 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy078b08b1
Seq. No.
                  26288
                  137639 1.R1040
Contig ID
5'-most EST
                  ncj700977918.hl
Seq. No.
                  26289
                  137647 1.R1040
Contig ID
5'-most EST
                  ncj700977927.hl
```



5'-most EST ncj700977960.h1

Seq. No. 26291

Contig ID 137676\_1.R1040 5'-most EST gsv701051166.h1

Method BLASTX
NCBI GI g2499931
BLAST score 724
E value 1.0e-76
Match length 183
% identity 77

NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)

>gi 2129534\_pir\_\_S71272 adenine phosphoribosyltransferase

(EC 2.4.2.7) - Arabidopsis thaliana

>gi 1321681 emb CAA65609 (X96866) adenine

phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No. 26292

Contig ID 137677\_1.R1040 5'-most EST ncj700986622.h1

Seq. No. 26293

Contig ID 137695 1.R1040 5'-most EST jex700905884.h1

Seq. No. 26294

Contig ID 137703\_1.R1040 5'-most EST ncj700978013.h1

Method BLASTN
NCBI GI g2695860
BLAST score 67

E value 2.0e-29
Match length 146
% identity 90

NCBI Description Pisum sativum mRNA for

3-deoxy-D-manno-2-octulosonate-8-phosphate synthase, clone

pPS40

Seq. No. 26295

Contig ID 137707 1.R1040 5'-most EST ncj700978019.h1

Seq. No. 26296

Contig ID 137726\_1.R1040 5'-most EST pxt700942557.h1

Seq. No. 26297

Contig ID 137729\_1.R1040 5'-most EST jsh701063755.h1

Seq. No. 26298

Contig ID 137797 1.R1040 5'-most EST pcp700992060.h1

Method BLASTX
NCBI GI g2062171
BLAST score 166
E value 8.0e-12



Match length 87 % identity 45

NCBI Description (AC001645) DNA binding protein (CDC27SH) isolog [Arabidopsis thaliana]

26299 Seq. No.

137846 1.R1040 Contig ID 5'-most EST vzy700750680.hl

Method BLASTX g3287683 NCBI GI BLAST score 243 E value 9.0e-21 Match length 110 % identity 19

NCBI Description (AC003979) Similar to apoptosis protein MA-3 gb D50465 from

Mus musculus. [Arabidopsis thaliana]

Seq. No. 26300

137855 1.R1040 Contig ID 5'-most EST rlr700895922.hl

Method BLASTX NCBI GI q3080385 BLAST score 179 7.0e-13 E value Match length 92 43 % identity

NCBI Description (AL022603) serine/threonine protein kinase [Arabidopsis

thaliana] >gi 3402760 emb CAA20206.1 (AL031187) serine/threonine kinase - like protein [Arabidopsis

thaliana]

26301 Seq. No.

137861 1.R1040 Contig ID 5'-most EST asn701142772.hl

Seq. No. 26302

Contig ID 137874 1.R1040 5'-most EST leu701146878.hl

Seq. No. 26303

137874 2.R1040 Contig ID 5'-most EST leu701155970.hl

Seq. No. 26304

137916 1.R1040 Contig ID 5'-most EST  $ncj700\overline{9}78354.h1$ 

Method BLASTX NCBI GI q417570 BLAST score 388 E value 1.0e-58 Match length 141 % identity 87

NCBI Description DIHYDROOROTATE DEHYDROGENASE PRECURSOR (DIHYDROOROTATE OXIDASE) (DHODEHASE) >qi 478676 pir S23762 dihydroorotate

oxidase (EC 1.3.3.1) - Arabidopsis thaliana >gi 16449\_emb\_CAA44695\_ (X62909) dihydroorotate

dehydrogenase [Arabidopsis thaliana]



Seq. No. 26305

Contig ID 137917\_1.R1040 5'-most EST zhf700955804.h1

Seq. No. 26306

Contig ID 137924\_1.R1040 5'-most EST zhf700964637.h1

Method BLASTX
NCBI GI g1084334
BLAST score 348
E value 7.0e-33
Match length 81
% identity 80

NCBI Description calcium-dependent protein kinase (EC 2.7.1.-) 1 -

Arabidopsis thaliana >gi\_604880\_dbj\_BAA04829\_ (D21805) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No. 26307

Contig ID 137933\_1.R1040 5'-most EST ncj700978380.h1

Seq. No. 26308

Contig ID 137950\_1.R1040 5'-most EST ncj700978404.h1

Method BLASTX
NCBI GI g2462825
BLAST score 234
E value 1.0e-26
Match length 73
% identity 85

NCBI Description (AF000657) contains Procite 'RNP1' putative RNA-binding

region [Arabidopsis thaliana]

Seq. No. 26309

Contig ID 137955\_1.R1040 5'-most EST fde700874521.h1

Method BLASTX
NCBI GI g4204793
BLAST score 588
E value 6.0e-84
Match length 273
% identity 31

NCBI Description (U52079) P-glycoprotein [Solanum tuberosum]

Seq. No. 26310

Contig ID 137960\_1.R1040

5'-most EST uC-gmrominsoy205f03b1

Method BLASTN
NCBI GI g3821780
BLAST score 34
E value 2.0e-09
Match length 34
% identity 59

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 26311



```
137966 1.R1040
Contig ID
                   zzp700833230.h1
5'-most EST
                   26312
Seq. No.
                   138009 1.R1040
Contig ID
5'-most EST
                   pxt700945573.h1
Method
                   BLASTX
NCBI GI
                   q3341694
BLAST score
                   342
                   2.0e-32
E value
Match length
                   86
% identity
                   79
                  (AC003672) PREG-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   138015 1.R1040
Contig ID
5'-most EST
                   ncj700978509.hl
                   26314
Seq. No.
Contig ID
                   138016 1.R1040
5'-most EST
                   ncj700978510.h1
Seq. No.
                   26315
                   138038 1.R1040
Contig ID
                   jC-qmst02400006b07d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4539314
BLAST score
                   146
E value
                   4.0e-09
Match length
                   56
% identity
                   55
                  (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
                   26316
Seq. No.
                   138053 1.R1040
Contig ID
                   zhf700964503.h1
5'-most EST
                   BLASTX
Method
                   q4539010
NCBI GI
                   310
BLAST score
                   1.0e-28
E value
                   104
Match length
                   48
% identity
                   (AL049481) putative DNA-directed RNA polymerase
NCBI Description
                   [Arabidopsis thaliana]
                   26317
Seq. No.
                   138065 1.R1040
Contig ID
5'-most EST
                   epx701\overline{104375.h1}
                   26318
Seq. No.
                   138075 1.R1040
Contig ID
                   ncj700978611.h1
5'-most EST
                   BLASTX
Method
```

4115

g1086833

2.0e-14 91

191

NCBI GI BLAST score

E value

Match length



% identity 41
NCBI Description
CU41264) coded for by C. elegans cDNA CEESN26F; coded for
by C. elegans cDNA CEESI89F; similar to 60S acidic
ribosomal protein Po (L10) [Caenorhabditis elegans]

Seq. No. 26319

Contig ID 138105\_1.R1040 5'-most EST pxt700941695.h1

Method BLASTX
NCBI GI g4558556
BLAST score 155
E value 1.0e-22
Match length 101
% identity 60

NCBI Description (AC007138) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 26320

Contig ID 138118\_1.R1040 5'-most EST ncj700978667.h1

Seq. No. 26321

Contig ID 138121\_1.R1040 5'-most EST ncj700978672.h1

Method BLASTX
NCBI GI g1685005
BLAST score 516
E value 4.0e-52
Match length 273
% identity 36

NCBI Description (U32644) immediate-early salicylate-induced

glucosyltransferase [Nicotiana tabacum]

Seq. No. 26322

Contig ID 138143\_1.R1040 5'-most EST uC-gmropic091e02b1

Seq. No. 26323

Contig ID 138149\_1.R1040 5'-most EST sat701010327.h1

Method BLASTX
NCBI GI g4063744
BLAST score 149
E value 9.0e-10
Match length 58
% identity 55

NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26324

Contig ID 138180\_1.R1040 5'-most EST ncj700978777.h1

Method BLASTX
NCBI GI g2494905
BLAST score 210
E value 1.0e-16
Match length 157
% identity 35



MICROTUBULE-ASSOCIATED PROTEIN YTM1 >gi 2132107 pir S67174 NCBI Description

hypothetical protein YOR272w - yeast (Saccharomyces

cerevisiae) >gi\_1279699\_emb\_CAA61778\_ (X89633) hypothetical

protein [Saccharomyces cerevisiae]

>gi\_1420610\_emb\_CAA99497\_ (Z75180) ORF YOR272w [Saccharomyces cerevisiae] >gi 1928989 (U92821)

microtubule-associated protein [Saccharomyces cerevisiae]

26325 Seq. No.

138189 1.R1040 Contig ID 5'-most EST zhf700963468.hl

Method BLASTX NCBI GI q3157941 151 BLAST score E value 1.0e-09 Match length 47 53 % identity

(AC002131) Contains similarity to hypothetical protein NCBI Description

gb\_U95973 from A. thaliana. [Arabidopsis thaliana]

26326 Seq. No.

138197 1.R1040 Contig ID 5'-most EST rry700808448.h1

26327 Seq. No.

138202 1.R1040 Contig ID uC-gmropic021a11b1 5'-most EST

Seq. No. 26328

138204 1.R1040 Contig ID 5'-most EST epx701108921.h1

26329 Seq. No.

138222 1.R1040 Contig ID 5'-most EST zhf700959203.h1

BLASTX Method NCBI GI g2285885 BLAST score 542 2.0e-55 E value 139 Match length 73 % identity

(D89631) sulfate transporter [Arabidopsis thaliana] NCBI Description

Seq. No. 26330

138224 1.R1040 Contig ID uC-gmropic025f07b1 5'-most EST

Method BLASTX q1362017 NCBI GI 328 BLAST score 1.0e-30 E value 113 Match length 66 % identity

NCBI Description zinc finger protein 4 - Arabidopsis thaliana >gi\_790679

(L39647) zinc finger protein [Arabidopsis thaliana]

26331 Seq. No.

138230 2.R1040 Contig ID



5'-most EST uC-gmropic012b05b1

Seq. No. 26332

Contig ID 138230\_3.R1040 5'-most EST pmv700892280.h1

Seq. No. 26333

Contig ID 138269\_1.R1040

5'-most EST uC-gmflminsoy042e10b1

Method BLASTX
NCBI GI g2462831
BLAST score 200
E value 2.0e-15
Match length 78
% identity 62

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26334

Contig ID 138276\_1.R1040 5'-most EST jC-gmle01810062e01a1

Seq. No. 26335

Contig ID 138291\_1.R1040 5'-most EST ncj700978978.h1

Seq. No. 26336

Contig ID 138313\_1.R1040 5'-most EST epx701107330.h1

Seq. No. 26337

Contig ID 138314 1.R1040 5'-most EST rca701000761.h1

Seq. No. 26338

Contig ID 138324 1.R1040

5'-most EST jC-gmst02400053a11d1

Method BLASTX
NCBI GI g2145356
BLAST score 246
E value 6.0e-21
Match length 56
% identity 77

NCBI Description (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi\_3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No. 26339

Contig ID 138333\_1.R1040 5'-most EST ncj700979044.h1

Seq. No. 26340

Contig ID 138341\_1.R1040 5'-most EST jC-gmst02400063h12a1

Method BLASTN
NCBI GI g2352083
BLAST score 134
E value 4.0e-69
Match length 410

```
% identity
                  Arabidopsis thaliana serine/threonine kinase (SIK1) mRNA,
NCBI Description
                   complete cds
                   26341
Seq. No.
                   138373 1.R1040
Contig ID
                   gsv701044663.h1
5'-most EST
                   26342
Seq. No.
                   138400 1.R1040
Contig ID
                   k11701\overline{2}08735.h1
5'-most EST
                   BLASTX
Method
                   q4580397
NCBI GI
                   177
BLAST score
                   4.0e-13
E value
                   98
Match length
% identity
                   42
                   (AC007171) putative RNA helicase [Arabidopsis thaliana]
NCBI Description
                   26343
Seq. No.
                   138456 1.R1040
Contig ID
5'-most EST
                   ncj700979345.hl
Method
                   BLASTX
                   q4544460
NCBI GI
                   280
BLAST score
                   1.0e-24
E value
                   146
Match length
                   39
% identity
                   (AC006592) putative reverse transcriptase [Arabidopsis
NCBI Description
                   thaliana]
                   26344
Seq. No.
                   138462 1.R1040
Contig ID
                   wrg700787528.hl
5'-most EST
                   BLASTX
Method
                   g1076274
NCBI GI
BLAST score
                   357
                   9.0e-34
E value
                   143
Match length
                   49
% identity
                  cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)
NCBI Description
                   26345
Seq. No.
                   138471 1.R1040
Contig ID
                   ncj700\overline{9}87631.h1
5'-most EST
                   BLASTX
Method
                   q4454043
NCBI GI
BLAST score
                    167
```

Method BLASTX
NCBI GI 94454043
BLAST score 167
E value 6.0e-12
Match length 54
% identity 56

NCBI Description (AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 26346

Contig ID 138475\_1.R1040 5'-most EST jC-gmro02910034f08a1



Seq. No. 26347

Contig ID 138477\_1.R1040 5'-most EST eep700866060.h1

Seq. No. 26348

Contig ID 138510\_1.R1040 5'-most EST eep700864728.h1

Method BLASTX
NCBI GI g2191136
BLAST score 225
E value 1.0e-18
Match length 91
% identity 52

NCBI Description (AF007269) Similar to UTP-Glucose Glucosyltransferase;

coded for by A. thaliana cDNA T46230; coded for by A.

thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidopsis thaliana]

Seq. No. 26349

Contig ID 138513\_1.R1040 5'-most EST pcp700990402.h1

Seq. No. 26350

Contig ID 138514\_1.R1040 5'-most EST leu701149785.h1

Seq. No. 26351

Contig ID 138518 1.R1040

5'-most EST jC-gmf102220138d02a1

Seq. No. 26352

Contig ID 138546\_1.R1040 5'-most EST zhf700964179.h1

Method BLASTX
NCBI GI g4056506
BLAST score 166
E value 7.0e-12
Match length 62

% identity 50

NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 26353

Contig ID 138554\_1.R1040 5'-most EST ncj700982030.h1

Method BLASTN
NCBI GI g2304954
BLAST score 41
E value 7.0e-14
Match length 101
% identity 95

NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No. 26354

Contig ID 138558 1.R1040 5'-most EST zpv700761529.h1

Method BLASTX NCBI GI g4160300



```
BLAST score
                   8.0e-12
E value
                   78
Match length
                   46
% identity
                   (AJ011893) cyclin D3.1 protein [Nicotiana tabacum]
NCBI Description
                   26355
Seq. No.
                   138573 1.R1040
Contig ID
                   ncj700979537.h2
5'-most EST
                   BLASTX
Method
                   g1617268
NCBI GI
BLAST score
                   294
                   5.0e-27
E value
                   88
Match length
                   66
% identity
                   (Z72153) acyl CoA synthetase [Brassica napus]
NCBI Description
                   26356
Seq. No.
                   138587 1.R1040
Contig ID
                   ncj700980527.hl
5'-most EST
                   BLASTX
Method
                   g2244891
NCBI GI
BLAST score
                   168
E value
                   5.0e-12
                   73
Match length
                   51
% identity
                   (Z97338) strong similarity to cytochrome P450 [Arabidopsis
NCBI Description
                   thaliana]
                   26357
Seq. No.
                   138607 1.R1040
Contig ID
                   ncj700979629.h2
5'-most EST
Seq. No.
                   26358
                   138607 2.R1040
Contig ID
                   \mathtt{sat701\overline{0}02872.h1}
5'-most EST
                   26359
Seq. No.
                   138609 1.R1040
Contig ID
                   awf700842139.hl
5'-most EST
                    26360
Seq. No.
                    138609 2.R1040
Contig ID
5'-most EST
                    asn701138345.hl
                    26361
Seq. No.
                    138611 1.R1040
Contig ID
                    pxt700944838.h1
5'-most EST
                    BLASTX
Method
NCBI GI
                    q4539386
                    367
BLAST score
                    2.0e-35
E value
Match length
                    86
 % identity
```

NCBI Description (AL035526) extensin-like protein [Arabidopsis thaliana]

Seq. No.

26362

4121



Contig ID 138616\_1.R1040 5'-most EST ncj700979642.h2

Seq. No. 26363

Contig ID 138629\_1.R1040

5'-most EST jC-gmf102220115d06a1

Seq. No. 26364

Contig ID 138652\_1.R1040 5'-most EST dpv701100659.h1

Seq. No. 26365

Contig ID 138675 1.R1040 5'-most EST hrw701056979.h1

Seq. No. 26366

Contig ID 138675\_2.R1040 5'-most EST wrg700786026.h2

Seq. No. 26367

Contig ID 138692\_1.R1040 5'-most EST ncj700979777.h2

Seq. No. 26368

Contig ID 138721\_1.R1040 5'-most EST jC-gmle01810064g11a1

Method BLASTX
NCBI GI g2529686
BLAST score 473
E value 2.0e-54

Match length 125 % identity 78

NCBI Description (AC002535) putative G-beta-repeat containing protein, 5'

partial [Arabidopsis thaliana]

Seq. No. 26369

Contig ID 138724\_1.R1040 5'-most EST ncj700979845.h2

Method BLASTX
NCBI GI g4539459
BLAST score 400
E value 4.0e-39
Match length 106
% identity 68

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 26370

Contig ID 138756\_1.R1040 5'-most EST pxt700943842.h1

Method BLASTX
NCBI GI g1170409
BLAST score 369
E value 1.0e-35
Match length 93
% identity 76

NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22) >gi 549887 (U09336) homeobox protein [Arabidopsis thaliana]



>gi\_549888 (U09337) homeobox protein [Arabidopsis thaliana] >gi 4490724 emb CAB38927.1 (AL035709) homeobox protein HAT22 [Arabidopsis thaliana]

26371 Seq. No. 138767 1.R1040 Contig ID  $g43961\overline{1}3$ 5'-most EST Method BLASTX q3402704 NCBI GI 547 BLAST score 7.0e-56 E value 187 Match length % identity 63 (AC004261) hypothetical protein [Arabidopsis thaliana] NCBI Description

138794 1.R1040 Contig ID 5'-most EST ncj700980025.h1 BLASTN Method NCBI GI q2264314 33 BLAST score 7.0e-09

26372

E value 105 Match length % identity 83

Seq. No.

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MQK4, complete sequence [Arabidopsis thaliana]

26373 Seq. No. 138812 1.R1040 Contig ID ncj700980082.hl 5'-most EST

BLASTX Method g3123130 NCBI GI 208 BLAST score 4.0e-29 E value 108 Match length % identity 45

HYPOTHETICAL 61.8 KD TRP-ASP REPEATS CONTAINING PROTEIN NCBI Description T32G6.2 IN CHROMOSOME II >gi 2618685 (AC002510) putative small nuclear ribonucleoprotein Prp4p [Arabidopsis thaliana] >gi\_3241948 (AC004625) putative small nuclear

ribonucleoprotein Prp4p [Arabidopsis thaliana]

26374 Seq. No.

138816 1.R1040 Contig ID epx701104215.h1 5'-most EST

Seq. No. 26375

138821 1.R1040 Contig ID  $ncj700\overline{9}80106.h1$ 5'-most EST

BLASTX Method q2501491 NCBI GI 169 BLAST score 2.0e-12 E value 81 Match length 43 % identity

FLAVONOL 3-O-GLUCOSYLTRANSFERASE 1 (UDP-GLUCOSE FLAVONOID NCBI Description 3-O-GLUCOSYLTRANSFERASE 1) >gi\_542014\_pir\_\_\$41950



UTP-glucose glucosyltransferase - cassava >gi\_453246\_emb\_CAA54609\_ (X77459) UTP-glucose glucosyltransferase [Manihot esculenta]

Seq. No. 26376

Contig ID 138852\_1.R1040 5'-most EST ncj700980211.h1

Method BLASTX
NCBI GI g4185599
BLAST score 199
E value 1.0e-15
Match length 89
% identity 46

NCBI Description (AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana

triflora]

Seq. No. 26377

Contig ID 138853\_1.R1040 5'-most EST leu701153701.h1

Method BLASTX
NCBI GI g2580584
BLAST score 412
E value 2.0e-40
Match length 133
% identity 62

NCBI Description (AF000976) 7-O-methyltransferase [Medicago sativa]

Seq. No. 26378

Contig ID 138867\_1.R1040 5'-most EST ncj700980250.h1

Seq. No. 26379

Contig ID 138914\_1.R1040 5'-most EST ncj700980359.h1

Seq. No. 26380

Contig ID 138972\_1.R1040

5'-most EST uC-gmrominsoy241g11b1

Seq. No. 26381

Contig ID 138975\_1.R1040 5'-most EST smc700748186.h1

Seq. No. 26382

Contig ID 138988\_1.R1040 5'-most EST ncj700980503.h1

Method BLASTX
NCBI GI g4454043
BLAST score 568
E value 1.0e-58
Match length 140
% identity 74

NCBI Description (AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 26383

Contig ID 138992\_1.R1040 5'-most EST ncj700983574.h1



Method BLASTX
NCBI GI g4455192
BLAST score 359
E value 9.0e-50
Match length 168
% identity 65

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 26384

Contig ID 139000 1.R1040 5'-most EST pmv700889384.h1

Method BLASTX
NCBI GI g3522938
BLAST score 345
E value 3.0e-32
Match length 187
% identity 43

NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 26385

Contig ID 139001\_1.R1040 5'-most EST fC-gmro7000746535d1

Method BLASTX
NCBI GI g3860250
BLAST score 576
E value 3.0e-59
Match length 213
% identity 88

NCBI Description (AC005824) putative chloroplast prephenate dehydratase

[Arabidopsis thaliana]

Seq. No. 26386

Contig ID 139009\_1.R1040 5'-most EST bth700847360.h1

Method BLASTX
NCBI GI g2494736
BLAST score 259
E value 3.0e-22
Match length 125
% identity 44

NCBI Description GLUCOSE INHIBITED DIVISION PROTEIN A

>gi\_1001595\_dbj\_BAA10223\_ (D64000) glucose inhibited

division protein A [Synechocystis sp.]

Seq. No. 26387

Contig ID 139017\_1.R1040

5'-most EST jC-gmro02910012d03d1

Method BLASTX
NCBI GI g3834323
BLAST score 283
E value 3.0e-25
Match length 87
% identity 60

NCBI Description (AC005679) F9K20.25 [Arabidopsis thaliana]

Seq. No. 26388

Contig ID 139024\_1.R1040



5'-most EST pmv700890942.h1

Method BLASTX
NCBI GI g2244898
BLAST score 256
E value 3.0e-22
Match length 111
% identity 47

NCBI Description (Z97338) strong similarity to protein phosphatase 2A

regulatory chain, 74K [Arabidopsis thaliana]

Seq. No. 26389

Contig ID 139027\_1.R1040 5'-most EST zsg701127504.h1

Method BLASTX
NCBI GI g1076821
BLAST score 489
E value 3.0e-49
Match length 135
% identity 70

NCBI Description probable 1-acyl-glycerol-3-phosphate acyltransferase -

maize >gi\_575960\_emb\_CAA82638\_ (Z29518)

1-acyl-glycerol-3-phosphate acyltransferase (putative) [Zea

mays]

Seq. No. 26390

Contig ID 139045 1.R1040 5'-most EST ncj700980593.h1

Seq. No. 26391

Contig ID 139100\_1.R1040

5'-most EST jC-gmf $\overline{1}$ 02220138c04a1

Seq. No. 26392

Contig ID 139100\_2.R1040 5'-most EST ncj700980690.h1

Seq. No. 26393

Contig ID 139104 1.R1040 5'-most EST ncj700980695.h1

Method BLASTX
NCBI GI g2244839
BLAST score 304
E value 7.0e-32
Match length 131
% identity 21

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26394

Contig ID 139106\_1.R1040 5'-most EST ncj700980706.h1

Seq. No. 26395

Contig ID 139114\_1.R1040 5'-most EST txt700736867.h1

Seq. No. 26396

Contig ID 139186\_1.R1040



5'-most EST ncj700980850.h1

Seq. No. 26397

Contig ID 139194 1.R1040 5'-most EST jsh701064920.h1

Seq. No. 26398

Contig ID 139195\_1.R1040 5'-most EST epx701104057.h1

Seq. No. 26399

Contig ID 139204 2.R1040 5'-most EST ncj700986459.h1

Method BLASTX
NCBI GI g3201554
BLAST score 202
E value 5.0e-18
Match length 103
% identity 50

NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No. 26400

Contig ID 139207\_1.R1040

NCBI Description (AC003981) F22013.28 [Arabidopsis thaliana]

Seq. No. 26401

Contig ID 139217\_1.R1040 5'-most EST uC-gmropic065c09b1

Method BLASTX
NCBI GI g1176658
BLAST score 271
E value 1.0e-23
Match length 111
% identity 50

NCBI Description HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II

>gi 726363 (U23168) No definition line found

[Caenorhabditis elegans]

Seq. No. 26402

Contig ID 139232\_2.R1040 5'-most EST zhf700952549.h1

Seq. No. 26403

Contig ID 139267\_1.R1040 5'-most EST pxt700945232.h1

Method BLASTX
NCBI GI g3096919
BLAST score 576
E value 2.0e-59
Match length 142



Seq. No. 26404

Contig ID 139279\_1.R1040 5'-most EST ncj700980985.h1

Seq. No. 26405

Contig ID 139286\_1.R1040 5'-most EST ncj700980994.h1

Method BLASTX
NCBI GI g3355478
BLAST score 163
E value 3.0e-11
Match length 97
% identity 41

NCBI Description (AC004218) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26406

Contig ID 139289\_1.R1040 5'-most EST leu701152205.h1

Method BLASTX
NCBI GI g3603401
BLAST score 351
E value 4.0e-33
Match length 111
% identity 59

NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No. 26407

Contig ID 139291\_1.R1040

5'-most EST uC-gmflminsoy042c11b1

Method BLASTX
NCBI GI g2651302
BLAST score 486
E value 5.0e-49
Match length 141
% identity 63

NCBI Description (AC002336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26408

Contig ID 139303\_1.R1040 5'-most EST ncj700981028.h1

Seq. No. 26409

Contig ID 139323\_1.R1040 5'-most EST ncj700981065.h1

Method BLASTX
NCBI GI g4006854
BLAST score 238
E value 3.0e-20
Match length 96
% identity 53

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 26410



139338 1.R1040 Contig ID leu701152581.hl 5'-most EST Seq. No. 26411 139339 1.R1040 Contig ID 5'-most EST  $gsv701\overline{0}55401.h1$ BLASTX Method g3785989 NCBI GI BLAST score 539 3.0e-55 E value 139 Match length 75 % identity (AC005560) unknown protein [Arabidopsis thaliana] NCBI Description 26412 Seq. No. 139345 1.R1040 Contig ID 5'-most EST wrg700788384.hl BLASTX Method g629562 NCBI GI BLAST score 812 E value 4.0e-87 172 Match length 87 % identity sulfate adenylyltransferase (EC 2.7.7.4) - Arabidopsis NCBI Description thaliana >gi\_2129743\_pir S68024 sulfate adenylyltransferase (EC 2.7.7.4) precursor (clone APS2) -Arabidopsis thaliana >gi\_487404\_emb\_CAA55799\_ (X79210) sulfate adenylyltransferase [Arabidopsis thaliana] >gi\_1228104 (U06276) ATP sulfurylase [Arabidopsis thaliana] >gi 1378028 (U40715) ATP sulfurylase precursor [Arabidopsis thaliana] >gi 1575324 (U59737) ATP sulfurylase [Arabidopsis thaliana] 26413 Seq. No. 139346 1.R1040 Contig ID 5'-most EST uC-gmronoir008f03b1 BLASTX Method q2828289 NCBI GI 154 BLAST score 5.0e-10 E value Match length 59 % identity 51 (AL021687) hypothetical protein [Arabidopsis thaliana] NCBI Description 26414 Seq. No. 139346 2.R1040 Contig ID 5'-most EST zzp700833537.hl 26415 Seq. No. 139400 1.R1040 Contiq ID

g5126598 5'-most EST

Seq. No. 26416

Contig ID 139404 1.R1040 ncj700981213.hl 5'-most EST

Method BLASTX NCBI GI q116923



BLAST score 325 E value 3.0e-30 Match length 118 % identity 57

NCBI Description COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)

>gi\_111414\_pir\_\_S13520 beta-COP protein - rat
>gi\_55819\_emb\_CAA40505\_ (X57228) beta COP [Rattus

norvegicus]

Seq. No.

26417

Contig ID 5'-most EST

139409\_1.R1040

jC-gmf102220146c08a1

Seq. No.

26418

Contig ID 5'-most EST

139409\_2.R1040 bth700844803.h1

Seq. No.

26419

Contig ID 5'-most EST 139431\_1.R1040 ncj700985758.h1

Method BLASTX
NCBI GI g4204295
BLAST score 205
E value 3.0e-16
Match length 98
% identity 41

NCBI Description (AC003027) lcl\_prt\_seq No definition line found

[Arabidopsis thaliana]

Seq. No.

Contig ID

26420 139482\_1.R1040 ncj700981336.h1

Seq. No.

26421

Contig ID 5'-most EST

5'-most EST

139525\_1.R1040 sat701002827.h1

Seq. No.

26422

Contig ID

139528 1.R1040

5'-most EST

jC-gmle01810037f03a2

Seq. No.

26423

Contig ID 5'-most EST

139535\_1.R1040 ncj700981420.h1

Method NCBI GI BLASTX g3775993

BLAST score E value

359 5.0e-34

Match length

71 96

% identity NCBI Description

(AJ010460) RNA helicase [Arabidopsis thaliana]

Seq. No.

26424

Contig ID 5'-most EST

139545\_1.R1040 pcp700989648.h1

Method NCBI GI BLASTX g4469012



BLAST score 172 E value 5.0e-12 Match length 62 % identity 55

NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26425

Contig ID 139546 1.R1040 5'-most EST ncj700981436.h1

Method BLASTX
NCBI GI g3201554
BLAST score 558
E value 1.0e-83
Match length 228
% identity 66

NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No. 26426

Contig ID 139549\_1.R1040 5'-most EST vzy700752472.h1

Seq. No. 26427

Contig ID 139560\_1.R1040 5'-most EST zhf700958364.h1

Method BLASTN
NCBI GI g2104674
BLAST score 89

E value 2.0e-42 Match length 219 % identity 91

NCBI Description V.faba mRNA for transcription factor containing bZIP

Seq. No. 26428

Contig ID 139572\_1.R1040 5'-most EST ncj700981485.h1

Seq. No. 26429

Contig ID 139578 1.R1040 5'-most EST ncj700981491.h1

Seq. No. 26430

Contig ID 139592\_1.R1040 5'-most EST uC-gmropic012b06b1

Seq. No. 26431

Contig ID 139596 1.R1040

5'-most EST jC-gmle01810010b04a1

Seq. No. 26432

Contig ID 139609\_1.R1040 5'-most EST ncj700981547.h1

Seq. No. 26433

Contig ID 139610\_1.R1040

5'-most EST jC-gmle01810015a04d1

Seq. No. 26434



139613 1.R1040 Contig ID jC-gmst02400060e10a1 5'-most EST 26435 Seq. No. 139635 1.R1040 Contig ID jC-gmro02910013d12d1 5'-most EST 26436 Seq. No. 139664 1.R1040 Contig ID rlr700896745.hl 5'-most EST BLASTX Method NCBI GI q3193288 177 BLAST score 6.0e-13E value 112 Match length 44 % identity (AF069298) similar to bacterial and fungi pectinesterases NCBI Description [Arabidopsis thaliana] 26437 Seq. No. 139665 1.R1040 Contig ID 5'-most EST ncj700988637.hl Method BLASTX g3819099 NCBI GI BLAST score 521 3.0e-53 E value Match length 138 70 % identity NCBI Description (AJ009825) copper amine oxidase [Cicer arietinum] 26438 Seq. No. 139672 1.R1040 Contig ID 5'-most EST gsv701055318.hl Seq. No. 26439 139685 1.R1040 Contig ID uC-gmrominsoy111h01b1 5'-most EST BLASTX Method q1817544 NCBI GI 189 BLAST score 3.0e-14E value 85 Match length 44 % identity (D83025) proline oxidase precursor [Arabidopsis thaliana] NCBI Description 26440 Seq. No. 139690 1.R1040 Contig ID  $gsv701\overline{0}51537.h1$ 5'-most EST 26441 Seq. No. 139700 1.R1040 Contig ID uC-gmrominsoy167b10b1 5'-most EST

Method BLASTX
NCBI GI g4490342
BLAST score 297
E value 9.0e-27
Match length 160



% identity 50

NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No. 26442

Contig ID 139701 1.R1040 5'-most EST leu701150580.h1

Seq. No. 26443

Contig ID 139717\_1.R1040 5'-most EST ncj700981712.h1

Seq. No. 26444

Contig ID 139790\_1.R1040 5'-most EST ncj700981842.h1

Method BLASTX
NCBI GI g2980806
BLAST score 145
E value 3.0e-09
Match length 36
% identity 69

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 26445

Contig ID 139808\_1.R1040 5'-most EST zpv700759887.h1

Seq. No. 26446

Contig ID 139809\_1.R1040 5'-most EST hrw701060688.h1

Method BLASTX
NCBI GI g282964
BLAST score 344
E value 2.0e-32
Match length 81
% identity 75

NCBI Description transforming protein (myb) homolog (clone myb.Ph3) - garden petunia >gi 20563 emb CAA78386 (Z13996) protein 1 [Petunia

x hybrida]

Seq. No. 26447

Contig ID 139827 1.R1040

5'-most EST jC-gmf102220114e07d1

Seq. No. 26448

Contig ID 139828 1.R1040 5'-most EST xpa700792448.h1

Method BLASTX
NCBI GI 94454026
BLAST score 384
E value 1.0e-41
Match length 138
% identity 65

NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No. 26449

Contig ID 139836 1.R1040 5'-most EST ncj700981939.h1



Method BLASTN
NCBI GI g559505
BLAST score 128
E value 1.0e-65
Match length 368
% identity 84

NCBI Description P.hybrida mRNA for S-adenosylmethionine-synthetase

Seq. No. 26450

Contig ID 139845 1.R1040 5'-most EST ncj700981952.h1

Method BLASTX
NCBI GI g3335353
BLAST score 194
E value 4.0e-15
Match length 78
% identity 47

NCBI Description (AC004512) Similar to cytochrome P450 gb\_X90458 from A.

thaliana. [Arabidopsis thaliana]

Seq. No. 26451

Contig ID 139861\_1.R1040 5'-most EST kl1701205476.h1

Method BLASTX
NCBI GI g3646336
BLAST score 392
E value 8.0e-38
Match length 121
% identity 68

NCBI Description (AJ001682) MdMADS9 [Malus domestica]

Seq. No. 26452

Contig ID 139874\_1.R1040 5'-most EST dpv701100857.h1

Method BLASTX
NCBI GI g1429226
BLAST score 315
E value 6.0e-29
Match length 96
% identity 64

NCBI Description (X98861) TFIIA [Arabidopsis thaliana]

Seq. No. 26453

Contig ID 139889\_1.R1040

5'-most EST uC-gmrominsoy108e12b1

Method BLASTX
NCBI GI g2497034
BLAST score 177
E value 8.0e-13
Match length 109
% identity 41

NCBI Description HYPOTHETICAL 55.5 KD PROTEIN ZK1128.2 IN CHROMOSOME III

>gi\_3881502\_emb\_CAA87421\_ (Z47357) ZK1128.2 [Caenorhabditis

elegans]

Seq. No. 26454

Contig ID 139937\_1.R1040



5'-most EST fua701040927.hl

Seq. No. 26455

Contig ID 139941\_1.R1040 5'-most EST gsf700698307.h1

Seq. No. 26456

Contig ID 139965\_1.R1040 5'-most EST ncj700983310.h1

Method BLASTN
NCBI GI g1217993
BLAST score 217
E value 1.0e-119
Match length 413
% identity 88

NCBI Description Glycine max dynamin-like protein SDL12A mRNA, complete cds

Seq. No. 26457

Contig ID 139977\_1.R1040 5'-most EST gsv701046585.h1

Seq. No. 26458

Contig ID 139989\_1.R1040 5'-most EST asn701141023.h1

Method BLASTX
NCBI GI g2880047
BLAST score 540
E value 3.0e-57
Match length 181
% identity 69

NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26459

Contig ID 140018\_1.R1040 5'-most EST kl1701205510.h1

Method BLASTX
NCBI GI g3249098
BLAST score 245
E value 2.0e-20
Match length 99
% identity 52

NCBI Description (AC003114) ESTs gb\_T04610, gb\_N38459, gb\_T45174, gb\_R30481 and gb\_N64971 come from this gene. [Arabidopsis thaliana]

Seq. No. 26460

Contig ID 140025\_1.R1040

5'-most EST g5676821

Seq. No. 26461

Contig ID 140029\_1.R1040 5'-most EST gsv701053383.h1

Seq. No. 26462

Contig ID 140030\_1.R1040 5'-most EST eep700863841.h1

Seq. No. 26463



```
140030 3.R1040
Contig ID
                  fde700\overline{8}76315.h1
5'-most EST
                  26464
Seq. No.
                   140033 1.R1040
Contig ID
                  uC-gmrominsoy029h05b1
5'-most EST
                  BLASTX
Method
                   g231573
NCBI GI
BLAST score
                   266
                   3.0e-26
E value
                   94
Match length
                   70
% identity
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                   >qi 99970 pir S24757 asparaginase (EC 3.5.1.1) -
                   narrow-leaved blue lupine >gi_19135_emb_CAA43099_ (X60691)
                   developing seed L-asparaginase [Lupinus angustifolius]
                   26465
Seq. No.
                   140070 1.R1040
Contig ID
                   jC-gmro02910019a06a1
5'-most EST
Seq. No.
                   26466
                   140070 2.R1040
Contig ID
5'-most EST
                   zsq701123769.h1
                   26467
Seq. No.
                   140072 1.R1040
Contig ID
5'-most EST
                   ncj700982317.hl
Seq. No.
                   26468
                   140079 1.R1040
Contig ID
5'-most EST
                   g5677849
                   26469
Seq. No.
                   140091 1.R1040
Contig ID
                   ncj700982406.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2244831
BLAST score
                   174
                   4.0e-13
E value
                   37
Match length
                   92
% identity
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   26470
                   140097 1.R1040
Contig ID
5'-most EST
                   fC-qmro7000748540r1
Method
                   BLASTN
                   q392822
NCBI GI
```

BLAST score 456 0.0e + 00E value Match length 464

100

NCBI Description Glycine max Williams cellulase gene, partial cds

Seq. No. 26471

% identity

Contig ID 140101 1.R1040



5'-most EST g5752519

Seq. No. 26472

Contig ID 140108\_1.R1040 5'-most EST ncj700982429.h1

Seq. No. 26473

Contig ID 140109\_1.R1040 5'-most EST ncj700982430.h1

Seq. No. 26474

Contig ID 140122\_1.R1040 5'-most EST ncj700982460.h1

Seq. No. 26475

Contig ID 140143\_1.R1040 5'-most EST ncj700982503.h1

Seq. No. 26476

Contig ID 140178\_1.R1040 5'-most EST zhf700961136.h1

Seq. No. 26477

Contig ID 140193 1.R1040 5'-most EST fua701041857.h1

Seq. No. 26478

Contig ID 140251\_1.R1040 5'-most EST ncj700982660.h1

Method BLASTN
NCBI GI g294667
BLAST score 210
E value 1.0e-114
Match length 530
% identity 85

NCBI Description Castor bean chloroplast beta-ketoacyl-ACP synthase (50 kDa

synthase) mRNA, complete cds

Seq. No. 26479

Contig ID 140262\_1.R1040 5'-most EST ncj700982674.h1

Method BLASTX
NCBI GI g4006878
BLAST score 401
E value 4.0e-39
Match length 134
% identity 55

NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No. 26480

Contig ID 140271\_1.R1040 5'-most EST ncj700982684.h1

Seq. No. 26481

Contig ID 140295\_1.R1040 5'-most EST ncj700982722.h1



Seq. No. 26482 Contig ID 140304 1.R1040 5'-most EST kmv700739574.h1 Method BLASTX NCBI GI g2262157 BLAST score 361 E value 1.0e-34

96 % identity 69 (AC002329) putative ligand-gated ion channel protein NCBI Description

[Arabidopsis thaliana]

Seq. No. 26483

Match length

Contig ID 140329 1.R1040 5'-most EST ncj700982775.h1

Method BLASTX NCBI GI g3785977 BLAST score 233 E value 1.0e-19 Match length 92 % identity 53

NCBI Description (AC005560) putative growth regulator protein [Arabidopsis

thaliana]

Seq. No. 26484

140330 1.R1040 Contig ID 5'-most EST leu701156303.h1

Method BLASTX NCBI GI g629561 BLAST score 440 E value 2.0e-43 Match length 217 % identity 41

NCBI Description SRG1 protein - Arabidopsis thaliana

>gi\_479047\_emb\_CAA55654\_ (X79052) SRG1 [Arabidopsis

thalianal

Seq. No. 26485

Contig ID 140382 1.R1040 5'-most EST ncj700982879.h1

Method BLASTX NCBI GI q3152572 BLAST score 322 E value 3.0e-30 Match length 78 % identity 90

(AC002986) Contains homology to DNAJ heatshock protein NCBI Description

gb\_U32803 from Haemophilus influenzae. [Arabidopsis

thaliana]

Seq. No. 26486

Contig ID 140385 1.R1040 5'-most EST  $jsh701\overline{0}64350.h1$ 

Method BLASTX NCBI GI g4006918 BLAST score 319 E value 2.0e-29



Match length 121 % identity 53

NCBI Description (Z99708) peroxidase like protein [Arabidopsis thaliana]

Seq. No. 26487

Contig ID 140394 1.R1040 5'-most EST kl1701212683.h1

Seq. No. 26488

Contig ID 140395\_1.R1040 5'-most EST ncj700982901.h1

Seq. No. 26489

Contig ID 140399\_1.R1040 5'-most EST jex700907547.h1

Seq. No. 26490

Contig ID 140416\_1.R1040 5'-most EST ncj700982958.h1

Method BLASTX
NCBI GI g2244833
BLAST score 263
E value 7.0e-23
Match length 137
% identity 44

NCBI Description (Z97337) centromere protein homolog [Arabidopsis thaliana]

Seq. No. 26491

Contig ID 140421 1.R1040 5'-most EST ncj700982975.h1

Seq. No. 26492

Contig ID 140470\_1.R1040 5'-most EST kwa701015680.h1

Seq. No. 26493

Contig ID 140493\_1.R1040 5'-most EST ncj700983103.h1

Method BLASTN
NCBI GI g2104523
BLAST score 35
E value 3.0e-10
Match length 67
% identity 88

NCBI Description Arabidopsis thaliana BAC T10M13 from chromosome IV, from

10.8 cM to 11.6 cM, complete sequence

Seq. No. 26494

Contig ID 140533 1.R1040 5'-most EST gsv701046889.h1

Seq. No. 26495

Contig ID 140543 1.R1040

5'-most EST g5752614

Seq. No. 26496

Contig ID 140551\_1.R1040



5'-most EST ncj700983211.h1

Seq. No. 26497

Contig ID 140556\_1.R1040 5'-most EST bth700849719.h1

Seq. No. 26498

Contig ID 140559\_1.R1040 5'-most EST ncj700983222.h1

Seq. No. 26499

Contig ID 140564\_1.R1040 5'-most EST ncj700983234.h1

Seq. No. 26500

Contig ID 140597 1.R1040

5'-most EST jC-gmro02800025g08d1

Seq. No. 26501

Contig ID 140610\_1.R1040 5'-most EST ncj700983319.h1

Method BLASTX
NCBI GI g1723738
BLAST score 213
E value 3.0e-17
Match length 104
% identity 20

NCBI Description HYPOTHETICAL 55.1 KD PROTEIN IN TRX1-RTA1 INTERGENIC REGION

>gi\_2131699\_pir\_\_S64534 hypothetical protein YGR211w yeast (Saccharomyces cerevisiae) >gi\_1323379\_emb\_CAA97238\_
(Z72996) ORF YGR211w [Saccharomyces cerevisiae] >gi\_3510466
(AF019769) zinc finger protein [Saccharomyces cerevisiae]

Seq. No. 26502

Contig ID 140638 1.R1040 5'-most EST gsv701047757.h1

Seq. No. 26503

Contig ID 140665\_1.R1040 5'-most EST ncj700983409.h1

Seq. No. 26504

Contig ID 140670\_1.R1040

5'-most EST jC-gmst02400063c02a1

Method BLASTX
NCBI GI 9728483
BLAST score 915
E value 5.0e-99
Match length 208
% identity 82

NCBI Description (L41046) endo-1,4-beta-glucanase [Pisum sativum]

Seq. No. 26505

Contig ID 140682\_1.R1040 5'-most EST xpa700793272.h1

Method BLASTX NCBI GI g2316016

```
425
```

BLAST score 425 E value 4.0e-42 Match length 112 % identity 73

NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No. 26506

Contig ID 140695\_1.R1040 5'-most EST pmv700891626.h1

Method BLASTX
NCBI GI g2244987
BLAST score 346
E value 1.0e-32
Match length 156
% identity 45

NCBI Description (Z97340) similarity to protein kinase - slime mold

(Dictyostelium) [Arabidopsis thaliana]

Seq. No. 26507

Contig ID 140696\_1.R1040

5'-most EST jC-gmro02910012b11a1

Seq. No. 26508

Contig ID 140697\_1.R1040

5'-most EST jC-gmro02910019b04d1

Seq. No. 26509

Contig ID 140706\_1.R1040 5'-most EST ncj700983470.h1

Seq. No. 26510

Contig ID 140729\_1.R1040 5'-most EST zzp700831407.h1

Method BLASTX
NCBI GI g2154997
BLAST score 421
E value 4.0e-41
Match length 196
% identity 46

NCBI Description (Y12503) Man9-mannosidase [Sus scrofa]

Seq. No. 26511

Contig ID 140748\_1.R1040 5'-most EST cf1700863544.h1

Method BLASTX
NCBI GI g4490937
BLAST score 245
E value 8.0e-21
Match length 126
% identity 37

NCBI Description (AJ132261) hypothetical helicase K12H4.8-like protein [Homo

sapiens]

Seq. No. 26512

Contig ID 140752\_1.R1040 5'-most EST jC-gmle01810060e10a1



Contig ID 140767\_1.R1040 5'-most EST ncj700983583.h1

Method BLASTX
NCBI GI g224797
BLAST score 165
E value 5.0e-17
Match length 64
% identity 70

NCBI Description urease [Canavalia ensiformis]

Seq. No. 26514

Contig ID 140777\_1.R1040 5'-most EST uC-gmropic009a07b1

Method BLASTX
NCBI GI g3953470
BLAST score 403
E value 2.0e-39
Match length 85
% identity 88

NCBI Description (AC002328) F20N2.15 [Arabidopsis thaliana]

Seq. No. 26515

Contig ID 140781\_1.R1040 5'-most EST fua701040863.h1

Seq. No. 26516

Contig ID 140801\_1.R1040 5'-most EST uC-gmronoir073c03b1

Seq. No. 26517

Contig ID 140809\_1.R1040 5'-most EST ncj700983651.h1

Seq. No. 26518

Contig ID 140813\_1.R1040 5'-most EST ncj700983655.h1

Method BLASTX
NCBI GI g3128173
BLAST score 407
E value 2.0e-57
Match length 121
% identity 90

NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26519

Contig ID 140828\_1.R1040 5'-most EST kl1701212139.h1

Method BLASTN
NCBI GI g3695062
BLAST score 194
E value 1.0e-105
Match length 402
% identity 87

NCBI Description Lotus japonicus rac GTPase activating protein 3 mRNA,

partial cds



Contig ID 140837\_1.R1040 5'-most EST jC-gmst02400053a10d1

Seq. No. 26521

Contig ID 140844 1.R1040 5'-most EST zhf700964855.h1

Method BLASTX
NCBI GI g4218120
BLAST score 277
E value 1.0e-24
Match length 61
% identity 82

NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis

thaliana]

Seq. No. 26522

Contig ID 140880\_1.R1040 5'-most EST asn701136306.h1

Method BLASTX
NCBI GI g4455326
BLAST score 675
E value 4.0e-71
Match length 171
% identity 71

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 26523

Contig ID 140888\_1.R1040 5'-most EST ncj700986805.h1

Seq. No. 26524

Contig ID 140902\_1.R1040 5'-most EST pcp700995354.h1

Seq. No. 26525

Contig ID 140916\_1.R1040 5'-most EST ncj700983850.h1

Seq. No. 26526

Contig ID 140937\_1.R1040 5'-most EST ncj700983884.h1

Method BLASTX
NCBI GI g2352492
BLAST score 559
E value 3.0e-66
Match length 197
% identity 67

NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis

thaliana] >gi 2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

Seq. No. 26527

Contig ID 140957\_1.R1040 5'-most EST leu701152930.h1

Method BLASTX NCBI GI g3785987



BLAST score 2.0e-09 E value 51 Match length 57 % identity

(AC005560) hypothetical protein [Arabidopsis thaliana] NCBI Description

26528 Seq. No.

140957 3.R1040 Contig ID  $k11701\overline{2}06601.h1$ 5'-most EST

Seq. No. 26529

140961 1.R1040 Contig ID ncj700983993.hl 5'-most EST

Seq. No. 26530

140962 1.R1040 Contig ID 5'-most EST bth700849269.hl

Seq. No. 26531

140985 1.R1040 Contig ID  $ncj700\overline{9}84068.h1$ 5'-most EST

Method BLASTX NCBI GI q2443886 BLAST score 148 2.0e-09 E value Match length 89 34 % identity

(AC002294) Unknown protein [Arabidopsis thaliana] NCBI Description

26532 Seq. No.

140986 1.R1040 Contig ID uC-gmropic025c08b1 5'-most EST

26533 Seq. No.

141007 1.R1040 Contig ID ncj700984122.hl 5'-most EST

Seq. No. 26534

141042 1.R1040 Contig ID ncj700984174.h1 5'-most EST

BLASTX Method g1304227 NCBI GI BLAST score 362 3.0e-37 E value 146 Match length 47 % identity

(D63781) Epoxide hydrolase [Glycine max] NCBI Description

>gi 2764804 emb CAA55293\_ (X78547) epoxide hydrolase

[Glycine max]

26535 Seq. No.

141047 1.R1040 Contig ID ncj700984182.hl 5'-most EST

BLASTX Method NCBI GI g3367537 BLAST score 470 5.0e-47E value



Match length 132 % identity 64

NCBI Description

(AC004392) Contains similarity to ANK repeat region of Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi\_485107 from Caenorhabditis elegans cosmid gb\_U00049. This gene is continued from unannotated gene on BAC F19K23 gb\_AC000375. [Arabid

Seq. No. 26536

Contig ID 141051\_1.R1040 5'-most EST ncj700984187.h1

Method BLASTX
NCBI GI g4539314
BLAST score 206
E value 4.0e-16
Match length 73
% identity 55

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 26537

Contig ID 141055\_1.R1040 5'-most EST ncj700984193.h1

Method BLASTX
NCBI GI g4218120
BLAST score 210
E value 5.0e-17
Match length 47
% identity 83

NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis

thaliana]

Seq. No. 26538

Contig ID 141061\_1.R1040 5'-most EST eep700864079.h1

Method BLASTX
NCBI GI g2088651
BLAST score 173
E value 2.0e-12
Match length 105
% identity 43

NCBI Description (AF002109) hypersensitivity-related gene 201 isolog

[Arabidopsis thaliana]

Seq. No. 26539

Contig ID 141088\_1.R1040 5'-most EST ncj700984246.h1

Seq. No. 26540

Contig ID 141091 1.R1040 5'-most EST ncj700984251.h1

Method BLASTN
NCBI GI g3869075
BLAST score 58
E value 5.0e-24
Match length 287
% identity 84

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



## MXK3, complete sequence [Arabidopsis thaliana]

```
26541
Sea. No.
                  141094 1.R1040
Contig ID
                  zhf700954649.h1
5'-most EST
Seq. No.
                  26542
                  141097_1.R1040
Contig ID
                  ncj700984263.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g541913
BLAST score
                  363
E value
                  5.0e-35
Match length
                  84
                  79
% identity
                  oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) -
NCBI Description
                  rape >gi 435011 emb CAA52069 (X73849) oleoyl-[acyl-carrier
                  protein] hydrolase [Brassica napus]
                  26543
Seq. No.
                  141114 1.R1040
Contig ID
5'-most EST
                  uC-gmropic020c06b1
                  26544
Seq. No.
                  141136 1.R1040
Contig ID
                  uC-gmropic035b03b1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4006876
BLAST score
                   235
                   2.0e-19
E value
Match length
                   92
% identity
                   61
                  (Z99707) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   26545
Seq. No.
                   141136 2.R1040
Contig ID
5'-most EST
                   asn701140108.hl
                   26546
Seq. No.
                   141146 1.R1040
Contig ID
                   ncj700984337.hl
5'-most EST
                   26547
Seq. No.
                   141161 1.R1040
Contig ID
                   fC-gmle700555881b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1170949
BLAST score
                   227
                   1.0e-18
E value
                   82
Match length
                   55
% identity
                   SERINE/THREONINE-PROTEIN KINASE MHK >gi 481207_pir_ S38327
NCBI Description
                   protein kinase - Arabidopsis thaliana >gi_166811 (L07249)
```

Seq. No. 26548

Contig ID 141178\_1.R1040

protein kinase [Arabidopsis thaliana]



```
sat701003559.hl
5'-most EST
                   26549
Seq. No.
                   141221 1.R1040
Contig ID
                   ncj700984530.h1
5'-most EST
Seq. No.
                   26550
                   141239 1.R1040
Contig ID
5'-most EST
                   ncj700984573.hl
                   BLASTX
Method
NCBI GI
                   q3212868
BLAST score
                   534
E value
                   2.0e-54
                   170
Match length
                   62
% identity
                   (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                   26551
Seq. No.
                   141260 1.R1040
Contig ID
                   sat701007938.hl
5'-most EST
                   BLASTX
Method
                   q1350783
NCBI GI
BLAST score
                   168
E value
                   4.0e-12
                   80
Match length
                   53
% identity
                   RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR
NCBI Description
                   >qi 282883 pir S27756 receptor-like protein kinase
                   precursor - Arabidopsis thaliana >gi_166850 (M84660)
                    receptor-like protein kinase [Arabidopsis thaliana]
                   >gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]
                    26552
Seq. No.
                    141286 1.R1040
Contig ID
                   ncj700984706.hl
5'-most EST
Method
                    BLASTX
NCBI GI
                    q4490756
BLAST score
                    187
E value
                    2.0e-16
Match length
                    106
                    41
% identity
NCBI Description (AL035708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    26553
                    141300 1.R1040
Contig ID
5'-most EST
                    ncj700984726.h1
Method
                    BLASTX
                    q3080427
NCBI GI
BLAST score
                    1541
                    1.0e-172
E value
```

338 Match length 88 % identity

(AL022604) putative protein [Arabidopsis thaliana] NCBI Description

26554 Seq. No.

141303 1.R1040 Contig ID



5'-most EST jC-gmst02400055f01d1

Method BLASTX
NCBI GI g2288887
BLAST score 164
E value 3.0e-11
Match length 44
% identity 70

NCBI Description (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis

thaliana] >gi 3250736\_emb\_CAA76803\_ (Y17593) mevalonate

diphosphate decarboxylase [Arabidopsis thaliana]

>gi\_3786002 (AC005499) mevalonate diphosphate decarboxylase

[Arabidopsis thaliana]

Seq. No. 26555

Contig ID 141332\_1.R1040 5'-most EST ncj700984770.h1

Method BLASTX
NCBI GI g3152559
BLAST score 490
E value 5.0e-49
Match length 197
% identity 49

NCBI Description (AC002986) Similarity to A. thaliana gene product

F21M12.20, gb AC000132. EST gb Z25651 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 26556

Contig ID 141335\_1.R1040 5'-most EST epx701110420.h1

Seq. No. 26557

Contig ID 141345\_1.R1040 5'-most EST ncj700984788.h1

Method BLASTX
NCBI GI g2244852
BLAST score 207
E value 1.0e-16
Match length 51
% identity 80

NCBI Description (297337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26558

Contig ID 141404\_1.R1040 5'-most EST ncj700984884.h1

Method BLASTX
NCBI GI g4204293
BLAST score 183
E value 6.0e-14
Match length 83
% identity 45

NCBI Description (AC003027) lcl\_prt\_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 26559

Contig ID 141442\_1.R1040 5'-most EST leu701154394.h1



Contig ID 141448\_1.R1040 5'-most EST kl1701211248.h1

Seq. No. 26561

Contig ID 141466\_1.R1040 5'-most EST ncj700984989.h1

Seq. No. 26562

Contig ID 141510\_1.R1040 5'-most EST jex700907689.h1

Seq. No. 26563

Contig ID 141530\_2.R1040 5'-most EST jex700903484.h1

Method BLASTX
NCBI GI g4006900
BLAST score 227
E value 6.0e-19
Match length 76
% identity 57

NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26564

Contig ID 141566\_1.R1040

5'-most EST uC-gmrominsoy195d07b1

Method BLASTX
NCBI GI g3702323
BLAST score 464
E value 2.0e-46
Match length 131
% identity 73

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 26565

Contig ID 141571 1.R1040 5'-most EST asn701135056.h1

Seq. No. 26566

Contig ID 141584 1.R1040 5'-most EST sat701014302.h1

Seq. No. 26567

Contig ID 141588\_1.R1040 5'-most EST kl1701215142.h1

Method BLASTX
NCBI GI g1777312
BLAST score 145
E value 1.0e-08
Match length 35
% identity 80

NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No. 26568

Contig ID 141605\_1.R1040 5'-most EST jsh701064332.h1



Method BLASTX
NCBI GI g1532165
BLAST score 222
E value 3.0e-18
Match length 85
% identity 53

NCBI Description (U63815) similar to dehydrogenase encoded by GenBank Accession Number S39508; localized according to blastn similarity to EST sequences; therefore, the coding span

corresponds only to an area of similarity since the

initation codon and stop

Seq. No. 26569

Contig ID 141636 1.R1040 5'-most EST kll701203753.h2

Seq. No. 26570

Contig ID 141650\_1.R1040 5'-most EST uC-gmropic108g04b1

Seq. No. 26571

Contig ID 141650\_2.R1040

5'-most EST uC-gmrominsoy256e09b1

Seq. No. 26572

Contig ID 141663\_1.R1040 5'-most EST zhf700962075.h1

Seq. No. 26573

Contig ID 141666\_1.R1040 5'-most EST kl1701214514.h1

Seq. No. 26574

Contig ID 141691\_1.R1040 5'-most EST ncj700985352.h1

Method BLASTX
NCBI GI 94314358
BLAST score 380
E value 1.0e-36
Match length 128
% identity 56

NCBI Description (AC006340) putative kinesin heavy chain protein

[Arabidopsis thaliana]

Seq. No. 26575

Contig ID 141733\_1.R1040

5'-most EST jC-gmf102220052a02a1

Seq. No. 26576

Contig ID 141739\_1.R1040

5'-most EST uC-gmflminsoy044g10b1

Method BLASTX
NCBI GI g4538987
BLAST score 279
E value 3.0e-24
Match length 228
% identity 25



(AJ133777) gamma-adaptin 2 [Arabidopsis thaliana]

Seq. No. 26577

NCBI Description

Contig ID 141771\_1.R1040 5'-most EST zzp700834386.h1

Seq. No. 26578

Contig ID 141773\_1.R1040 5'-most EST pcp700992358.h1

Method BLASTX
NCBI GI g2244815
BLAST score 143
E value 5.0e-09
Match length 51
% identity 57

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26579

Contig ID 141782 1.R1040

5'-most EST uC-gmrominsoy060f03b1

Method BLASTX
NCBI GI g2632103
BLAST score 207
E value 2.0e-16
Match length 70
% identity 60

NCBI Description (Z98759) arginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 26580

Contig ID 141782\_2.R1040 5'-most EST smc700748696.h1

Seq. No. 26581

Contig ID 141784\_1.R1040

5'-most EST jC-gmst02400052d09a1

Method BLASTX
NCBI GI g3618320
BLAST score 192
E value 2.0e-14
Match length 111
% identity 42

NCBI Description (AB001888) zinc finger protein [Oryza sativa]

Seq. No. 26582

Contig ID 141849\_1.R1040 5'-most EST wrg700790875.h1

Seq. No. 26583

Contig ID 141863 1.R1040

5'-most EST jC-gmst02400071f06a1

Seq. No. 26584

Contig ID 141867\_1.R1040 5'-most EST ncj700985591.h1

Seq. No. 26585

Contig ID 141877\_1.R1040



```
5'-most EST
                  ncj700985611.hl
                  BLASTX
Method
NCBI GI
                  g2702268
                  396
BLAST score
                  2.0e-38
E value
Match length
                  114
% identity
                  66
                  (AC003033) putative cellulase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  26586
                  141877 2.R1040
Contig ID
5'-most EST
                  epx701109545.h1
                  BLASTX
Method
NCBI GI
                  g2702268
                  223
BLAST score
                  2.0e-18
E value
                  81
Match length
                  57
% identity
                  (AC003033) putative cellulase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  26587
                  141881 1.R1040
Contig ID
5'-most EST
                  ncj700985615.h1
                  BLASTX
Method
NCBI GI
                  q4210449
BLAST score
                  362
                   5.0e-34
E value
                   273
Match length
% identity
NCBI Description
                  (AB016471) ARR1 protein [Arabidopsis thaliana]
Seq. No.
                   26588
Contig ID
                   141903 1.R1040
                   pcp700995658.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3805851
BLAST score
                   400
E value
                   6.0e-39
Match length
                   102
                   72
% identity
NCBI Description
                  (AL031986) putative protein [Arabidopsis thaliana]
Seq. No.
                   26589
Contig ID
                   141943 1.R1040
5'-most EST
                  pmv700890950.h1
                   26590
Seq. No.
                   141956 1.R1040
Contig ID
```

ncj700985737.h1 5'-most EST

Seq. No. 26591

141997 1.R1040 Contig ID 5'-most EST  $asn701\overline{1}32792.h1$ 

26592 Seq. No.

Contig ID 142003 1.R1040 5'-most EST ncj700985810.h1

```
BLASTX
Method
                  g807698
NCBI GI
                  361
BLAST score
                  2.0e-34
E value
                  129
Match length
                  57
% identity
                  (D32206) prepro-cucumisin [Cucumis melo]
NCBI Description
                  26593
Seq. No.
                  142010 1.R1040
Contig ID
5'-most EST
                  leu701152243.h1
                  26594
Seq. No.
                  142017 1.R1040
Contig ID
                  zhf700952286.h1
5'-most EST
                  26595
Seq. No.
                   142022 1.R1040
Contig ID
                  ncj700987179.h1
5'-most EST
                   26596
Seq. No.
                   142024 1.R1040
Contig ID
                   pcp700989817.h1
5'-most EST
                   BLASTX
Method
                   g2651316
NCBI GI
                   225
BLAST score
                   1.0e-18
E value
                   62
Match length
                   79
% identity
                  (AC002336) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   26597
                   142025 1.R1040
Contig ID
```

5'-most EST wrg700790609.h2

26598 Seq. No.

142044 1.R1040 Contig ID ncj700985869.h15'-most EST

26599 Seq. No.

142046 1.R1040 Contig ID 5'-most EST  $ncj700\overline{9}85871.h1$ 

Seq. No. 26600

142103 1.R1040 Contig ID 5'-most EST ncj700985949.h1

26601 Seq. No.

142104 1.R1040 Contig ID

jC-qmst02400029d04a1 5'-most EST

BLASTX Method g1553133 NCBI GI 159 BLAST score 1.0e-10 E value Match length 119 % identity

NCBI Description (U64722) actin-fragmin kinase [Physarum polycephalum]



Contig ID 142117\_1.R1040 5'-most EST ncj700987991.h1

Method BLASTN
NCBI GI g4140025
BLAST score 186
E value 1.0e-100
Match length 428

% identity 86
NCBI Description Vigna mungo UF3GaT mRNA for flavonoid 3-O-galactosyl

transferase, complete cds

Seq. No. 26603

Contig ID 142123\_1.R1040 5'-most EST epx701105074.h1

Seq. No. 26604

Contig ID 142133\_1.R1040 5'-most EST smc700747118.h1

Seq. No. 26605

Contig ID 142139\_1.R1040 5'-most EST gsv701056689.h1

Seq. No. 26606

Contig ID 142148\_1.R1040 5'-most EST ncj700986016.h1

Seq. No. 26607

Contig ID 142193\_1.R1040 5'-most EST zhf700959032.h1

Seq. No. 26608

Contig ID 142193\_2.R1040 5'-most EST jex700906403.h1

Seq. No. 26609

Contig ID 142206\_1.R1040

5'-most EST uC-gmflminsoy075a05b1

Seq. No. 26610

Contig ID 142232\_1.R1040

5'-most EST jC-gmle01810022c01a1

Method BLASTX
NCBI GI g4490325
BLAST score 398
E value 7.0e-39
Match length 113
% identity 69

NCBI Description (AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26611

Contig ID 142237\_1.R1040 5'-most EST ncj700986140.h1 Method BLASTX

Method BLASTX NCBI GI g2443887



BLAST score 520 E value 4.0e-53 Match length 130 % identity 73

NCBI Description

(AC002294) Similar to transcription factor

gb\_Z46606\_1658307 and others [Arabidopsis thaliana]

Seq. No. 26612

Contig ID 142239\_1.R1040 5'-most EST zhf700952977.h1

Seq. No. 26613

Contig ID 142253\_1.R1040 5'-most EST zhf700965103.h1

Seq. No. 26614

Contig ID 142267\_1.R1040 5'-most EST ncj700986195.h1

Seq. No. 26615

Contig ID 142272\_1.R1040 5'-most EST ncj700986207.h1

Seq. No. 26616

Contig ID 142314\_1.R1040 5'-most EST uC-gmropic112h07b1

Method BLASTX
NCBI GI g2501356
BLAST score 666
E value 4.0e-70
Match length 138
% identity 88

NCBI Description TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK)

>gi\_1658322\_emb\_CAA90427\_ (Z50099) transketolase precursor

[Solanum tuberosum]

Seq. No. 26617

Contig ID 142317\_1.R1040 5'-most EST ncj700986301.h1

Seq. No. 26618

Contig ID 142325\_1.R1040

5'-most EST uC-gmflminsoy036d01b1

Seq. No. 26619

Contig ID 142355 1.R1040 5'-most EST asn701142632.h1

Seq. No. 26620

Contig ID 142361\_1.R1040 5'-most EST kl1701208980.h1

Method BLASTX
NCBI GI g4104056
BLAST score 456
E value 9.0e-46
Match length 107
% identity 73



NCBI Description (AF031194) S276 [Triticum aestivum]

Seq. No. 26621

Contig ID 142375\_1.R1040 5'-most EST crh700854918.h1

Seq. No. 26622

Contig ID 142379\_1.R1040

5'-most EST uC-gmflminsoy067b12b1

Seq. No. 26623

Contig ID 142385\_1.R1040 5'-most EST ncj700986408.h1

Method BLASTX
NCBI GI g4185499
BLAST score 335
E value 4.0e-31
Match length 150
% identity 44

NCBI Description (AF096095) fertilization-independent seed 2 protein

[Arabidopsis thaliana] >gi 4185501 (AF096096)

fertilization-independent seed 2 protein [Arabidopsis

thaliana]

Seq. No. 26624

Contig ID 142400\_1.R1040 5'-most EST zhf700964744.h1

Seq. No. 26625

Contig ID 142416\_1.R1040 5'-most EST jC-gmro02800033e10a1

Method BLASTX
NCBI GI g2262173
BLAST score 441
E value 6.0e-44
Match length 112

Match length 112 % identity 78

NCBI Description (AC002329) NADPH thioredoxin reductase [Arabidopsis

thaliana]

Seq. No. 26626

Contig ID 142419\_1.R1040 5'-most EST jex700906483.h1

Method BLASTX
NCBI GI g1345132
BLAST score 376
E value 8.0e-44
Match length 117
% identity 80

NCBI Description (U47029) ERECTA [Arabidopsis thaliana]

>gi\_1389566\_dbj\_BAA11869\_ (D83257) receptor protein kinase

[Arabidopsis thaliana] >gi\_3075386 (AC004484) receptor

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 26627

Contig ID 142424\_1.R1040 5'-most EST kmv700740451.h1



Contig ID 142425\_1.R1040 5'-most EST ncj700986457.h1

Seq. No. 26629

Contig ID 142452 1.R1040 5'-most EST ncj700986494.h1

Seq. No. 26630

Contig ID 142472\_1.R1040 5'-most EST ncj700986527.h1

Seq. No. 26631

Contig ID 142473 1.R1040

5'-most EST uC-gmflminsoy064c11b1

Method BLASTX
NCBI GI g4539452
BLAST score 348
E value 4.0e-33
Match length 98
% identity 60

NCBI Description (AL049500) putative phosphoribosylanthranilate transferase

[Arabidopsis thaliana]

Seq. No. 26632

Contig ID 142478\_1.R1040

5'-most EST uC-gmrominsoy157f04b1

Seq. No. 26633

Contig ID 142488\_1.R1040 5'-most EST ncj700986543.h1

Seq. No. 26634

Contig ID 142498\_1.R1040 5'-most EST hrw701060354.h1

Seq. No. 26635

Contig ID 142501\_1.R1040 5'-most EST ncj700987295.h1

Seq. No. 26636

Contig ID 142504\_1.R1040 5'-most EST smc700746405.h1

Seq. No. 26637

Contig ID 142505\_1.R1040 5'-most EST jex700907810.h1

Seq. No. 26638

Contig ID 142511\_1.R1040 5'-most EST epx701107806.h1

Method BLASTX
NCBI GI g2618684
BLAST score 292
E value 7.0e-42
Match length 105



% identity 83

NCBI Description (AC002510) putative

UDP-N-acetylglucosamine--dolichyl-phosphate

N-acetylglucosaminephosphotransferase [Arabidopsis

thaliana] >gi\_3241947 (AC004625) putative UDP-N-acetylglucosamine--dolichyl-phosphate

N-acetylglucosaminephosphotransferase [Arabidopsis

thaliana]

Seq. No. 26639

Contig ID 142526 1.R1040 5'-most EST wrg700791886.h1

Seq. No. 26640

Contig ID 142531\_1.R1040 5'-most EST ncj700986608.h1

Method BLASTX
NCBI GI g509810
BLAST score 160
E value 6.0e-11
Match length 76
% identity 46

NCBI Description (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No. 26641

Contig ID 142533\_1.R1040 5'-most EST ncj700986612.h1

Method BLASTX
NCBI GI g4544403
BLAST score 259
E value 6.0e-22
Match length 81
% identity 56

NCBI Description (AC007047) putative glucan endo-1,3-beta-D-glucosidase

precursor [Arabidopsis thaliana]

Seq. No. 26642

Contig ID 142533 2.R1040 5'-most EST kl1701212260.h1

Method BLASTX
NCBI GI g4544403
BLAST score 152
E value 8.0e-10
Match length 48
% identity 54

NCBI Description (AC007047) putative glucan endo-1,3-beta-D-glucosidase

precursor [Arabidopsis thaliana]

Seq. No. 26643

Contig ID 142533\_3.R1040 5'-most EST fC-gmf1700901194a1

Method BLASTX
NCBI GI g4544403
BLAST score 141
E value 6.0e-09
Match length 96
% identity 35





(AC007047) putative glucan endo-1,3-beta-D-glucosidase NCBI Description precursor [Arabidopsis thaliana]

Seq. No.

26644 Contig ID 142558 1.R1040 ncj700986645.hl 5'-most EST

26645 Seq. No.

Contig ID 142562 1.R1040 ncj700986652.hl 5'-most EST

26646 Seq. No.

142592 1.R1040 Contig ID 5'-most EST bth700849607.h1

26647 Seq. No.

142595 1.R1040 Contig ID 5'-most EST zsg701125958.hl

Seq. No. 26648

142596 1.R1040 Contig ID ncj700986706.h15'-most EST

BLASTX Method NCBI GI q3738297 BLAST score 312 E value 2.0e-28 130 Match length 16 % identity

(AC005309) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 26649

142610 1.R1040 Contig ID  $ncj700\overline{9}86731.h1$ 5'-most EST

26650 Seq. No.

Contig ID 142615 1.R1040 5'-most EST ncj700986737.h1

26651 Seq. No.

142628 1.R1040 Contig ID 5'-most EST sat701010007.h2

BLASTX Method NCBI GI q477430 BLAST score 418 3.0e-41E value Match length 122 % identity

NCBI Description nucleolar protein p120 - mouse (fragment)

Seq. No. 26652

Contig ID 142642 1.R1040 5'-most EST vzy700750782.h1

Seq. No. 26653

142681 1.R1040 Contig ID 5'-most EST ncj700986835.hl



Contig ID 142716\_1.R1040 5'-most EST vzy700753607.h1

Seq. No. 26655

Contig ID 142721\_1.R1040 5'-most EST kl1701212835.h1

Seq. No. 26656

Contig ID 142733\_2.R1040 5'-most EST leu701151255.h1

Method BLASTX
NCBI GI g4103757
BLAST score 256
E value 3.0e-22
Match length 55
% identity 91

NCBI Description (AF027376) MADS1 [Corylus avellana]

Seq. No. 26657

Contig ID 142759\_1.R1040 5'-most EST pcp700990417.h1

Seq. No. 26658

Contig ID 142792\_1.R1040 5'-most EST ncj700987043.h1

Method BLASTX
NCBI GI g3201554
BLAST score 396
E value 1.0e-66
Match length 169
% identity 76

NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No.

Contig ID 142801\_1.R1040 5'-most EST ncj700987054.h1

Seq. No. 26660

Contig ID 142832 1.R1040

5'-most EST uC-gmrominsoy111h09b1

26659

Method BLASTX
NCBI GI g2459437
BLAST score 197
E value 3.0e-15
Match length 77
% identity 62

NCBI Description (AC002332) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26661

Contig ID 142837\_1.R1040 5'-most EST ncj700987110.h1

Seq. No. 26662

Contig ID 142861\_1.R1040

5'-most EST uC-gmflminsoy007a10b1

Method BLASTX

4160



g4544436 NCBI GI 295 BLAST score 5.0e-28 E value 139 Match length 49 % identity (AC006592) anthocyanidin-3-glucoside rhamnosyltransferase, NCBI Description 3' partial [Arabidopsis thaliana] 26663 Seq. No. Contig ID 142866 1.R1040  $leu701\overline{1}56129.h1$ 5'-most EST

Method BLASTX
NCBI GI g3242728
BLAST score 221
E value 9.0e-18
Match length 204
% identity 39

NCBI Description (AC003040) unknown protein [Arabidopsis thaliana]

Seq. No. 26664

Contig ID 142871\_1.R1040 5'-most EST ncj700987156.h1

Seq. No. 26665

Contig ID 142883 1.R1040

5'-most EST jC-gmst02400065e08a2

Method BLASTX
NCBI GI g2760839
BLAST score 228
E value 1.0e-18
Match length 101
% identity 49

NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 26666

Contig ID 142885\_1.R1040 5'-most EST dpv701100860.h1

Method BLASTX
NCBI GI g4193320
BLAST score 465
E value 7.0e-47
Match length 99
% identity 84

NCBI Description (AF045473) histone deacetylase [Zea mays]

Seq. No. 26667

Contig ID 142907\_1.R1040

5'-most EST jC-gmfl02220137a09a1

Seq. No. 26668

Contig ID 142913 1.R1040

5'-most EST  $jC-gmf\overline{1}02220080b07a1$ 

Seq. No. 26669

Contig ID 142915\_1.R1040 5'-most EST ncj700987212.h1

Method BLASTX



NCBI GI g3122595 BLAST score 118 E value 1.0e-10 Match length 57 % identity 55

NCBI Description PROBABLE RNA-DEPENDENT HELICASE P72 (DEAD-BOX PROTEIN P72)

>gi\_1592565 (U59321) DEAD-box protein p72 [Homo sapiens]

>gi\_2832596 emb CAB09792 (Z97056) dJ434P1.3 [Homo sapiens]

Seq. No. 26670

Contig ID 142920\_1.R1040 5'-most EST uC-gmropic037d11b1

Seq. No. 26671

Contig ID 142923 1.R1040 5'-most EST kmv700741889.h1

Seq. No. 26672

Contig ID 142945\_1.R1040 5'-most EST eep700864944.h1

Seq. No. 26673

Contig ID 142957 1.R1040

5'-most EST uC-gmrominsoy169a02b1

Method BLASTX
NCBI GI g2494034
BLAST score 602
E value 2.0e-62
Match length 188
% identity 62

NCBI Description DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1) >gi 2129573 pir S71467 diacylglycerol kinase -

Arabidopsis thaliana >gi\_1374772\_dbj\_BAA09856\_ (D63787)

diacylglycerol kinase [Arabidopsis thaliana]

Seq. No. 26674

Contig ID 142960\_1.R1040

5'-most EST jC-gmfl02220136b04a1

Method BLASTX
NCBI GI g2245004
BLAST score 495
E value 5.0e-50
Match length 160
% identity 57

NCBI Description (Z97341) similarity to membrane transport protein

[Arabidopsis thaliana]

Seq. No. 26675

Contig ID 142966\_1.R1040 5'-most EST asn701139805.h1

Seq. No. 26676

Contig ID 142994 1.R1040

5'-most EST jC-gmro02910075e08a1

Seq. No. 26677

Contig ID 142995\_1.R1040



5'-most EST zhf700953284.h1

Method BLASTX
NCBI GI g3004565
BLAST score 280
E value 8.0e-25
Match length 86
% identity 69

NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 26678

Contig ID 143010 1.R1040

5'-most EST uC-gmrominsoy042d06b1

Method BLASTX
NCBI GI g2995370
BLAST score 156
E value 1.0e-10
Match length 66
% identity 39

NCBI Description (AL022245) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 26679

Contig ID 143018\_1.R1040 5'-most EST pxt700944424.h1

Seq. No. 26680

Contig ID 143025\_1.R1040 5'-most EST ncj700987375.h1

Method BLASTX
NCBI GI g2920706
BLAST score 145
E value 2.0e-09
Match length 62
% identity 48

NCBI Description (Y13568) beta-xylosidase [Emericella nidulans]

Seq. No. 26681

Contig ID 143055\_1.R1040

5'-most EST uC-gmrominsoy245a02b1

Seq. No. 26682

Contig ID 143057\_1.R1040 5'-most EST ncj700987429.h1

Seq. No. 26683

Contig ID 143118\_1.R1040 5'-most EST ncj700987533.h1

Method BLASTX
NCBI GI g4151068
BLAST score 488
E value 2.0e-49
Match length 97
% identity 93

NCBI Description (Y10862) ribonucleotide reductase [Nicotiana tabacum]

Seq. No. 26684

Contig ID 143126\_1.R1040 5'-most EST ncj700987549.h1



BLASTX Method g1491710 NCBI GI 125 BLAST score 3.0e-10 E value 65 Match length 41 % identity (X96506) alpha subunit; forms heterodimer with NC2 NCBI Description alpha/Dr1 [Homo sapiens] 26685 Seq. No. 143179 1.R1040 Contig ID jC-gmfl02220073g11a1 5'-most EST 26686 Seq. No. 143238 1.R1040 Contig ID 5'-most EST  $ncj700\overline{9}87731.h1$ 26687 Seq. No. 143253 1.R1040 Contig ID uC-gmrominsoy111d06b1 5'-most EST BLASTX Method NCBI GI q2501296 BLAST score 301 4.0e-27 E value 77 Match length 71 % identity DNA GYRASE SUBUNIT B >gi\_1652801\_dbj\_BAA17720\_ (D90908) DNA NCBI Description gyrase B subunit [Synechocystis sp.] 26688 Seq. No. 143259 1.R1040 Contig ID 5'-most EST  $ncj700\overline{9}87765.h1$ 26689 Seq. No. 143278 1.R1040 Contig ID gsv701048101.h1 5'-most EST Seq. No. 26690 143278 3.R1040 Contig ID 5'-most EST zzp700835694.h1 26691 Seq. No. 143286 1.R1040 Contig ID ncj700987804.hl 5'-most EST BLASTX Method q4467111 NCBI GI BLAST score 333 4.0e-31 E value

99 Match length % identity 66

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 26692

143291 1.R1040 Contig ID 5'-most EST jC-qmst02400029g04a1

Method BLASTN NCBI GI q166411



BLAST score 195 E value 1.0e-105 Match length 463 % identity 85

NCBI Description Medicago sativa NADH-glutamate synthase mRNA, comlete cds

Seq. No. 26693

Contig ID 143326 1.R1040 5'-most EST jsh701067464.h1

Method BLASTX
NCBI GI g4204285
BLAST score 408
E value 9.0e-40
Match length 167
% identity 49

NCBI Description (AC003027) 1cl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 26694

Contig ID 143333\_1.R1040 5'-most EST ncj700987868.h1

Seq. No. 26695

Contig ID 143335 1.R1040

5'-most EST jC-gmro02910063d01a1

Seq. No. 26696

Contig ID 143342\_1.R1040 5'-most EST jC-gmro02800035f12d1

Method BLASTX
NCBI GI g3319341
BLAST score 224
E value 3.0e-18
Match length 44
% identity 82

NCBI Description (AF077407) similar to Medicago sativa nucleic acid binding

protein Alfin-1 (GB:L07291) [Arabidopsis thaliana]

Seq. No. 26697

Contig ID 143375\_1.R1040 5'-most EST bth700845896.h1

Method BLASTX
NCBI GI g2983347
BLAST score 163
E value 5.0e-11
Match length 89
% identity 43

NCBI Description (AE000707) hemolysin [Aquifex aeolicus]

Seq. No. 26698

Contig ID 143401\_1.R1040 5'-most EST zsg701126126.h1

Method BLASTX
NCBI GI g4455359
BLAST score 226
E value 7.0e-19
Match length 77



% identity

(AL035524) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

26699

Contig ID 5'-most EST 143463 1.R1040

Method

ncj700988163.hl

NCBI GI

BLASTN g16508

BLAST score

75

E value Match length

4.0e-34 147

% identity

88

NCBI Description

A.thaliana DNA for S-adenosylmethionine synthetase gene

sam-1 >gi 166871 gb M55077 ATHSAM A.thaliana

S-adenosylmethionine synthetase gene, complete cds

Seq. No.

26700

Contig ID 5'-most EST 143470 1.R1040 zhf700955313.h1

Method NCBI GI BLASTX

BLAST score

g1495251 565

E value Match length 2.0e-58

% identity

124 87

NCBI Description

(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.

26701

Contig ID 5'-most EST 143472 1.R1040 zhf700952045.hl

Method

BLASTX

NCBI GI

g1172441

BLAST score

163

E value

7.0e-11

Match length

48

% identity

67 POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi\_99685\_pir\_\_S21883

NCBI Description

DNA-binding protein POSF21 - Arabidopsis thaliana >gi 16429 emb CAA43366 (X61031) posF21 [Arabidopsis

thaliana]

Seq. No.

26702

Contig ID

143472 2.R1040

5'-most EST

smc700744982.h1

Seq. No.

26703

Contig ID

143477 1.R1040 sat701012012.hl

5'-most EST

26704

Seq. No. Contig ID

143519 1.R1040

5'-most EST

ncj700988274.h1

Seq. No.

26705

Contig ID

143520 1.R1040

5'-most EST

ncj700988275.hl

Method

BLASTX



81

58

Match length

NCBI Description

% identity

```
g2832664
NCBI GI
                   214
BLAST score
                   1.0e-17
E value
                   73
Match length
                   58
% identity
                   (AL021710) pollen-specific protein - like [Arabidopsis
NCBI Description
                  thaliana]
                   26706
Seq. No.
                   143582 1.R1040
Contig ID
                   ncj700988393.hl
5'-most EST
Method
                   BLASTX
                   q4455278
NCBI GI
BLAST score
                   128
                   4.0e-10
E value
Match length
                   90
% identity
                   43
                  (AL035527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   26707
Seq. No.
                   143588 1.R1040
Contig ID
                   uC-gmflminsoy075c09b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2660677
BLAST score
                   722
                   2.0e-76
E value
                   251
Match length
                   59
% identity
                  (AC002342) unknown protein [Arabidopsis thaliana]
NCBI Description
                   26708
Seq. No.
                   143607 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy035b02b1
                   26709
Seq. No.
                   143621 1.R1040
Contig ID
                   fC-qmle700871981f3
5'-most EST
                   BLASTX
Method
                   q2623300
NCBI GI
BLAST score
                   1045
                   1.0e-114
E value
                   372
Match length
                   55
% identity
                   (AC002409) putative protein phosphatase 2C [Arabidopsis
NCBI Description
                   thaliana]
                   26710
Seq. No.
                   143639 1.R1040
Contig ID
                   1eu701\overline{1}47859.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3510254
                   227
BLAST score
E value
                   8.0e-19
```

(AC005310) putative zinc transporter [Arabidopsis thaliana]



Contig ID 143649\_1.R1040 5'-most EST ncj700988522.h1

Seq. No. 26712

Contig ID 143656\_1.R1040 5'-most EST ncj700988535.h1

Seq. No. 26713

Contig ID 143658\_1.R1040 5'-most EST ncj700988541.h1

Seq. No. 26714

Contig ID 143668\_1.R1040 5'-most EST ncj700988559.h1

Method BLASTX
NCBI GI g1169128
BLAST score 228
E value 1.0e-18
Match length 111
% identity 42

NCBI Description SERINE/THREONINE-PROTEIN KINASE CTR1 >gi\_166680 (L08789)

protein kinase [Arabidopsis thaliana] >gi\_166682 (L08790)

protein kinase [Arabidopsis thaliana]

Seq. No. 26715

Contig ID 143680\_1.R1040

5'-most EST jC-gmro02910016e12a1

Seq. No. 26716

Contig ID 143730\_1.R1040 5'-most EST zhf700964905.h1

Seq. No. 26717

Contig ID 143735\_1.R1040 5'-most EST ncj700988655.h1

Method BLASTX
NCBI GI g1245343
BLAST score 242
E value 2.0e-20
Match length 76
% identity 58

NCBI Description (U50194) tripeptidylpeptidase II [Rattus norvegicus]

Seq. No. 26718

Contig ID 143755\_1.R1040 5'-most EST gsv701044887.h1

Method BLASTX
NCBI GI g2160182
BLAST score 345
E value 2.0e-32
Match length 104
% identity 66

NCBI Description (AC000132) ESTs gb\_ATTS1236, gb\_T43334, gb\_N97019, gb\_AA395203

come from this gene. [Arabidopsis thaliana]

Seq. No. 26719



Contig ID 143765\_1.R1040 5'-most EST pst700645716.h1

Method BLASTX
NCBI GI g2245009
BLAST score 201
E value 7.0e-16
Match length 54
% identity 70

NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26720

Contig ID 143912\_1.R1040 5'-most EST txt700731337.h1

Seq. No. 26721

Contig ID 143912\_2.R1040 5'-most EST zhf700958462.h1

Seq. No. 26722

Contig ID 143936\_1.R1040 5'-most EST kl1701207242.h1

Seq. No. 26723

Contig ID 143962\_1.R1040 5'-most EST txt700731496.h1

Method BLASTX
NCBI GI g1174718
BLAST score 178
E value 2.0e-13
Match length 41
% identity 83

NCBI Description PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR

>gi\_322579\_pir\_\_JQ1674 receptor protein kinase TMK1 (EC
2.7.1.-) precursor - Arabidopsis thaliana >gi 166888

(L00670) protein kinase [Arabidopsis thaliana]

Seq. No. 26724

Contig ID 144083\_1.R1040 5'-most EST kl1701202564.h1

Seq. No. 26725

Contig ID 144117\_1.R1040

5'-most EST g5342789
Method BLASTX
NCBI GI g1705678
BLAST score 364
E value 1.0e-34
Match length 108
% identity 72

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING

PROTEIN HOMOLOG) (VCP) >gi\_862480 (U20213) valosin-containing protein [Glycine max]

Seq. No. 26726

Contig ID 144139\_2.R1040 5'-most EST txt700731771.h1

Method BLASTX

```
NCBI GI
                  q1055161
BLAST score
                  221
                  7.0e-18
E value
                  122
Match length
                  24
% identity
                  (U40029) similar to human 100 kDa coactivator (U22055)
NCBI Description
                  [Caenorhabditis elegans]
Seq. No.
                  144141 1.R1040
Contig ID
                  rlr700900684.hl
5'-most EST
Seq. No.
                  26728
                  144156 1.R1040
Contig ID
                  txt700731814.h1
5'-most EST
                  BLASTX
Method
                  g3269285
NCBI GI
BLAST score
                   349
                   3.0e-33
E value
                   78
Match length
                   82
% identity
                  (AL030978) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   26729
Contig ID
                   144164 1.R1040
                   gsv701045873.hl
5'-most EST
Method
                   BLASTX
                   q2981439
NCBI GI
BLAST score
                   205
                   2.0e-16
E value
                   63
Match length
                   67
% identity
                  (AF051853) t-SNARE SED5 [Arabidopsis thaliana]
NCBI Description
                   26730
Seq. No.
                   144178 1.R1040
Contig ID
                   txt700731848.hl
5'-most EST
                   BLASTX
Method
                   q4325324
NCBI GI
                   470
BLAST score
                   5.0e-47
E value
                   98
Match length
                   90
% identity
                   (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis
NCBI Description
                   thaliana]
                   26731
Seq. No.
                   144277 1.R1040
Contig ID
                   txt700732015.h1
5'-most EST
```

Method BLASTX
NCBI GI g1841357
BLAST score 364
E value 1.0e-34
Match length 122
% identity 58

NCBI Description (D85382) mitochondrial ribosomal protein S11 (nuclear

encoded) [Oryza sativa]



Seq. No. 26732
Contig ID 144293\_1.R1040
5'-most EST ujr700646608.h1

Seq. No. 26733

Contig ID 144297 1.R1040 5'-most EST kl1701212153.h1

Seq. No. 26734

Contig ID 144315\_1.R1040 5'-most EST txt700732787.h1

Seq. No. 26735

Contig ID 144329 1.R1040 5'-most EST txt700732113.h1

Seq. No. 26736

Contig ID 144345\_1.R1040

5'-most EST uC-gmrominsoy167c09b1

Method BLASTN
NCBI GI g3702738
BLAST score 34
E value 1.0e-09
Match length 50
% identity 92

% identity 92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWJ3, complete sequence [Arabidopsis thaliana]

Seq. No. 26737

Contig ID 144348 1.R1040 5'-most EST fua701037950.h1

Method BLASTX
NCBI GI g2507300
BLAST score 237
E value 3.0e-20
Match length 57
% identity 74

NCBI Description ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD

SUBUNIT) (A1 40 KD SUBUNIT) (RF-C 40 KD SUBUNIT) (RFC40) >gi\_1590811 (M87338) replication factor C, 40-kDa subunit [Homo sapiens] >gi\_2914760 (AF045555) replication factor C subunit 2 [Homo sapiens] >gi\_4506487\_ref\_NP\_002905.1\_pRFC2\_

replication factor C (activator 1) 2 (40kD)

Seq. No. 26738

Contig ID 144359\_1.R1040 5'-most EST gsv701045178.h1

Seq. No. 26739

Contig ID 144390\_1.R1040 5'-most EST txt700732216.h1

Method BLASTX
NCBI GI g2827552
BLAST score 214
E value 1.0e-17
Match length 77



% identity

NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

26740 Seq. No.

144398 1.R1040 Contig ID txt700732226.hl 5'-most EST

26741 Seq. No.

144403 1.R1040 Contig ID dpv701098967.hl 5'-most EST

BLASTX Method NCBI GI g2204236 539 BLAST score 3.0e-55 E value Match length 141 77 % identity

NCBI Description (Y13861) enoyl-ACP reductase [Nicotiana tabacum]

26742 Seq. No.

144473 1.R1040 Contig ID txt700732364.hl 5'-most EST

Seq. No. 26743

144488 1.R1040 Contig ID txt700732403.h1 5'-most EST

Seq. No. 26744

144489 1.R1040 Contig ID

5'-most EST jC-qmst02400001g06a1

BLASTX Method NCBI GI g3335378 BLAST score 364 E value 2.0e-34 Match length 90

% identity 76

(AC003028) Myb-related transcription activator [Arabidopsis NCBI Description

thaliana]

Seq. No. 26745

144509 1.R1040 Contig ID uC-gmropic074a10b1 5'-most EST

45

Method BLASTX g3152940 NCBI GI BLAST score 196 5.0e-15 E value 92 Match length

% identity (AF065483) sorting nexin 1 [Homo sapiens] NCBI Description

26746 Seq. No.

144509 2.R1040 Contig ID dpv701097363.hl 5'-most EST

26747 Seq. No.

144514 1.R1040 Contig ID awf700841065.hl 5'-most EST

Method BLASTX



NCBI GI g2262115
BLAST score 332
E value 1.0e-30
Match length 233
% identity 32

NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No. 26748

Contig ID 144529\_1.R1040

5'-most EST uC-gmrominsoy041d07b1

Seq. No. 26749

Contig ID 144543 1.R1040 5'-most EST txt700732511.h1

Seq. No. 26750

Contig ID 144549\_1.R1040 5'-most EST kl1701205179.h1

Method BLASTX
NCBI GI g3033384
BLAST score 443
E value 6.0e-44
Match length 142
% identity 63

NCBI Description (AC004238) putative CTP synthase [Arabidopsis thaliana]

Seq. No. 26751

Contig ID 144562\_1.R1040 5'-most EST leu701157138.h1

Method BLASTX
NCBI GI g3297824
BLAST score 141
E value 1.0e-08
Match length 94
% identity 39

NCBI Description (AL031032) bZIP transcription factor - like protein

[Arabidopsis thaliana]

Seq. No. 26752

Contig ID 144570\_1.R1040 5'-most EST txt700732562.h1

Method BLASTN
NCBI GI g2605511
BLAST score 121
E value 2.0e-61
Match length 356
% identity 83

NCBI Description Glycine max mRNA for beta subunit of beta conglycinin,

complete cds

Seq. No. 26753

Contig ID 144589\_2.R1040 5'-most EST fua701041692.h1

Seq. No. 26754

Contig ID 144608\_1.R1040 5'-most EST txt700732661.h1



Method BLASTN
NCBI GI g2995454
BLAST score 317
E value 1.0e-178
Match length 521
% identity 90

NCBI Description L.luteus mRNA for tRNA-glutamine synthetase

Seq. No. 26755

Contig ID 144609 1.R1040 5'-most EST pxt700943328.h1

Method BLASTX
NCBI GI g3702338
BLAST score 269
E value 6.0e-24
Match length 80
% identity 66

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 26756

Contig ID 144639 1.R1040 5'-most EST txt700732737.h1

Seq. No. 26757

Contig ID 144643\_1.R1040 5'-most EST hrw701061473.h1

Method BLASTX
NCBI GI g3341684
BLAST score 236
E value 4.0e-20
Match length 87
% identity 49

NCBI Description (AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26758

Contig ID 144648\_1.R1040 5'-most EST fC-gmse700837723c1

Method BLASTX
NCBI GI g3641252
BLAST score 516
E value 2.0e-52
Match length 169
% identity 65

NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus

domestica]

Seq. No. 26759

Contig ID 144670 1.R1040 5'-most EST txt700732816.h1

Seq. No. 26760

Contig ID 144688 1.R1040 5'-most EST epx701109140.h1

Method BLASTX
NCBI GI g267442
BLAST score 257
E value 8.0e-22



Match length 15% identity 40 NCBI Description HY

HYPOTHETICAL 18.7 KD PROTEIN IN RHLE-DING INTERGENIC REGION (F160) >gi 147599 (L02123) YbiA [Escherichia coli]

>gi\_1787017 (AE000182) orf, hypothetical protein
[Escherichia coli] >gi\_4062356\_dbj\_BAA35458\_ (D90716)
Hypothetical 18.7 kd protein in rhlE-dinG/rarB intergenic
region (F160). [Escherichia coli] >gi\_4062360\_dbj\_BAA35464\_
(D90717) Hypothetical 18.7 kd protein in rhlE-dinG/rarB

intergenic region (F160). [Escherichia coli]

Seq. No. 26761

Contig ID 144708\_1.R1040 5'-most EST zhf700954866.h1

Seq. No. 26762

Contig ID 144802\_1.R1040 5'-most EST uC-gmropic062a07b1

Seq. No. 26763

Contig ID 144809\_1.R1040 5'-most EST txt700733086.h1

Seq. No. 26764

Contig ID 144810\_1.R1040 5'-most EST zpv700759801.h1

Seq. No. 26765

Contig ID 144819\_1.R1040 5'-most EST pmv700889162.h1

Method BLASTX
NCBI GI g120777
BLAST score 827
E value 2.0e-88
Match length 251
% identity 61

NCBI Description SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH)

>qi 147901 (M88334) succinic semialdehyde dehydrogenase

[Escherichia coli] >gi\_1789015 (AE000351)

succinate-semialdehyde dehydrogenase, NADP-dependent

activity [Escherichia coli]

Seq. No. 26766

Contig ID 144819\_2.R1040

5'-most EST jC-gmf102220071c03d1

Method BLASTX
NCBI GI g120777
BLAST score 223
E value 3.0e-18
Match length 66
% identity 61

NCBI Description SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH)

>qi 147901 (M88334) succinic semialdehyde dehydrogenase

[Escherichia coli] >gi 1789015 (AE000351)

succinate-semialdehyde dehydrogenase, NADP-dependent

activity [Escherichia coli]



Contig ID 144874\_1.R1040 5'-most EST rca701002368.h1

Seq. No. 26768

Contig ID 144909 1.R1040 5'-most EST txt700733296.h1

Seq. No. 26769

Contig ID 144952 1.R1040 5'-most EST txt700733379.h1

Seq. No. 26770

Contig ID 144964 1.R1040 5'-most EST txt700733408.h1

Seq. No. 26771

Contig ID 145017\_1.R1040 5'-most EST zsg701119121.h1

Method BLASTX
NCBI GI g3219269
BLAST score 279
E value 1.0e-48
Match length 117
% identity 81

NCBI Description (AB015314) MAP kinase kinase 3 [Arabidopsis thaliana]

Seq. No. 26772

Contig ID 145028 1.R1040 5'-most EST txt700733518.h1

Method BLASTX
NCBI GI g2880046
BLAST score 147
E value 2.0e-09
Match length 65
% identity 46

NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26773

Contig ID 145043\_1.R1040 5'-most EST jC-gmf102220078a05a1

Seq. No. 26774

Contig ID 145056\_1.R1040 5'-most EST txt700737183.h1

Seq. No. 26775

Contig ID 145106\_1.R1040 5'-most EST gsv701043865.h1

Seq. No. 26776

Contig ID 145110\_1.R1040

5'-most EST g5126515

Method BLASTX

NCBI GI g2323410

BLAST score 994

E value 1.0e-108



Match length 376 % identity 54

NCBI Description (AF015913) Skb1Hs [Homo sapiens]

Seq. No. 26777

Contig ID 145133 1.R1040 5'-most EST txt700733710.h1

Method BLASTX
NCBI GI g2213626
BLAST score 144
E value 7.0e-09
Match length 153
% identity 30

NCBI Description (AC000103) F21J9.18 [Arabidopsis thaliana]

Seq. No. 26778

Contig ID 145156\_1.R1040 5'-most EST uC-gmropic111c10b1

Method BLASTX
NCBI GI g3885334
BLAST score 193
E value 7.0e-15
Match length 50
% identity 66

NCBI Description (AC005623) putative argonaute protein [Arabidopsis

thaliana]

Seq. No. 26779

Contig ID 145196\_1.R1040 5'-most EST txt700733827.h1

Seq. No. 26780

Contig ID 145197\_3.R1040 5'-most EST jex700908479.h1

Seq. No. 26781

Contig ID 145201\_1.R1040 5'-most EST txt700733833.h1

Method BLASTN
NCBI GI g2687440
BLAST score 118
E value 5.0e-60
Match length 138
% identity 96

NCBI Description Tellima grandiflora large subunit 26S ribosomal RNA gene,

partial sequence

Seq. No. 26782

Contig ID 145226\_1.R1040 5'-most EST kmv700737717.h1

Seq. No. 26783

Contig ID 145232\_1.R1040 5'-most EST txt700733885.h1

Method BLASTX NCBI GI g4263704 BLAST score 362



E value 2.0e-34
Match length 136
% identity 50

NCBI Description (AC006223) putative sugar starvation-induced protein

[Arabidopsis thaliana]

Seq. No. 26784

Contig ID 145236\_1.R1040 5'-most EST txt700733890.h1

Seq. No. 26785

Contig ID 145300\_1.R1040 5'-most EST txt700734006.h1

Method BLASTX
NCBI GI g3184285
BLAST score 296
E value 5.0e-27
Match length 96
% identity 65

NCBI Description (AC004136) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26786

Contig ID 145328\_1.R1040 5'-most EST zzp700832617.h1

Seq. No. 26787

Contig ID 145330\_1.R1040 5'-most EST pxt700945528.h1

Method BLASTX
NCBI GI g2894611
BLAST score 155
E value 2.0e-10
Match length 47
% identity 70

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 26788

Contig ID 145330\_2.R1040 5'-most EST kl1701215222.h1

Seq. No. 26789

Contig ID 145340\_1.R1040 5'-most EST txt700734093.h1

Seq. No. 26790

Contig ID 145393\_1.R1040 5'-most EST txt700734230.h1

Method BLASTX
NCBI GI g3123161
BLAST score 94
E value 8.0e-09
Match length 111
% identity 38

NCBI Description HYPOTHETICAL 77.0 KD TRP-ASP REPEATS CONTAINING PROTEIN

F35G12.4 IN CHROMOSOME III >gi\_3876723\_emb\_CAA86335

(Z46242) similar to beta-transducin;  $\overline{\text{cDNA}}$  EST EMBL:  $\overline{\text{Z}}$ 14703 comes from this gene;  $\overline{\text{cDNA}}$  EST EMBL:D67532 comes from this



gene; cDNA EST EMBL:D69055 comes from this gene; cDNA EST EMBL:D64515 comes from this gene; cDNA EST EMBL:D655

 Seq. No.
 26791

 Contig ID
 145499\_1.R1040

 5'-most EST
 txt700734406.h1

Seq. No. 26792

Contig ID 145502\_1.R1040 5'-most EST txt700734410.h1

Seq. No. 26793

Contig ID 145514\_1.R1040

5'-most EST uC-gmrominsoy307f01b1

Method BLASTX
NCBI GI g3142291
BLAST score 487
E value 6.0e-49
Match length 167
% identity 54

NCBI Description (AC002411) Contains similarity to adenylate cyclase

gb AF012921 from Magnaporthe grisae. EST gb\_Z24512 comes

from this gene. [Arabidopsis thaliana]

Seq. No. 26794

Contig ID 145544\_1.R1040 5'-most EST zpv700761035.h1

Method BLASTX
NCBI GI g4249416
BLAST score 291
E value 4.0e-26
Match length 89
% identity 58

NCBI Description (AC006072) putative exoribonuclease (also contains zinc-finger C2H2-type domain) [Arabidopsis thaliana]

Seq. No. 26795

Contig ID 145570\_1.R1040 5'-most EST dpv701101324.h1

Method BLASTX
NCBI GI g3377843
BLAST score 151
E value 6.0e-10
Match length 102
% identity 41

NCBI Description (AF076274) contains similarity to rat p47 protein

(GB:AB002086) [Arabidopsis thaliana]

Seq. No. 26796

Contig ID 145635\_1.R1040 5'-most EST jC-gmro02910062d04a1

Method BLASTX
NCBI GI g2911042
BLAST score 682
E value 3.0e-89
Match length 226
% identity 79

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(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No. 26797 Contig ID 145698\_1.R1040

NCBI Description

5'-most EST gsv701055801.h1

Method BLASTX
NCBI GI g4218011
BLAST score 442
E value 6.0e-44
Match length 101
% identity 80

NCBI Description (AC006135) putative protein kinase [Arabidopsis thaliana]

>gi\_4309721\_gb\_AAD15491\_ (AC006439) putative

serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 26798

Contig ID 145700\_1.R1040 5'-most EST pmv700888891.h1

Method BLASTX
NCBI GI g3132478
BLAST score 311
E value 1.0e-28
Match length 146
% identity 47

NCBI Description (AC003096) bZIP-like protein [Arabidopsis thaliana]

Seq. No. 26799

Contig ID 145704\_1.R1040

5'-most EST jC-gmle01810066b02d1

Seq. No. 26800

Contig ID 145713\_1.R1040 5'-most EST pmv700888646.h1

Seq. No. 26801

Contig ID 145743\_1.R1040 5'-most EST crh700852487.h1

Method BLASTX
NCBI GI g2244996
BLAST score 262
E value 7.0e-37
Match length 131
% identity 59

NCBI Description (Z97341) similarity to a membrane-associated salt-inducible

protein [Arabidopsis thaliana]

Seq. No. 26802

Contig ID 145763 1.R1040 5'-most EST smc700746937.h1

Seq. No. 26803

Contig ID 145785\_1.R1040

5'-most EST jC-gmst02400013e01a1

Seq. No. 26804

Contig ID 145786\_1.R1040



```
smc700744318.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3549667
BLAST score
                   587
                   6.0e-61
E value
                  136
Match length
                  85
% identity
                   (AL031394) Arabidopsis dynamin-like protein ADL2
NCBI Description
                   [Arabidopsis thaliana]
                   26805
Seq. No.
                  145799 1.R1040
Contig ID
5'-most EST
                  dpv701\overline{1}00879.h1
Seq. No.
                   26806
                   145803 1.R1040
Contig ID
5'-most EST
                   txt700734949.hl
                   26807
Seq. No.
                   145828 1.R1040
Contig ID
5'-most EST
                   pmv700893370.h1
                  BLASTX
Method
                   g1169198
NCBI GI
                   267
BLAST score
                   2.0e-23
E value
Match length
                   92
                   59
% identity
                   DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR
NCBI Description
                   >gi 479738_pir__S35270 hypothetical protein - Arabidopsis
                   thaliana >gi_166926 (L11367) [Arabidopsis thaliana
                   unidentified mRNA sequence, complete cds.], gene product
                   [Arabidopsis thaliana]
                   26808
Seq. No.
                   145839 1.R1040
Contig ID
5'-most EST
                   awf700837802.h1
Method
                   BLASTX
                   q3386597
NCBI GI
                   169
BLAST score
                   1.0e-11
E value
Match length
                   48
% identity
                   71
                   (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3702347 (AC005397) putative permease [Arabidopsis
                   thaliana]
Seq. No.
                   26809
Contig ID
                   145844 1.R1040
5'-most EST
                   kl1701202434.h1
                   BLASTX
Method
NCBI GI
                   q3452263
```

BLAST score 435 4.0e-53 E value Match length 133 % identity

(AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis NCBI Description thaliana]



Seq. No. 26810
Contig ID 145846\_1.R1040
5'-most EST txt700735025.h1

BLAST score 227

E value 7.0e-19
Match length 102
% identity 46

NCBI Description QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)

>gi\_2137015\_pir\_\_S68430 queuine tRNA-ribosyltransferase (EC
2.4.2.29), 60K chain - rabbit >gi\_623547 (L37420) queuine

tRNA-ribosyltransferase [Oryctolagus cuniculus]

Seq. No. 26811

Contig ID 145866\_1.R1040 5'-most EST txt700735055.h1

Seq. No. 26812

Contig ID 145873 1.R1040 5'-most EST leu701153435.h1

Seq. No. 26813

Contig ID 145884\_1.R1040 5'-most EST txt700735091.h1

Seq. No. 26814

Contig ID 145929\_1.R1040 5'-most EST txt700735202.h1

Method BLASTX
NCBI GI g2494174
BLAST score 444
E value 3.0e-60
Match length 180
% identity 67

NCBI Description GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi\_497979 (U10034)

glutamate decarboxylase [Arabidopsis thaliana]

Seq. No. 26815

Contig ID 145967 1.R1040 5'-most EST pxt700944894.h1

Seq. No. 26816

Contig ID 146045\_1.R1040 5'-most EST txt700735414.h1

Seq. No. 26817

Contig ID 146091\_1.R1040 5'-most EST txt700735488.h1

Seq. No. 26818

Contig ID 146129 1.R1040 5'-most EST txt700735551.h1

Method BLASTX NCBI GI g440965



BLAST score 281 E value 4.0e-25 Match length 88 % identity 67

NCBI Description (S66876) orf in promoter of Lhca3.St.1 [Solanum

tuberosum=potatoes, Peptide Chloroplast, 137 aa] [Solanum

tuberosum]

Seq. No. 26819

Contig ID 146149 1.R1040 5'-most EST kl1701202403.h1

Seq. No. 26820

Contig ID 146156 1.R1040 5'-most EST txt700735610.h1

Seq. No. 26821

Contig ID 146163\_1.R1040 5'-most EST txt700735623.h1

Seq. No. 26822

Contig ID 146168\_1.R1040 5'-most EST txt700735630.h1

Seq. No. 26823

Contig ID 146204\_1.R1040 5'-most EST xpa700793442.h1

Method BLASTN
NCBI GI g210811
BLAST score 124
E value 2.0e-63
Match length 296
% identity 92

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 26824

Contig ID 146232\_1.R1040 5'-most EST txt700735759.h1

Method BLASTX
NCBI GI g3953463
BLAST score 188
E value 3.0e-14
Match length 65
% identity 49

NCBI Description (AC002328) F20N2.8 [Arabidopsis thaliana]

Seq. No. 26825

Contig ID 146237\_1.R1040 5'-most EST zhf700962523.h1

Seq. No. 26826

Contig ID 146240\_1.R1040 5'-most EST hrw701058854.h1

Method BLASTX NCBI GI g3021409 BLAST score 252

爱



8.0e-22 E value 86 Match length 17 % identity

(Y12781) transducin (beta) like 1 protein [Homo sapiens] NCBI Description

26827 Seq. No.

146248 1.R1040 Contig ID uC-gmropic104f07b1 5'-most EST

26828 Seq. No.

146258 1.R1040 Contig ID txt700735801.h1 5'-most EST

26829 Seq. No.

146261 1.R1040 Contig ID

5'-most EST uC-gmrominsoy086c07b1

26830 Seq. No.

146338 1.R1040 Contig ID jsh701067558.hl 5'-most EST

Seq. No. 26831

146351 1.R1040 Contig ID txt700735962.h1 5'-most EST

26832 Seq. No.

146360 1.R1040 Contig ID txt700735975.h1 5'-most EST

BLASTX Method g3386604 NCBI GI 322 BLAST score 3.0e-30 E value 82 Match length

76 % identity

(AC004665) putative protein kinase [Arabidopsis thaliana] NCBI Description

26833 Seq. No.

146411 1.R1040 Contig ID fua701040350.h1 5'-most EST

Seq. No. 26834

146414 1.R1040 Contig ID 5'-most EST kl1701214317.h1

Method BLASTX NCBI GI g3746064 BLAST score 145 6.0e-09 E value Match length 45 % identity

(AC005311) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 26835

146423 1.R1040 Contig ID

uC-gmflminsoy010g10b1 5'-most EST

Method BLASTX NCBI GI q4091810 BLAST score 204



E value 9.0e-16
Match length 112
% identity 54

NCBI Description (AF053345) fatty acid elongase 3-ketoacyl-CoA synthase 1

[Arabidopsis thaliana]

Seq. No. 26836

Contig ID 146450 1.R1040 5'-most EST txt700736183.h1

Method BLASTX
NCBI GI g1707945
BLAST score 295
E value 4.0e-27
Match length 81
% identity 69

NCBI Description GLYCOGEN OPERON PROTEIN GLGX HOMOLOG

>gi 1403478 emb CAA98327 (Z74020) glgX [Mycobacterium

tuberculosis]

Seq. No. 26837

Contig ID 146452\_1.R1040 5'-most EST epx701108278.h1

Seq. No. 26838

Contig ID 146456 1.R1040 5'-most EST txt700736189.h1

Seq. No. 26839

Contig ID 146502 1.R1040 5'-most EST hrw701062412.h1

Seq. No. 26840

Contig ID 146531\_2.R1040 5'-most EST uC-gmropic107e10b1

Seq. No. 26841

Contig ID 146538\_1.R1040 5'-most EST txt700736335.h1

Seq. No. 26842

Contig ID 146599\_1.R1040 5'-most EST txt700736452.h1

Method BLASTX
NCBI GI g3850587
BLAST score 212
E value 4.0e-17
Match length 86
% identity 52

NCBI Description (AC005278) Strong similarity to gi\_2244780 hypothetical protein from Arabidopsis thaliana chromosome 4 contig

gb Z97335. [Arabidopsis thaliana]

Seq. No. 26843

Contig ID 146647\_1.R1040

5'-most EST jC-gmfl02220132ab10d1

Seq. No. 26844



146706 1.R1040 Contig ID zhf700960906.hl 5'-most EST

BLASTX Method g3024898 NCBI GI 304 BLAST score 4.0e-45 E value 153 Match length 65 % identity

PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA NCBI Description

HELICASE KIAA0224 (HA4657) >gi 1504028\_dbj\_BAA13213 (D86977) similar to putative ATP-dependent RNA helicase K03H1.2 of C.elegans(S41025) [Homo sapiens] >gi\_3123906 (AF038391) pre-mRNA splicing factor [Homo sapiens]

26845 Seq. No.

146707 1.R1040 Contig ID bth700847556.h1 5'-most EST

BLASTX Method g4115379 NCBI GI 266 BLAST score E value 2.0e-27 Match length 119 55 % identity

(AC005967) putative carbonyl reductase [Arabidopsis NCBI Description

thaliana]

26846 Seq. No.

146736 1.R1040 Contig ID 5'-most EST jC-gmro02910013f05a1

26847 Seq. No.

Contig ID 146745 1.R1040 5'-most EST jC-qmf102220061d11a1

BLASTX Method NCBI GI q2826884 BLAST score 352 E value 6.0e-33 151 Match length 51 % identity

(AJ223635) transcription factor IIA large subunit NCBI Description

[Arabidopsis thaliana]

26848 Seq. No.

146792 1.R1040 Contig ID kmv700740644.h1 5'-most EST

BLASTN Method g3510343 NCBI GI 47 BLAST score 2.0e-17 E value 95 Match length % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MJC20, complete sequence [Arabidopsis thaliana]

Seq. No. 26849

146801 1.R1040 Contig ID 5'-most EST txt700736866.h1



```
26850
Seq. No.
                   146811 1.R1040
Contig ID
                   txt700736883.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1046278
                   361
BLAST score
                   8.0e-35
E value
                   93
Match length
                   77
% identity
                  (U28645) PvAlf [Phaseolus vulgaris]
NCBI Description
                   26851
Seq. No.
                   146883 1.R1040
Contig ID
                   txt700737027.h1
5'-most EST
                   26852
Seq. No.
                   146911 1.R1040
Contig ID
                   jsh701\overline{0}65542.h1
5'-most EST
                   26853
Seq. No.
                   147007 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810006g05a1
                   26854
Seq. No.
                   147027 1.R1040
Contig ID
                   sat701010749.h1
5'-most EST
                   BLASTX
Method
                   g4263524
NCBI GI
BLAST score
                   169
                   4.0e-12
E value
Match length
                   95
                   40
% identity
                   (AC004044) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   26855
Seq. No.
                   147058 1.R1040
Contig ID
                   uC-gmrominsoy125f08b1
5'-most EST
                   BLASTX
Method
                   g116923
NCBI GI
                   329
BLAST score
                   1.0e-30
E value
                   107
Match length
                   58
% identity
                   COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
NCBI Description
                   >gi_111414_pir__S13520 beta-COP protein - rat
                   >gi 55819 emb CAA40505 (X57228) beta COP [Rattus
                   norvegicus]
                   26856
Seq. No.
                   147058 2.R1040
Contig ID
                   sat701005136.hl
5'-most EST
```

Method BLASTX
NCBI GI g116923
BLAST score 211
E value 6.0e-17
Match length 75

```
% identity
                  COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
NCBI Description
                  >gi_111414_pir__S13520 beta-COP protein - rat
                  >gi 55819 emb CAA40505 (X57228) beta COP [Rattus
                  norvegicus]
                   26857
Seq. No.
                   147062 1.R1040
Contig ID
                   g5126378
5'-most EST
                  BLASTX
Method
                   q2462749
NCBI GI
BLAST score
                   265
                   4.0e-23
E value
                   145
Match length
                   41
% identity
                   (AC002292) Putative Serine/Threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   26858
Seq. No.
                   147070 1.R1040
Contig ID
                   k11701\overline{2}11321.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3924599
BLAST score
                   153
E value
                   6.0e-10
                   126
Match length
                   29
% identity
                   (AF069442) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
                   26859
Seq. No.
                   147072 1.R1040
Contig ID
                   txt700737512.hl
5'-most EST
                   26860
Seq. No.
                   147114 1.R1040
Contig ID
                   txt700737589.h1
 5'-most EST
                   BLASTX
Method
                   q2160156
NCBI GI
BLAST score
                   441
                   7.0e-44
E value
                   122
Match length
                   70
 % identity
                   (AC000132) Strong similarity to S. pombe leucyl-tRNA
 NCBI Description
                   synthetase (gb_Z73100). [Arabidopsis thaliana]
                   26861
 Seq. No.
                   147125 1.R1040
 Contig ID
                   txt700737617.h1
 5'-most EST
```

Contig ID 147148\_1.R1040 5'-most EST zhf700963702.h1

Method BLASTN
NCBI GI g1370187
BLAST score 185
E value 1.0e-99
Match length 265



% identity 92 NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB7D

Seq. No. 26863

Contig ID 147174\_1.R1040 5'-most EST rrt700645903.h1

Seq. No. 26864

Contig ID 147180\_1.R1040 5'-most EST rrt700645913.h1

Seq. No. 26865

Contig ID 147183 1.R1040 5'-most EST rrt700645918.h1

Seq. No. 26866

Contig ID 147195\_1.R1040 5'-most EST jC-gmst02400004a11d1

Seq. No. 26867

Contig ID 147212\_1.R1040 5'-most EST fC-gmro700843925h2

Seq. No. 26868

Contig ID 147212\_2.R1040 5'-most EST jsh701068555.h1

Seq. No. 26869

Contig ID 147213\_1.R1040 5'-most EST zhf700952872.h1

Method BLASTX
NCBI GI g2829923
BLAST score 410
E value 2.0e-40
Match length 108
% identity 42

NCBI Description (AC002291) Similar to uridylyl transferases [Arabidopsis

thaliana]

Seq. No. 26870

Contig ID 147214\_1.R1040 5'-most EST rrt700645957.h1

Method BLASTX
NCBI GI g4559356
BLAST score 209
E value 6.0e-17
Match length 72
% identity 12

NCBI Description (AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26871

Contig ID 147225\_1.R1040



Match length 187 % identity 32

NCBI Description (AC002392) putative anthranilate

N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis

thaliana]

Seq. No. 26872

Contig ID 147311\_1.R1040 5'-most EST rrt700646090.h1

Seq. No. 26873

Contig ID 147323 1.R1040 5'-most EST wrg700785919.h2

Method BLASTX
NCBI GI g3024871
BLAST score 171
E value 2.0e-12
Match length 71
% identity 48

NCBI Description HYPOTHETICAL 77.3 KD PROTEIN SLL0005

>gi 1001579\_dbj\_BAA10206\_ (D64000) ABC1-like [Synechocystis

sp.]

Seg. No. 26874

Contig ID 147349\_1.R1040 5'-most EST wrg700785953.h2

Method BLASTX
NCBI GI g1076315
BLAST score 381
E value 4.0e-37
Match length 83
% identity 86

NCBI Description cytochrome P450 - Arabidopsis thaliana

>gi\_853719\_emb\_CAA60793\_ (X87367) CYP90 protein

[Arabidopsis thaliana] >gi\_871988\_emb\_CAA60794\_ (X87368)

CYP90 protein [Arabidopsis thaliana]

Seq. No. 26875

Contig ID 147389\_1.R1040 5'-most EST bth700846474.h1

Method BLASTX
NCBI GI g3913425
BLAST score 663
E value 7.0e-70
Match length 133
% identity 95

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi\_2275203 (AC002337) RNA helicase isolog

[Arabidopsis thaliana]

Seq. No. 26876

Contig ID 147396\_1.R1040 5'-most EST sat701007529.h1

Seq. No. 26877

Contig ID 147396 2.R1040 5'-most EST wrg700786022.h2

BLAST score

Match length

E value

224 3.0e-18



```
26878
Seq. No.
                   147407 1.R1040
Contig ID
                   asn701\overline{1}35857.h1
5'-most EST
                   26879
Seq. No.
                   147410 1.R1040
Contig ID
                   fC-gmle7000786045a1
5'-most EST
                   BLASTX
Method
                   g131754
NCBI GI
BLAST score
                   145
                   1.0e-08
E value
Match length
                   81
                   41
% identity
                   PPLZ02 PROTEIN >gi_99973_pir__S11881 hypothetical protein
NCBI Description
                    (clone pPLZ2) - large-leaved lupine >gi_19507_emb_CAA36069_
                    (X51767) put. pPLZ2 product (AA 1-164) [Lupinus
                   polyphyllus]
                   26880
Seq. No.
                    147412 1.R1040
Contig ID
                    fde700873366.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                    g2829895
                    336
BLAST score
E value
                    6.0e-32
                    81
Match length
                    78
% identity
                   (AC002311) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    26881
Seq. No.
                    147420_1.R1040
Contig ID
5'-most EST
                    wrg700786058.h2
Method
                    BLASTX
                    q3776025
NCBI GI
BLAST score
                    410
                    2.0e-40
E value
                    97
Match length
                    78
% identity
                   (AJ010474) RNA helicase [Arabidopsis thaliana]
NCBI Description
                    26882
Seq. No.
                    147448 1.R1040
Contig ID
                    fua701\overline{0}40174.h1
5'-most EST
                    26883
Seq. No.
                    147468 1.R1040
Contig ID
                    asn701\overline{1}36493.h1
5'-most EST
                    26884
Seq. No.
                    147499 1.R1040
Contig ID
                    zhf700\overline{9}58443.h1
 5'-most EST
                    BLASTX
Method
                    q4455131
NCBI GI
```



```
% identity
                  (AF129433) histone deacetylase HDA2 [Drosophila
NCBI Description
                  melanogaster]
                  26885
Seq. No.
                  147516 1.R1040
Contig ID
                  pcp700993668.hl
5'-most EST
                  BLASTX
Method
                  q3023070
NCBI GI
                  229
BLAST score
E value
                  2.0e-19
Match length
                  84
% identity
                  (AF053702) hypothetical protein [Mesembryanthemum
NCBI Description
                  crystallinum]
                  26886
Seq. No.
                  147521 1.R1040
Contig ID
                  fC-qmle7000786228a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3411266
BLAST score
                   458
                   2.0e-63
E value
Match length
                   147
% identity
                   79
                  (AF080567) pullulanase-type starch debranching enzyme [Zea
NCBI Description
                  mays]
                   26887
Seq. No.
                   147568 1.R1040
Contig ID
                   sat701004052.h1
5'-most EST
                   BLASTX
Method
                   q4263784
NCBI GI
BLAST score
                   275
                   2.0e-47
E value
Match length
                   176
% identity
                   (AC006068) putative glycogenin-2 protein [Arabidopsis
NCBI Description
                   thaliana]
                   26888
Seq. No.
                   147604 1.R1040
Contig ID
                   fua701037144.h1
5'-most EST
Method
                   BLASTX
                   g1703292
NCBI GI
                   434
BLAST score
                   2.0e-53
E value
```

Match length 131 78 % identity

NCBI Description HIGH AFFINITY AMMONIUM TRANSPORTER >gi 551219 emb\_CAA53473

(X75879) amt1 [Arabidopsis thaliana]

26889 Seq. No.

147626 1.R1040 Contig ID wrg700786484.h1 5'-most EST

26890 Seq. No.



Contig ID 147653 1.R1040 5'-most EST wrg700792050.h1

Method BLASTX
NCBI GI g3193330
BLAST score 315
E value 6.0e-29
Match length 131
% identity 50

NCBI Description (AF069299) contains similarity to Medicago sativa corC

(GB:L22305) [Arabidopsis thaliana]

Seq. No. 26891

Contig ID 147675 1.R1040

5'-most EST jC-gmro02910037e08d1

Method BLASTX
NCBI GI g2764806
BLAST score 373
E value 9.0e-36
Match length 91
% identity 74

NCBI Description (X78548) epoxide hydrolase [Glycine max]

Seq. No. 26892

Contig ID 147680\_1.R1040

5'-most EST g5753630

Seq. No. 26893

Contig ID 147719\_1.R1040 5'-most EST wrg700786807.h2

Seq. No. 26894

Contig ID 147726\_1.R1040 5'-most EST wrg700786703.h2

Seq. No. 26895

Contig ID 147731\_1.R1040 5'-most EST vzy700752415.h1

Method BLASTX
NCBI GI g4220512
BLAST score 200
E value 6.0e-16
Match length 53
% identity 68

NCBI Description (AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No. 26896

Contig ID 147732\_2.R1040 5'-most EST yuv700862822.h1

Seq. No. 26897

Contig ID 147737\_1.R1040 5'-most EST wrg700788813.h2

Method BLASTN
NCBI GI g168702
BLAST score 255
E value 1.0e-141
Match length 279



% identity

NCBI Description Corn 22 kDa zein protein gene, complete cds

Seq. No.

26898

Contig ID 5'-most EST 147740 1.R1040  $leu701\overline{1}54242.h1$ 

Seq. No.

26899

Contig ID 5'-most EST 147753 1.R1040 wrg700788061.h1

Seq. No.

26900

Contig ID 5'-most EST 147765 1.R1040 wrg700786754.h2

Seq. No.

26901

Contig ID 5'-most EST 147792 1.R1040 wrg700786840.h2

Method -NCBI GI BLAST score BLASTN q168681 243

E value Match length 1.0e-134 259

% identity

98 NCBI Description

Maize 19 kDa zein mRNA, clone cZ19D1, complete cds. >gi 270686 gb I03333 Sequence 8 from Patent US

26902 Seq. No.

Contig ID

147793 1.R1040 wrg700786793.h2

5'-most EST

Seq. No. Contig ID 26903 147803 1.R1040

5'-most EST

fC-gmro7000747078r1

Method NCBI GI BLASTX g4432846

BLAST score

372

E value

2.0e-35

Match length % identity

121 64

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.

26904

Contig ID 5'-most EST 147821 1.R1040 wrg700786834.h2

Seq. No.

26905

Contig ID

147832 1.R1040

5'-most EST

jC-gmst02400039h12a1

Seq. No.

26906

Contig ID 5'-most EST 147887 1.R1040 wrg700786944.h2

Seq. No.

26907

Contig ID

147887 2.R1040

5'-most EST

smc700744330.h1



Contig ID 147911\_1.R1040 5'-most EST zhf700960751.h1

Method BLASTX
NCBI GI g3033384
BLAST score 221
E value 8.0e-18
Match length 55
% identity 75

NCBI Description (AC004238) putative CTP synthase [Arabidopsis thaliana]

Seq. No. 26909

Contig ID 147930 1.R1040

5'-most EST g4293163

Seq. No. 26910

Contig ID 147940\_1.R1040 5'-most EST rlr700900634.h1

Seq. No. 26911

Contig ID 147941\_1.R1040 5'-most EST jsh701067675.h1

Method BLASTX
NCBI GI g129726
BLAST score 201
E value 1.0e-15
Match length 129
% identity 38

NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL

4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55) >gi\_68464\_pir\_\_ISBOSS protein disulfide-isomerase (EC 5.3.4.1) precursor - bovine >gi 163497 (M17596) PDI (E.C.5.3.4.1) [Bos taurus]

Seq. No. 26912

Contig ID 147953\_1.R1040 5'-most EST gsv701054945.h1

Seq. No. 26913

Contig ID 147986\_1.R1040

5'-most EST g4396513
Method BLASTX
NCBI GI g3482913
BLAST score 169
E value 6.0e-12
Match length 127
% identity 32

NCBI Description (AC003970) Similar to MtN21, gi\_2598575, Megicago

truncatula nodulation induced gene [Arabidopsis thaliana]

Seq. No. 26914

Contig ID 147995\_1.R1040 5'-most EST wrg700787103.h2

Seq. No. 26915

Contig ID 147999\_1.R1040

Contig ID 5'-most EST

Method



```
5'-most EST
                  uC-gmrominsoy298e04b1
                  BLASTX
Method
NCBI GI
                  g4455153
                  158
BLAST score
                   2.0e-10
E value
                  107
Match length
% identity
                   68
                  (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
                   26916
Seq. No.
                   148010 1.R1040
Contig ID
                   fua701037886.hl
5'-most EST
                   BLASTN
Method
                   g170645
NCBI GI
                   334
BLAST score
                   0.0e + 00
E value
                   477
Match length
                   93
% identity
                  Vigna aconitifolia pyrroline-5-carboxylate synthetase
NCBI Description
                   associated mRNA sequence. >gi 2471746 gb I47781_I47781
                   Sequence 1 from patent US
                   26917
Seq. No.
                   148015 1.R1040
Contig ID
5'-most EST
                   wrq700787129.h2
Method
                   BLASTX
NCBI GI
                   g4519671
BLAST score
                   228
                   1.0e-18
E value
Match length
                   70
% identity
                   57
                   (AB017693) transfactor [Nicotiana tabacum]
NCBI Description
Seq. No.
                   26918
Contig ID
                   148045 1.R1040
5'-most EST
                   wrg700787173.h2
                   BLASTX
Method
NCBI GI
                   g3152558
BLAST score
                   519
E value
                   9.0e-53
Match length
                   139
                   74
% identity
                   (AC002986) Similar to M. tuberculosis gene gb Z96072 and M.
NCBI Description
                   leprae gene gb 400019. [Arabidopsis thaliana]
Seq. No.
                   26919
Contig ID
                   148051 1.R1040
5'-most EST
                   wrg700787183.h2
                   26920
Seq. No.
Contig ID
                   148066 1.R1040
5'-most EST
                   wrg700787217.h2
Seq. No.
                   26921
```

148068 1.R1040

BLASTX

fC-qmle700788247a4

SEA.

```
NCBI GI
                  g4567279
BLAST score
                  432
                  1.0e-42
E value
Match length
                  105
% identity
                  74
                   (AC006841) putative serine/threonine protein kinase
NCBI Description
                  [Arabidopsis thaliana]
                  26922
Seq. No.
                  148088 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220148c07a1
                  26923
Seq. No.
                  148091_1.R1040
Contig ID
5'-most EST
                  g5127006
                  BLASTX
Method
                  g2160161
NCBI GI
                  207
BLAST score
                  5.0e-16
E value
                  162
Match length
                  11
% identity
                  (AC000132) F21M12.7 gene product [Arabidopsis thaliana]
NCBI Description
                  26924
Seq. No.
                  148098 1.R1040
Contig ID
5'-most EST
                  xzm700763723.h1
                  BLASTN
Method
                  g3493646
NCBI GI
BLAST score
                  79
                  3.0e-36
E value
Match length
                  187
% identity
                  86
                  Pimpinella brachycarpa transcription activator (MADS1)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  26925
                  148177 1.R1040
Contig ID
                  zzp700829984.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2194142
BLAST score
                  259
E value
                  4.0e-22
Match length
                  112
                  47
% identity
                  (AC002062) ESTs gb N38288, gb T43486, gb AA395242 come from
NCBI Description
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  26926
```

Contig ID 148184\_1.R1040 5'-most EST wrg700787429.h2

Seq. No. 26927

Contig ID 148191 1.R1040

5'-most EST g5606337
Method BLASTX
NCBI GI g4432846
BLAST score 398



3.0e-56 E value 268 Match length 47 % identity

(AC006283) unknown protein [Arabidopsis thaliana] NCBI Description

26928 Seq. No.

148193 1.R1040 Contig ID

g5607183 5'-most EST Method BLASTX NCBI GI q1084301 BLAST score 684 4.0e-72 E value 172 Match length

% identity 81

pyruvate, orthophosphate dikinase (EC 2.7.9.1) - common ice NCBI Description

plant >qi 559471 emb CAA55143 (X78347)

pyruvate, orthophosphate dikinase [Mesembryanthemum

crystallinum]

26929 Seq. No.

148203 1.R1040 Contig ID 5'-most EST wrg700787450.h2

Method BLASTX q4538911 NCBI GI BLAST score 151 3.0e-22 E value Match length 85 % identity 67

(AL049482) hypothetical protein [Arabidopsis thaliana] NCBI Description

26930 Seq. No.

148206 1.R1040 Contig ID 5'-most EST wrg700787453.h2

Method BLASTX g2499989 NCBI GI BLAST score 144 3.0e-09 E value Match length 85 39 % identity

PEPTIDYL-TRNA HYDROLASE (PTH) >gi 1001232 dbj BAA10473\_ NCBI Description

(D64003) peptidyl-tRNA hydrolase [Synechocystis sp.]

26931 Seq. No.

Contig ID 148220 1.R1040

5'-most EST g5509244 Method BLASTX NCBI GI q1001253 BLAST score 241 4.0e-20 E value 140 Match length 41 % identity

(D64003) hypothetical protein [Synechocystis sp.] NCBI Description

26932 Seq. No.

148254 1.R1040 Contig ID 5'-most EST zhf700956404.h1



```
Seq. No.
Contig ID
                   148264 1.R1040
5'-most EST
                   wrg700787537.h1
Seq. No.
                   26934
Contig ID
                   148276 1.R1040
5'-most EST
                   jC-gmst02400043f08a1
Sea. No.
                   26935
Contig ID
                   148282 1.R1040
5'-most EST
                   zhf700964075.h1
```

Seq. No. 26936 Contig ID 148288 1.R1040 5'-most EST pxt700943466.h1 BLASTX Method

NCBI GI g3414930 BLAST score 164 7.0e-11 E value Match length 113 % identity 34

(AF076599) FutA [Dictyostelium discoideum] NCBI Description

26937 Seq. No. Contig ID 148302 1.R1040  $uC-gmf\overline{l}minsoy022d03b1$ 5'-most EST

Seq. No. 26938 148306 1.R1040 Contig ID 5'-most EST jC-gmf102220141e08a1 Method BLASTX NCBI GI q2827701

BLAST score 149 E value 3.0e-09 Match length 101 % identity 34

NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

26939 Seq. No. Contig ID 148313 1.R1040 5'-most EST zhf700957008.h1 Seq. No. 26940

148353 1.R1040 Contig ID wrg700787647.h25'-most EST

26941 Seq. No. 148359 1.R1040 Contig ID 5'-most EST wrg700787654.h2

Method BLASTX NCBI GI g2827631 BLAST score 236 2.0e-19 E value Match length 90 % identity 62

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]



```
Seq. No.
```

Contig ID 148363 1.R1040 5'-most EST jex700906321.h1

Method BLASTX NCBI GI g2731443 BLAST score 214 5.0e-17 E value Match length 185 % identity 32

(U96923) [prot= cDNA of the qlycoamidase gene [Aspergillus NCBI Description

niger]

Seq. No.

26943 Contig ID 148385 1.R1040

5'-most EST uC-gmflminsoy079h05b1

26944 Seq. No.

Contig ID 148391 1.R1040

5'-most EST jC-gmro02800030g06a1

Method BLASTX NCBI GI g2414593 BLAST score 385 4.0e-37 E value Match length 155 % identity 52

(Z99258) molybdopterin biosynthesis [Schizosaccharomyces NCBI Description

pombe]

26945

Seq. No.

Contig ID 148395 1.R1040 5'-most EST fua701042184.h1

BLASTN Method NCBI GI q4322474 BLAST score 40 E value 3.0e-13 Match length 100 85 % identity

NCBI Description Eucalyptus globulus subsp. globulus putative MADS box

transcription factor ETL mRNA, complete cds

Seq. No. 26946

Contig ID 148397 1.R1040 5'-most EST leu701154637.h1

Seq. No. 26947

Contig ID 148401 1.R1040 5'-most EST wrg700789607.h2

Seq. No. 26948

Contig ID 148409 1.R1040 5'-most EST wrg700787720.h2

Seq. No. 26949

Contig ID 148424 1.R1040

5'-most EST uC-gmrominsoy307h06b1

Seq. No. 26950



Contig ID 148437\_1.R1040 5'-most EST wrg700787755.h2

Seq. No. 26951

Contig ID 148449\_1.R1040 5'-most EST wrg700787770.h2

Seq. No. 26952

Contig ID 148467\_1.R1040 5'-most EST zsg701121122.h1

Method BLASTN
NCBI GI g2477521
BLAST score 41
E value 1.0e-13
Match length 128

Match length 128 % identity 87

NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 26953

Contig ID 148467\_2.R1040 5'-most EST wrg700787790.h2

Seq. No. 26954

Contig ID 148481\_1.R1040 5'-most EST wrg700787814.h2

Seq. No. 26955

Contig ID 148520\_1.R1040 5'-most EST wrg700787858.h2

Method BLASTX
NCBI GI g3643604
BLAST score 212
E value 3.0e-17
Match length 98
% identity 4

NCBI Description (AC005395) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 26956

Contig ID 148543\_1.R1040 5'-most EST zhf700955802.h1

Method BLASTX
NCBI GI g2252840
BLAST score 356
E value 5.0e-34
Match length 107
% identity 59

NCBI Description (AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No. 26957

Contig ID 148551 1.R1040

5'-most EST jC-gmle01810033c09a2

Method BLASTX NCBI GI g4455367 BLAST score 454



E value 4.0e-45 Match length 164 % identity 57

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 26958

Contig ID 148557 1.R1040

5'-most EST jC-gmst02400014f08d1

Seq. No. 26959

Contig ID 148574\_1.R1040 5'-most EST pcp700994010.h1

Seq. No. 26960

Contig ID 148583\_1.R1040 5'-most EST wrg700787970.h1

Method BLASTX
NCBI GI g3540184
BLAST score 404
E value 1.0e-39
Match length 110
% identity 59

NCBI Description (AC004122) Similar to endoxylanases [Arabidopsis thaliana]

Seq. No. 26961

Contig ID 148590\_1.R1040 5'-most EST ujr700646607.h1

Method BLASTX
NCBI GI g1084301
BLAST score 986
E value 1.0e-107
Match length 214
% identity 86

NCBI Description pyruvate, orthophosphate dikinase (EC 2.7.9.1) - common ice

plant >gi\_559471 emb CAA55143 (X78347)

pyruvate, orthophosphate dikinase [Mesembryanthemum

crystallinum]

Seq. No. 26962

Contig ID 148600\_1.R1040 5'-most EST pcp700992466.h1

Method BLASTX
NCBI GI g2760836
BLAST score 156
E value 1.0e-10
Match length 67
% identity 20

NCBI Description (AC003105) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 26963

Contig ID 148625\_1.R1040 5'-most EST wrg700788049.h1

Seq. No. 26964

Contig ID 148627\_1.R1040 5'-most EST wrg700788052.h1



Method BLASTX
NCBI GI g3004655
BLAST score 327
E value 2.0e-30
Match length 140
% identity 52

NCBI Description (AF017777) waclaw [Drosophila melanogaster]

Seq. No. 26965

Contig ID 148629\_1.R1040 5'-most EST wrg700788056.h1

Seq. No. 26966

Contig ID 148632 1.R1040 5'-most EST all700863205.h1

Seq. No. 26967

Contig ID 148660\_1.R1040

5'-most EST g4291611

Seq. No. 26968

Contig ID 148697\_1.R1040 5'-most EST wrg700788214.h1

Seq. No. 26969

Contig ID 148720\_1.R1040 5'-most EST fua701038872.h1

Seq. No. 26970

Contig ID 148721\_1.R1040 5'-most EST gsv701051145.h1

Method BLASTX
NCBI GI g461729
BLAST score 251
E value 8.0e-22
Match length 63
% identity 75

NCBI Description 10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) >gi\_2146744\_pir\_S65597 probable chaperonin, 10K -

Zurliden in helden vir 100000 (100000), local

Arabidopsis thaliana >gi\_166662 (L02843) 10 kDa chaperonin

[Arabidopsis thaliana]

Seq. No. 26971

Contig ID 148780\_1.R1040 5'-most EST wrg700788389.h1

Method BLASTX
NCBI GI g2264382
BLAST score 257
E value 2.0e-22
Match length 79
% identity 58

NCBI Description (AC002354) putative tetracycline transporter-like protein

[Arabidopsis thaliana]

Seq. No. 26972

Contig ID 148827\_1.R1040 5'-most EST leu701152971.h1



BLASTX Method q3550661 NCBI GI 276 BLAST score 2.0e-24 E value Match length 66 % identity 40 (AJ001310) 39 kDa EF-Hand containing protein [Solanum NCBI Description tuberosum] 26973 Seq. No. 148874 1.R1040 Contig ID dpv701096930.h1 5'-most EST BLASTX Method g3298548 NCBI GI BLAST score 371 7.0e-36 E value Match length 95 76 % identity (AC004681) putative spliceosomal protein [Arabidopsis NCBI Description thaliana] Seq. No. 26974 148877 1.R1040 Contig ID wrg700788603.hl 5'-most EST Method BLASTX q3023930 NCBI GI BLAST score 135 E value 4.0e-12 49 Match length % identity 67 HISTONE DEACETYLASE 1 (HD1) >gi 2654077 gb AAB87685\_ NCBI Description (AF032919) histone deacetylase [Strongylocentrotus purpuratus] 26975 Seq. No. 148879 1.R1040 Contig ID 5'-most EST  $jsh701\overline{0}65770.h1$ BLASTX Method g3513747 NCBI GI BLAST score 251 2.0e-21

E value Match length 98 % identity 53

(AF080118) contains similarity to reverse transcriptases NCBI Description (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]

26976 Seq. No.

148904 1.R1040 Contig ID

q4295808 5'-most EST BLASTX Method q4218011 NCBI GI BLAST score 241 4.0e-20 E value Match length 172 % identity 41

(AC006135) putative protein kinase [Arabidopsis thaliana] NCBI Description

>gi 4309721 gb AAD15491 (AC006439) putative

26983



## serine/threonine protein kinase [Arabidopsis thaliana]

```
26977
Seq. No.
                  148917 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy078h07b1
Seq. No.
                  26978
                  149002 1.R1040
Contig ID
5'-most EST
                  euj700697968.h1
                  26979
Seq. No.
                  149009 1.R1040
Contig ID
5'-most EST
                  xpa700797596.h1
Method
                  BLASTX
NCBI GI
                  g3128176
BLAST score
                  384
                  1.0e-36
E value
                  150
Match length
                   47
% identity
                  (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
                  26980
Seq. No.
                  149015 1.R1040
Contig ID
5'-most EST
                   jsh701065581.h1
                  BLASTX
Method
                  g3033398
NCBI GI
BLAST score
                   467
                  1.0e-46
E value
                  113
Match length
                  76
% identity
NCBI Description
                   (AC004238) putative phosphoribosylaminoimidazolecarboxamide
                   formyltransferase [Arabidopsis thaliana]
                   26981
Seq. No.
                   149062 1.R1040
Contig ID
5'-most EST
                   wrq700789023.h2
                   BLASTX
Method
NCBI GI
                   g3643088
BLAST score
                   114
                   4.0e-09
E value
Match length
                   117
% identity
                   46
NCBI Description
                  (AF075581) protein phosphatase-2C; PP2C [Mesembryanthemum
                   crystallinum]
Seq. No.
                   26982
Contig ID
                   149065 1.R1040
5'-most EST
                   epx701107708.h1
Method
                   BLASTX
NCBI GI
                   g537313
BLAST score
                   1276
E value
                   1.0e-141
Match length
                   287
% identity
                   53
                  (L36159) unknown protein [Medicago sativa]
NCBI Description
```



Contig ID 149082\_1.R1040 5'-most EST fC-gmse7000751091d1

Seq. No. 26984

Contig ID 149095\_1.R1040 5'-most EST jex700905143.h1

Seq. No. 26985

Contig ID 149106 1.R1040 5'-most EST wrg700789096.h2

Method BLASTX
NCBI GI g3128228
BLAST score 584
E value 1.0e-60
Match length 118
% identity 92

NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis

thaliana] >gi\_3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

Seq. No. 26986

Contig ID 149115\_1.R1040 5'-most EST wrg700789117.h1

Seq. No. 26987

Contig ID 149117 1.R1040

5'-most EST jC-gmle01810060c09d1

Seq. No. 26988

Contig ID 149117 2.R1040

5'-most EST g5677527

Seq. No. 26989

Contig ID 149142 1.R1040 5'-most EST smc700748115.h1

Seq. No. 26990

Contig ID 149143\_1.R1040 5'-most EST wrg700789212.h2

Method BLASTX
NCBI GI g3355308
BLAST score 766
E value 2.0e-81
Match length 256
% identity 60

NCBI Description (AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]

Seq. No. 26991

Contig ID 149148\_1.R1040 5'-most EST pcp700993475.h1

Seq. No. 26992

Contig ID 149160 1.R1040



E value 1.0e-7
Match length 191
% identity 67

NCBI Description CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)

(O-ACETYLSERINE (THIOL)-LYASE) (CSASE)

>gi\_1071911\_pir\_\_S46438 cysteine synthase (EC 4.2.99.8) watermelon >gi\_540497\_dbj\_BAA05965\_ (D28777) cysteine

synthase [Citrullus lanatus]

Seq. No. 26993

Contig ID 149168\_1.R1040 5'-most EST wrg700789246.h2

Method BLASTX
NCBI GI g3953463
BLAST score 360
E value 1.0e-34
Match length 91
% identity 78

NCBI Description (AC002328) F20N2.8 [Arabidopsis thaliana]

Seq. No. 26994

Contig ID 149176\_1.R1040 5'-most EST wrg700789255.h2

Seq. No. 26995

Contig ID 149188\_1.R1040 5'-most EST wrg700789268.h2

Method BLASTX
NCBI GI g3980410
BLAST score 209
E value 2.0e-16
Match length 141
% identity 35

NCBI Description (AC004561) putative receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 26996

Contig ID 149193\_1.R1040 5'-most EST wrg700789275.h2

Seq. No. 26997

Contig ID 149193 2.R1040

5'-most EST uC-gmflminsoy080c11b1

Seq. No. 26998

Contig ID 149198\_1.R1040 5'-most EST wrg700789285.h2

Method BLASTX
NCBI GI g3402683
BLAST score 570
E value 9.0e-61
Match length 155
% identity 75

NCBI Description (AC004697) patatin-like protein [Arabidopsis thaliana]

Seq. No. 26999

Contig ID 149204\_1.R1040



5'-most EST hrw701061007.h1

Seq. No. 27000

Contig ID 149204\_2.R1040 5'-most EST uC-gmronoir015d09b1

Seq. No. 27001

Contig ID 149219\_1.R1040 5'-most EST uC-gmropic092b12b1

Seq. No. 27002

Contig ID 149228\_1.R1040 5'-most EST zhf700956157.h1

Method BLASTX
NCBI GI g4314357
BLAST score 262
E value 9.0e-23
Match length 153
% identity 32

NCBI Description (AC006340) putative nucleic acid binding protein

[Arabidopsis thaliana]

Seq. No. 27003

Contig ID 149229 1.R1040

5'-most EST uC-gmflminsoy046f04b1

Method BLASTX
NCBI GI g4567227
BLAST score 581
E value 5.0e-60
Match length 197
% identity 60

NCBI Description (AC007119) putative transport protein [Arabidopsis

thaliana]

Seq. No. 27004

Contig ID 149246\_1.R1040 5'-most EST wrg700789354.h2

Seq. No. 27005

Contig ID 149248 1.R1040 5'-most EST rca701001671.h1

Method BLASTX
NCBI GI g437327
BLAST score 689
E value 2.0e-72
Match length 130
% identity 94

NCBI Description (L04497) MYB A; putative [Gossypium hirsutum]

Seq. No. 27006

Contig ID 149250 1.R1040

5'-most EST uC-gmflminsoy012a03b1

Method BLASTN
NCBI GI g1218003
BLAST score 184
E value 5.0e-99
Match length 391



% identity 87

NCBI Description Glycine max dynamin-like protein SDL5A mRNA, complete cds

Seq. No. 27007

Contig ID 149281 1.R1040 5'-most EST crh700854590.h1

Method BLASTX
NCBI GI g2980777
BLAST score 262
E value 7.0e-23
Match length 123
% identity 45

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 27008

Contig ID 149293\_1.R1040 5'-most EST zzp700831677.h1

Seq. No. 27009

Contig ID 149296\_1.R1040 5'-most EST fde700875241.h1

Method BLASTX
NCBI GI g2435517
BLAST score 319
E value 7.0e-30
Match length 84
% identity 68

NCBI Description (AF024504) contains similarity to peptidase family A1

[Arabidopsis thaliana]

Seq. No. 27010

Contig ID 149333\_1.R1040 5'-most EST wrg700789476.h2

Seq. No. 27011

Contig ID 149339\_1.R1040 5'-most EST bth700843894.h1

Method BLASTX
NCBI GI g2129918
BLAST score 149
E value 5.0e-10
Match length 62
% identity 53

NCBI Description BPF-1 protein - parsley >gi\_396197\_emb\_CAA48413\_ (X68337)

BPF-1 [Petroselinum crispum] >gi\_441310\_emb\_CAA44518\_

(X62653) BPF-1 [Petroselinum crispum]

Seq. No. 27012

Contig ID 149342\_1.R1040 5'-most EST kl1701204637.h1

Method BLASTX
NCBI GI g2809246
BLAST score 260
E value 8.0e-23
Match length 70
% identity 67

NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]



Contig ID 149363 1.R1040 pmv700892134.h1 5'-most EST

BLASTX Method NCBI GI g529707 BLAST score 180 3.0e-16 E value 89 Match length 47 % identity

(U13070) No definition line found [Caenorhabditis elegans] NCBI Description

27014 Seq. No.

149364 1.R1040 Contig ID 5'-most EST wrg700789519.h2

Method BLASTX g3600061 NCBI GI BLAST score 181 E value 1.0e-13 Match length 44 % identity 70

(AF080120) contains similarity to DNA binding proteins NCBI Description

[Arabidopsis thaliana]

Seq. No. 27015

149371 1.R1040 Contig ID

5'-most EST q4300575Method BLASTX NCBI GI g1765899 BLAST score 753 E value 3.0e-80 Match length 174 74

% identity

(Y07917) Spot 3 protein [Arabidopsis thaliana] >gi\_1839244 NCBI Description (U86700) EGF receptor like protein [Arabidopsis thaliana]

Seq. No. 27016

149380 1.R1040 Contig ID 5'-most EST wrg700789542.h2

BLASTX Method NCBI GI q3695408 BLAST score 149 E value 1.0e-09 73 Match length % identity

(AF096373) contains similarity to Solanum lycopersicum NCBI Description

(tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >qi 4538956 emb CAB39780.1 (AL049488) probable

wound-induced protein [Arabidopsis thaliana]

27017 Seq. No.

Contig ID 149398 1.R1040  $k11701\overline{2}06935.h1$ 5'-most EST

Seq. No. 27018

149398 2.R1040 Contig ID 5'-most EST zsg701121559.h1



Contig ID 149413\_1.R1040 5'-most EST wrg700789585.h2

Seq. No. 27020

Contig ID 149425 1.R1040 5'-most EST zhf700961927.h1

Method BLASTX
NCBI GI g2369714
BLAST score 633
E value 5.0e-66
Match length 186
% identity 71

NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 27021

Contig ID 149425\_2.R1040 5'-most EST leu701146156.h1

Method BLASTX
NCBI GI g2369714
BLAST score 138
E value 1.0e-10
Match length 50
% identity 82

NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 27022

Contig ID 149450\_1.R1040 5'-most EST wrg700789631.h2

Method BLASTN
NCBI GI g3985958
BLAST score 50
E value 3.0e-19
Match length 170
% identity 82

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MZN1, complete sequence [Arabidopsis thaliana]

Seq. No. 27023

Contig ID 149458\_1.R1040 5'-most EST wrg700789641.h2

Seq. No. 27024

Contig ID 149462 1.R1040

5'-most EST jC-qmle01810087b04a1

Method BLASTX
NCBI GI g476961
BLAST score 586
E value 1.0e-60
Match length 167
% identity 71

NCBI Description chromodomain-helicase-DNA-binding protein, CHD-1 - mouse

Seq. No. 27025

Contig ID 149470\_1.R1040 5'-most EST vzy700755452.h1



```
27026
Seq. No.
                  149493 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400004g01d1
Seq. No.
                  27027
                  149535 1.R1040
Contig ID
                  wrg700789744.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1168654
BLAST score
                  312
E value
                  6.0e-29
Match length
                  78
                  69
% identity
NCBI Description
                  BETA-GALACTOSIDASE PRECURSOR (LACTASE)
                  >gi 542198 pir S41889 beta-galactosidase (EC 3.2.1.23) -
                  garden asparagus >gi 452712 emb CAA54525 (X77319)
                  beta-galactosidase [Asparagus officinalis]
Seq. No.
                  27028
                  149564 1.R1040
Contig ID
5'-most EST
                  cf1700863631.h1
                  BLASTX
Method
                  g2583123
NCBI GI
BLAST score
                  243
E value
                  1.0e-20
                  77
Match length
                  60
% identity
                  (AC002387) putative nucleotide sugar epimerase [Arabidopsis
NCBI Description
                  thaliana]
                  27029
Seq. No.
Contig ID
                  149596 1.R1040
5'-most EST
                  wrq700789823.h2
Seq. No.
                  27030
Contig ID
                  149615 1.R1040
5'-most EST
                  g4302093
Seq. No.
                  27031
Contig ID
                  149619 1.R1040
5'-most EST
                  jC-gmle01810004e04a1
Method
                  BLASTX
NCBI GI
                  q3328240
BLAST score
                  425
E value
                  6.0e-42
Match length
                  125
% identity
                  62
                  (AF064775) early nodule-specific protein [Medicago
NCBI Description
                  truncatula]
```

Contig ID 149635 1.R1040

5'-most EST jC-gmst02400045f07a1

Seq. No. 27033

Contig ID 149670\_1.R1040



5'-most EST bth700847278.h1

Seq. No. 27034

Contig ID 149676\_1.R1040 5'-most EST wrg700789950.h2

Seq. No. 27035

Contig ID 149678\_1.R1040

5'-most EST jC-gmst02400031g08d1

Seq. No. 27036

Contig ID 149680 1.R1040

5'-most EST jC-gmle01810012c09d1

Seq. No. 27037

Contig ID 149717 1.R1040 5'-most EST wrg700790013.h2

Seq. No. 27038

Contig ID 149721\_1.R1040 5'-most EST awf700838213.h1

Seq. No. 27039

Contig ID 149733\_1.R1040 5'-most EST wrg700790036.h2

Seq. No. 27040

Contig ID 149737 1.R1040 5'-most EST leu701147009.h1

Seq. No. 27041

Contig ID 149741 1.R1040 5'-most EST wrg700790044.h2

Seq. No. 27042

Contig ID 149790\_1.R1040 5'-most EST wrg700790186.h1

Method BLASTX
NCBI GI g3643611
BLAST score 480
E value 4.0e-48
Match length 103
% identity 86

NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No. 27043

Contig ID 149814\_1.R1040 5'-most EST asn701138651.h1

Method BLASTX
NCBI GI g3603401
BLAST score 304
E value 5.0e-28
Match length 92
% identity 63

NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No. 27044



Contig ID 149817 1.R1040

5'-most EST g5752548
Method BLASTX
NCBI GI g3757520
BLAST score 174
E value 2.0e-12
Match length 142
% identity 40

NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 27045

Contig ID 149844 1.R1040 5'-most EST wrg700790274.h2

Method BLASTN
NCBI GI g2293111
BLAST score 165
E value 1.0e-87
Match length 456
% identity 84

NCBI Description V.faba mRNA for potassium channel

Seq. No. 27046

Contig ID 149871 1.R1040 5'-most EST wrg700790603.h2

Method BLASTX
NCBI GI g498038
BLAST score 303
E value 5.0e-28
Match length 82
% identity 63

NCBI Description (L33792) lipid transfer protein [Senecio odorus]

Seq. No. 27047

Contig ID 149877\_1.R1040 5'-most EST wrg700790319.h2

Seq. No. 27048

Contig ID 149882 1.R1040 5'-most EST wrg700790324.h2

Seq. No. 27049

Contig ID 149883\_1.R1040 5'-most EST wrg700790325.h2

Seq. No. 27050

Contig ID 149889\_1.R1040 5'-most EST wrg700790435.h2

Seq. No. 27051

Contig ID 149893\_1.R1040 5'-most EST gsv701049523.h1

Seq. No. 27052

Contig ID 149911\_1.R1040 5'-most EST rca701001536.h1

Method BLASTX NCBI GI g3738298



BLAST score 166 E value 8.0e-12 Match length 93 % identity 41

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana] >gi 4249394 (AC006072) unknown protein [Arabidopsis

thaliana]

Seq. No. 27053

Contig ID 149912\_1.R1040 5'-most EST fC-gmst700790363y3

Method BLASTX
NCBI GI g462147
BLAST score 755
E value 1.0e-80
Match length 154
% identity 92

NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)

(PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi\_541866\_pir\_\_S41808 glucose-6-phosphate isomerase

(EC 5.3.1.9) - Arabidopsis thaliana

>gi\_415923\_emb\_CAA48940\_ (X69195) glucose-6-phosphate

isomerase [Arabidopsis thaliana]

Seq. No. 27054

Contig ID 149918 1.R1040

5'-most EST jC-gmst02400007h06a1

Seq. No. 27055

Contig ID 149923\_1.R1040 5'-most EST leu701146762.h1

Method BLASTX
NCBI GI g4140026
BLAST score 655
E value 1.0e-68
Match length 196
% identity 64

NCBI Description (AB009370) flavonoid 3-O-galactosyl transferase [Vigna

mungo]

Seq. No. 27056

Contig ID 149924 1.R1040

5'-most EST jC-gmf102220052g10a1

Method BLASTX
NCBI GI g3176725
BLAST score 375
E value 5.0e-36
Match length 151
% identity 48

NCBI Description (AC002392) unknown protein [Arabidopsis thaliana]

Seq. No. 27057

Contig ID 149925\_2.R1040 5'-most EST epx701104301.h1

Seq. No. 27058

Contig ID 149926\_1.R1040

```
wrg700790636.h2
5'-most EST
                  BLASTX
Method
                  g2854049
NCBI GI
                  148
BLAST score
                  3.0e-09
E value
Match length
                  80
                  39
% identity
                  (AF044260) receptor serine/threonine kinase; protein kinase
NCBI Description
                   [Oryza sativa]
                  27059
Seq. No.
                  149933 1.R1040
Contig ID
                  zhf700953875.h1
5'-most EST
                  BLASTX
Method
                  g4508077
NCBI GI
BLAST score
                  213
                  3.0e-17
E value
                  73
Match length
                  59
% identity
                  (AC005882) 62114 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   27060
                  149965 1.R1040
Contig ID
                   epx701104103.h1
5'-most EST
Method
                  BLASTX
                   q2961384
NCBI GI
                   169
BLAST score
                   4.0e-12
E value
                   83
Match length
                   35
% identity
                   (AL022141) aldehyde dehydrogenase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   27061
Seq. No.
                   149975 1.R1040
Contig ID
                   zzp700829909.h1
5'-most EST
                   BLASTX
Method
                   q2947062
NCBI GI
BLAST score
                   144
                   2.0e-09
E value
                   66
Match length
                   56
% identity
NCBI Description (AC002521) unknown protein [Arabidopsis thaliana]
Seq. No.
                   27062
                   150015 1.R1040
Contig ID
5'-most EST
                   fde700875304.h1
```

Method BLASTX
NCBI GI g3005983
BLAST score 461
E value 2.0e-46
Match length 104
% identity 84

NCBI Description (Y14387) lycopene epsilon-cyclase [Lycopersicon esculentum]

Seq. No. 27063

Contig ID 150033\_1.R1040



```
wrq700790543.h2
5'-most EST
                  27064
Seq. No.
                  150050 1.R1040
Contig ID
                  wrg700790567.h2
5'-most EST
                  27065
Seq. No.
                  150086 1.R1040
Contig ID
                  wrg700790621.h2
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4432848
                  158
BLAST score
                  7.0e-19
E value
                  80
Match length
                  74
% identity
                  (AC006300) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  27066
Seq. No.
                  150098_1.R1040
Contig ID
                  wrg700790641.h2
5'-most EST
Seq. No.
                  27067
                  150118 1.R1040
Contig ID
                  rca700997004.h1
5'-most EST
                  BLASTX
Method
                  q3914239
NCBI GI
BLAST score
                  209
                  1.0e-16
E value
                  73
Match length
                  53
% identity
                  PROTEIN PHOSPHATASE 2C ABI2 (PP2C)
NCBI Description
                  >gi_1945140_emb_CAA70163_ (Y08966) ABI2 protein phosphatase
                  2C [Arabidopsis thaliana] >gi 1945142 emb_CAA70162
                   (Y08965) ABI2 protein phosphatase 2C [Arabidopsis thaliana]
                  >gi 2564213_emb_CAA72538_ (Y11840) ABI2 [Arabidopsis
                  thaliana]
                  27068
Seq. No.
                  150131 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400006b05a1
Seq. No.
                  27069
                  150138 1.R1040
Contig ID
5'-most EST
                  sat701014816.h1
                   27070
Seq. No.
                  150146 1.R1040
Contig ID
                  wrq700790712.h1
5'-most EST
                   BLASTX
Method
```

Method BLASTX
NCBI GI g1167982
BLAST score 689
E value 3.0e-76
Match length 266
% identity 57

NCBI Description (U43892) ABC transporter-7 [Mus musculus]

Seq. No. 27071



419

Contig ID 150151\_1.R1040 5'-most EST jex700904456.h1

Method BLASTN
NCBI GI g534971
BLAST score 251
E value 1.0e-139

% identity 90
NCBI Description V.faba (var. minor) mRNA for alpha 1,4-glucan phosphorylase

L isoform

Seq. No. 27072

Match length

Contig ID 150178\_1.R1040 5'-most EST jC-qmf102220080q02a1

Method BLASTX
NCBI GI g2773249
BLAST score 175
E value 2.0e-12
Match length 77
% identity 45

NCBI Description (AF039707) glutamate carboxypeptidase II [Rattus

norvegicus]

Seq. No. 27073

Contig ID 150181\_1.R1040 5'-most EST wrg700790777.h1

Method BLASTX
NCBI GI g4262186
BLAST score 515
E value 3.0e-52
Match length 125
% identity 77

NCBI Description (AC005508) Highly similar to cullin 3 [Arabidopsis

thaliana]

Seq. No. 27074

Contig ID 150183\_1.R1040 5'-most EST bth700846128.h1

Seq. No. 27075

Contig ID 150245\_1.R1040 5'-most EST wrg700790893.h1

Method BLASTX
NCBI GI g2618689
BLAST score 362
E value 2.0e-34
Match length 106
% identity 74

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 27076

Contig ID 150246\_1.R1040 5'-most EST wrg700790894.h1

Seq. No. 27077

Contig ID 150272\_1.R1040 5'-most EST wrg700791278.h1



Seq. No. 27078

Contig ID 150285 1.R1040 5'-most EST wrg700790970.h1

Seq. No. 27079

Contig ID 150293 1.R1040 5'-most EST epx701107494.h1

Seq. No. 27080

Contig ID 150313\_1.R1040 5'-most EST uC-gmronoir064g02b1

Seq. No. 27081

Contig ID 150335\_1.R1040 5'-most EST zsg701118364.h1

Seq. No. 27082

Contig ID 150338\_1.R1040 5'-most EST wrg700791052.h1

Method BLASTX
NCBI GI g3420054
BLAST score 173
E value 1.0e-12
Match length 78
% identity 45

NCBI Description (AC004680) unknown protein [Arabidopsis thaliana]

Seq. No. 27083

Contig ID 150352\_1.R1040 5'-most EST wrg700791071.h1

Method BLASTX
NCBI GI g2674203
BLAST score 444
E value 2.0e-44
Match length 96
% identity 92

NCBI Description (AF036328) CLP protease regulatory subunit CLPX

[Arabidopsis thaliana]

Seq. No. 27084

Contig ID 150363\_1.R1040 5'-most EST eep700868248.h1

Seq. No. 27085

Contig ID 150365\_1.R1040

5'-most EST g5677813

Seq. No. 27086

Contig ID 150377 1.R1040

5'-most EST g5342507

Seq. No. 27087

Contig ID 150380\_1.R1040 5'-most EST wrg700791131.h1

Seq. No. 27088



Contig ID 150387\_1.R1040 5'-most EST vzy700756265.h1

Method BLASTX
NCBI GI g1174470
BLAST score 295
E value 1.0e-26
Match length 97
% identity 60

NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)

(INTEGRAL MEMBRANE PROTEIN 1) >gi\_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi\_1588285\_prf\_\_2208301A

integral membrane protein [Mus musculus]

Seq. No. 27089

Contig ID 150387\_2.R1040

5'-most EST g5753716
Method BLASTX
NCBI GI g1174470
BLAST score 253
E value 7.0e-22
Match length 70
% identity 63

NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)

(INTEGRAL MEMBRANE PROTEIN 1) >gi\_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi\_1588285 prf\_\_2208301A

integral membrane protein [Mus musculus]

Seq. No. 27090

Contig ID 150407\_1.R1040 5'-most EST wrg700791493.h1

Seq. No. 27091

Contig ID 150409\_1.R1040 5'-most EST jC-gmro02910012h12d1

Method BLASTX
NCBI GI g123178
BLAST score 358
E value 5.0e-34
Match length 77
% identity 88

NCBI Description HISTIDINOL DEHYDROGENASE, CHLOROPLAST PRECURSOR (HDH)

>gi\_99844\_pir\_\_A39358 histidinol dehydrogenase (EC
1.1.1.23) precursor, chloroplast - cabbage >gi\_167142
(M60466) histidinol dehydrogenase [Brassica oleracea]

Seq. No. 27092

Contig ID 150413\_1.R1040 5'-most EST asn701137565.h1

Seq. No. 27093

Contig ID 150413\_2.R1040

5'-most EST  $jC-gms\overline{t}02400008e07a1$ 

Seq. No. 27094

Contig ID 150425\_1.R1040 5'-most EST sat701004066.h1

Method BLASTX



```
q3135611
NCBI GI
                   354
BLAST score
                  1.0e-33
E value
                   109
Match length
                   62
% identity
                   (AF062485) cellulose synthase [Arabidopsis thaliana]
NCBI Description
                   27095
Seq. No.
                   150477 1.R1040
Contig ID
                   jC-gmle01810091g09a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2398831
                   392
BLAST score
                   8.0e-38
E value
                   213
Match length
                   43
% identity
                   (X75542) 4-coumarate:CoA ligase [Vanilla planifolia]
NCBI Description
                   27096
Seq. No.
                   150525 1.R1040
Contig ID
                   wrg700791515.h1
5'-most EST
Seq. No.
                   27097
                   150529 1.R1040
Contig ID
                   wrg700791520.h1
5'-most EST
                   27098
Seq. No.
                   150562 1.R1040
Contig ID
                   rca700999075.h1
5'-most EST
                   BLASTX
Method
                   g3096949
NCBI GI
                   262
BLAST score
E value
                   4.0e-34
                   88
Match length
                   74
% identity
                   (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                    [Arabidopsis thaliana] >gi 3894399 (AF067798) cyclic
                   nucleotide-gated cation channel [Arabidopsis thaliana]
                   27099
Seq. No.
                   150583 1.R1040
Contig ID
                   jsh701\overline{0}68834.h1
5'-most EST
                   27100
Seq. No.
                   150617 1.R1040
Contig ID
                   wrg700791687.hl
 5'-most EST
                   BLASTX
Method
                    q2864610
NCBI GI
BLAST score
                    168
                    6.0e-12
E value
```

% identity

Match length

(AL021811) putative protein [Arabidopsis thaliana] NCBI Description >gi\_4049336\_emb\_CAA22561\_ (AL034567) putative protein

[Arabidopsis thaliana]

Seq. No.

27101

45

64



```
150635 1.R1040
Contig ID
                  pxt700944468.h1
5'-most EST
                  BLASTX
Method
                  g2117620
NCBI GI
BLAST score
                  447
                  2.0e-44
E value
                  101
Match length
                  86
% identity
                  peroxidase (EC 1.11.1.7) 1A - alfalfa
NCBI Description
                  >gi_971558_emb_CAA62225_ (X90692) peroxidase1A [Medicago
                  sativa]
                  27102
Seq. No.
                  150638 1.R1040
Contig ID
                  leu701149501.h1
5'-most EST
Seq. No.
                  27103
                  150641 1.R1040
Contig ID
                  smc700745926.h1
5'-most EST
                  27104
Seq. No.
                  150666 1.R1040
Contig ID
                  vzy700755518.h1
5'-most EST
                  BLASTX
Method
                  g2129609
NCBI GI
                   284
BLAST score
                   1.0e-25
E value
                   82
Match length
                  70
% identity
                  HD-ZIP protein - Arabidopsis thaliana
NCBI Description
                   >gi 1212757 emb CAA91183 (Z54356) HD-ZIP (Arabidopsis
                   thaliana]
                   27105
Seq. No.
                   150677 1.R1040
Contig ID
                   wrg700791793.hl
5'-most EST
                   BLASTN
Method
                   g4115338
NCBI GI
BLAST score
                   104
                   2.0e-51
E value
Match length
                   207
                   26
% identity
NCBI Description Pisum sativum (Alaska) ubuquitin (PUB4) gene, complete cds
                   27106
Seq. No.
                   150699 1.R1040
Contig ID
                   jC-gmle01810088h12a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1169586
                   184
BLAST score
                   7.0e-14
E value
Match length
                   39
```

% identity

FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC NCBI Description

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (CY-F1) >gi\_542079 pir\_\_S41287 fructose-bisphosphatase (EC 3.1.3.11) - potato >gi 440591\_emb\_CAA54265\_ (X76946)



fructose-1,6-bisphosphatase [Solanum tuberosum]

Seq. No. 27107

Contig ID 150712 1.R1040

5'-most EST jC-gmf102220050b08d1

Seq. No. 27108

Contig ID 150715\_1.R1040 5'-most EST rca701002482.h1

Method BLASTX
NCBI GI g2673918
BLAST score 403
E value 4.0e-39
Match length 96
% identity 77

NCBI Description (AC002561) unknwon protein [Arabidopsis thaliana]

Seq. No. 27109

Contig ID 150721\_1.R1040 5'-most EST kmv700743705.h1

Method BLASTX
NCBI GI g2443350
BLAST score 172
E value 3.0e-19
Match length 95
% identity 53

NCBI Description (AB001380) cytochrome P450 [Glycyrrhiza echinata]

Seq. No. 27110

Contig ID 150726 1.R1040 5'-most EST wrg700791890.h1

Method BLASTX

NCBI GI g3176714

BLAST score 464

E value 3.0e-46

Match length 117

% identity 74

NCBI Description (AC002392) putative tRNA-splicing endonuclease positive

effector [Arabidopsis thaliana]

Seq. No. 27111

Contig ID 150738\_1.R1040 5'-most EST wrg700792261.h1

Method BLASTX
NCBI GI g3461813
BLAST score 279
E value 3.0e-25
Match length 83
% identity 64

NCBI Description (AC004138) putative sucrose/H+ symporter [Arabidopsis

thaliana]

Seq. No. 27112

Contig ID 150739\_1.R1040 5'-most EST leu701153333.h1

Method BLASTX NCBI GI g4567249

4223



BLAST score 514 E value 4.0e-52 Match length 133 % identity 68

NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27113

Contig ID 150757\_1.R1040 5'-most EST wrg700791938.h1

Seq. No. 27114

Contig ID 150761\_1.R1040 5'-most EST wrg700791948.h1

Seq. No. 27115

Contig ID 150784\_1.R1040 5'-most EST rca701000693.h1

Seq. No. 27116

Contig ID 150787\_1.R1040

5'-most EST g5753431

Method BLASTX

NCBI GI g3395435

BLAST score 216

E value 4.0e-17

Match length 139

% identity 41

NCBI Description (AC004683) myosin heavy chain-like protein [Arabidopsis

thaliana]

Seq. No. 27117

Contig ID 150801\_1.R1040 5'-most EST dpv701102331.h1

Method BLASTX
NCBI GI g1922248
BLAST score 260
E value 7.0e-23
Match length 68
% identity 75

NCBI Description (Y10087) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27118

Contig ID 150807\_1.R1040 5'-most EST wrg700792046.h1

Method BLASTX
NCBI GI g2245026
BLAST score 341
E value 3.0e-32
Match length 91
% identity 76

NCBI Description (297341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27119

Contig ID 150809\_1.R1040 5'-most EST wrg700792048.h1

Seq. No. 27120



Contig ID 150828\_1.R1040 5'-most EST kl1701207943.h1

Seq. No. 27121

Contig ID 150830\_1.R1040 5'-most EST jC-gmst02400051b01a1

Method BLASTX
NCBI GI g2443887
BLAST score 911
E value 2.0e-98
Match length 285
% identity 65

NCBI Description (AC002294) Similar to transcription factor

gb Z46606 1658307 and others [Arabidopsis thaliana]

Seq. No. 27122

Contig ID 150851\_1.R1040 5'-most EST gsv701056442.h1

Seq. No. 27123

Contig ID 150868 1.R1040 5'-most EST wrg700792214.h1

Seq. No. 27124

Contig ID 150869\_1.R1040 5'-most EST fde700875090.h1

Method BLASTX
NCBI GI g3600059
BLAST score 367
E value 3.0e-35
Match length 103
% identity 62

NCBI Description (AF080120) contains similarity to WB domains, G-beta

repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03)

[Arabidopsis thaliana]

Seq. No. 27125

Contig ID 150893\_2.R1040 5'-most EST hrw701059939.h1

Seq. No. 27126

Contig ID 150914\_1.R1040 5'-most EST kl1701214979.h1

Seq. No. 27127

Contig ID 150927\_1.R1040 5'-most EST pcp700988714.h1

Seq. No. 27128

Contig ID 150946\_1.R1040 5'-most EST pcp700988754.h1

Seq. No. 27129

Contig ID 150949\_1.R1040 5'-most EST pcp700990760.h1

Method BLASTX NCBI GI g3135269



BLAST score 4.0e-12 E value 81 Match length 51 % identity

(AC003058) unknown protein [Arabidopsis thaliana] NCBI Description

27130 Seq. No.

150955 1.R1040 Contig ID 5'-most EST pcp700988771.hl

27131 Seq. No.

150958 1.R1040 Contig ID 5'-most EST pcp700990778.hl

27132 Seq. No.

150967 1.R1040 Contig ID zhf700961446.hl 5'-most EST

27133 Seq. No.

150991 1.R1040 Contig ID pcp700988848.hl 5'-most EST

Method BLASTX NCBI GI q4056420 BLAST score 376 4.0e-36 E value 111 Match length 65 % identity

(ACO05322) ESTs gb\_T144077 and gb\_T43352 come from this NCBI Description

gene. [Arabidopsis thaliana]

27134 Seq. No.

Contig ID 150999 1.R1040 5'-most EST pcp700988872.h1

BLASTX Method NCBI GI g4097549 BLAST score 162 E value 8.0e-11 Match length 72 % identity 43

(U64907) ATFP4 [Arabidopsis thaliana] NCBI Description

Seq. No. 27135

Contig ID 151005 1.R1040  $zhf700\overline{9}61259.h1$ 5'-most EST

Method BLASTX q2072626 NCBI GI BLAST score 309 4.0e-28 E value Match length 108 62 % identity

(Y12904) hypothetical protein [Arabidopsis thaliana] NCBI Description

>qi 3281856 emb CAA19751 (AL031004) Transcription factor

II homolog [Arabidopsis thaliana]

27136 Seq. No.

151022 1.R1040 Contig ID 5'-most EST awf700838786.hl



Method BLASTX
NCBI GI g4558556
BLAST score 461
E value 3.0e-46
Match length 125
% identity 70

NCBI Description (AC007138) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 27137

Contig ID 151031\_2.R1040 5'-most EST uC-gmronoir014g07b1

Seq. No. 27138

Contig ID 151032\_1.R1040 5'-most EST zsg701118058.h2

Seq. No. 27139

Contig ID 151032\_2.R1040 5'-most EST jC-gmro02910063a07a1

Seq. No. 27140

Contig ID 151033\_1.R1040

5'-most EST jC-gmf102220062b09a1

Method BLASTX
NCBI GI g3928084
BLAST score 342
E value 3.0e-32
Match length 132
% identity 50

NCBI Description (AC005770) retrotransposon-like protein [Arabidopsis

thaliana]

Seq. No. 27141

Contig ID 151050\_1.R1040 5'-most EST pcp700991001.h1

Seq. No. 27142

Contig ID 151060\_1.R1040 5'-most EST zsg701125820.h1

Method BLASTX
NCBI GI g1617219
BLAST score 741
E value 2.0e-78
Match length 218
% identity 67

NCBI Description (X99301) CPD photolyase [Arabidopsis thaliana] >gi\_2984707

(AF053365) type II CPD photolyase PHR1 [Arabidopsis

thaliana]

Seq. No. 27143

Contig ID 151061 1.R1040 5'-most EST pmv700888961.h1

Seq. No. 27144

Contig ID 151061\_2.R1040 5'-most EST pcp700991019.h1



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27145
Seq. No.
                  151062 1.R1040
Contig ID
                  pcp700991020.hl
5'-most EST
                  27146
Seq. No.
                  151063 1.R1040
Contig ID
                  sat701010434.hl
5'-most EST
Seq. No.
                  27147
                  151064 1.R1040
Contig ID
                  pxt700944710.hl
5'-most EST
                  BLASTX
Method
                  q3738302
NCBI GI
                  396
BLAST score
                  3.0e-38
E value
Match length
                  202
                  46
% identity
                   (AC005309) tubby-like protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4249398 (AC006072) putative tubby protein [Arabidopsis
                  thaliana]
Seq. No.
                  27148
                  151069 1.R1040
Contig ID
                  pcp700989034.h1
5'-most EST
                  BLASTX
Method
                  g4539389
NCBI GI
                   320
BLAST score
                   5.0e-30
E value
                  82
Match length
                  77
% identity
                  (AL035526) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   27149
                   151075 1.R1040
Contig ID
                   sat701014344.h1
5'-most EST
                   BLASTX
Method
                   g2673947
NCBI GI
BLAST score
                   277
                   1.0e-24
E value
Match length
                   98
                   31
% identity
                   (U62931) multidrug resistance protein 1 [Aspergillus
NCBI Description
                   flavus] >gi 2673949 (U62932) multidrug resistance protein 1
                   [Aspergillus flavus]
                   27150
Seq. No.
```

151076 1.R1040 Contig ID

g5688315 5'-most EST

27151 Seq. No.

Contig ID 151083 1.R1040 5'-most EST pcp700991064.hl

BLASTX Method NCBI GI q3695019 BLAST score 225 E value 7.0e-19



Match length 81 % identity 54

NCBI Description (AF055848) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 27152

Contig ID 151087\_1.R1040 5'-most EST pcp700991071.h1

Seq. No. 27153

Contig ID 151095\_1.R1040 5'-most EST pcp700991080.h1

Seq. No. 27154

Contig ID 151127\_1.R1040 5'-most EST pcp700989157.h1

Method BLASTX
NCBI GI g2660670
BLAST score 469
E value 7.0e-48
Match length 117
% identity 83

NCBI Description (AC002342) putative Cu2+-transporting ATPase [Arabidopsis

thaliana]

Seq. No. 27155

Contig ID 151135\_1.R1040 5'-most EST fde700875359.h1

Method BLASTX
NCBI GI g4468804
BLAST score 178
E value 4.0e-13
Match length 108
% identity 23

NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 27156

Contig ID 151152\_1.R1040 5'-most EST kl1701214981.h1

Method BLASTX
NCBI GI g283966
BLAST score 590
E value 6.0e-61
Match length 173
% identity 67

NCBI Description activator 1 37K chain - human

Seq. No. 27157

Contig ID 151161\_1.R1040 5'-most EST pcp700989236.h1

Seq. No. 27158

Contig ID 151183\_1.R1040 5'-most EST zsq701122867.h1

Method BLASTN
NCBI GI g1396053
BLAST score 272
E value 1.0e-151



Match length 644 % identity 86

NCBI Description Pisum sativum mRNA for phosphoribosylanthranilate

transferase, partial cds

Seq. No. 27159

Contig ID 151188 1.R1040

5'-most EST jC-gmfl02220113a12d1

Method BLASTX
NCBI GI g3894193
BLAST score 155
E value 2.0e-10
Match length 56
% identity 52

NCBI Description (AC005662) putative strictosidine synthase [Arabidopsis

thaliana]

Seq. No. 27160

Contig ID 151203\_1.R1040

5'-most EST jC-gmfl02220089e02d1

Method BLASTX
NCBI GI g4512657
BLAST score 265
E value 4.0e-23
Match length 77
% identity 58

NCBI Description (AC006931) putative APG protein [Arabidopsis thaliana]

>gi\_4544463\_gb\_AAD22370.1\_AC006580\_2 (AC006580) putative

APG isolog protein [Arabidopsis thaliana]

Seq. No. 27161

Contig ID 151218\_1.R1040 5'-most EST sat701014153.h1

Seq. No. 27162

Contig ID 151244\_1.R1040 5'-most EST uC-gmropic006a01b1

Seq. No. 27163

Contig ID 151248\_1.R1040 5'-most EST pcp700989507.h1

Method BLASTX
NCBI GI g1168940
BLAST score 219
E value 9.0e-18
Match length 104
% identity 47

NCBI Description CHORISMATE MUTASE PRECURSOR (CM-1) >gi 629509 pir\_\_S38958

chorismate mutase precursor - Arabidopsis thaliana >gi\_429153\_emb\_CAA81286\_ (Z26519) chorismate mutase

precursor [Arabidopsis thaliana]

Seq. No. 27164

Contig ID 151249\_1.R1040 5'-most EST pcp700989509.h1

Seq. No. 27165



Contig ID 151252 1.R1040 5'-most EST asn701136972.h1

Seq. No. 27166

Contig ID 151256\_1.R1040 5'-most EST bth700847247.h1

Seq. No. 27167

Contig ID 151307 1.R1040

5'-most EST  $jC-gmf\overline{1}02220137e07a1$ 

Method BLASTX
NCBI GI g267421
BLAST score 176
E value 1.0e-12
Match length 106
% identity 49

NCBI Description DNA-REPAIR PROTEIN COMPLEMENTING XP-G CELLS HOMOLOG

(XERODERMA PIGMENTOSUM GROUP G COMPLEMENTING PROTEIN HOMOLOG) >gi\_422627\_pir\_\_S35994 DNA repair protein XPGC - African clawed frog >gi\_312433\_emb\_CAA49597 (X69977) XP-G

related factor [Xenopus laevis]

Seq. No. 27168

Contig ID 151324\_1.R1040 5'-most EST asn701142612.h1

Method BLASTX
NCBI GI g3540195
BLAST score 681
E value 7.0e-72
Match length 158
% identity 41

NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No. 27169

Contig ID 151334\_1.R1040 5'-most EST pcp700989637.h1

Method BLASTX
NCBI GI g4263818
BLAST score 251
E value 2.0e-21
Match length 134
% identity 43

NCBI Description (AC006067) unknown protein [Arabidopsis thaliana]

Seq. No. 27170

Contig ID 151361\_1.R1040 5'-most EST pcp700989680.h1

Seq. No. 27171

Contig ID 151366\_1.R1040 5'-most EST pcp700989685.h1

Seq. No. 27172

Contig ID 151373\_1.R1040 5'-most EST pcp700989794.h1

Seq. No. 27173

4231



Contig ID 151382\_1.R1040 5'-most EST pcp700989709.h1

Method BLASTX
NCBI GI g585053
BLAST score 335
E value 7.0e-59
Match length 205
% identity 57

NCBI Description MITOTIC CONTROL PROTEIN DIS3 >gi\_283075\_pir\_\_A41944 mitotic

control protein dis3+ - fission yeast (Schizosaccharomyces pombe) >gi\_173381 (M74094) mitotic control protein

[Schizosaccharomyces pombe] >gi\_3650393\_emb\_CAA21102\_

(AL031743) mitotic control protein dis3.

[Schizosaccharomyces pombe]

Seq. No. 27174

Contig ID 151382 2.R1040 5'-most EST hrw701060145.h1

Method BLASTX
NCBI GI g585053
BLAST score 265
E value 2.0e-23
Match length 93
% identity 57

NCBI Description MITOTIC CONTROL PROTEIN DIS3 >gi\_283075\_pir\_A41944 mitotic

control protein dis3+ - fission yeast (Schizosaccharomyces

pombe) >gi\_173381 (M74094) mitotic control protein [Schizosaccharomyces pombe] >gi\_3650393\_emb\_CAA21102\_

(AL031743) mitotic control protein dis3.

[Schizosaccharomyces pombe]

Seq. No. 27175

Contig ID 151391\_1.R1040 5'-most EST pcp700990227.h1

Seq. No. 27176

Contig ID 151402\_1.R1040 5'-most EST pcp700989740.h1

Method BLASTX
NCBI GI g4375829
BLAST score 449
E value 2.0e-59
Match length 143
% identity 81

NCBI Description (AJ011977) RNA-directed RNA polymerase [Arabidopsis

thaliana]

Seq. No. 27177

Contig ID 151408\_1.R1040 5'-most EST zhf700963853.h1

Method BLASTX
NCBI GI g3287695
BLAST score 403
E value 3.0e-44
Match length 119
% identity 76

NCBI Description (AC003979) Similar to hypothetical protein C34B7.2



gb\_1729503 from C. elegans cosmid gb\_Z83220. [Arabidopsis thaliana]

 Seq. No.
 27178

 Contig ID
 151408\_2.R1040

 5'-most EST
 hrw701058042.h1

 Method
 BLASTX

Method BLASIA NCBI GI g3287695 BLAST score 235 E value 6.0e-20 Match length 59 % identity 76

NCBI Description (AC003979) Similar to hypothetical protein C34B7.2

gb 1729503 from C. elegans cosmid gb\_Z83220. [Arabidopsis

thaliana]

Seq. No. 27179

Contig ID 151424\_1.R1040 5'-most EST pxt700945659.h1

Method BLASTX
NCBI GI g3341679
BLAST score 565
E value 2.0e-58
Match length 139
% identity 75

NCBI Description (AC003672) dynamin-like protein phragmoplastin 12

[Arabidopsis thaliana]

Seq. No. 27180

Contig ID 151453\_1.R1040 5'-most EST asn701134317.h1

Seq. No. 27181

Contig ID 151455 1.R1040 5'-most EST rca700999308.h1

Method BLASTX
NCBI GI g2911058
BLAST score 178
E value 3.0e-22
Match length 95
% identity 58

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 27182

Contig ID 151499\_1.R1040 5'-most EST pcp700989895.h1

Method BLASTX
NCBI GI g2500981
BLAST score 813
E value 2.0e-87
Match length 159
% identity 96

NCBI Description GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS)

>gi\_1084418\_pir\_\_S51685 glutamate--tRNA ligase (EC
6.1.1.17) - common tobacco >gi\_603867\_emb\_CAA58506\_
(X83524) glutamate--tRNA ligase [Nicotiana tabacum]



Seq. No. 27183

Contig ID 151503\_1.R1040 5'-most EST jC-gmf102220090d01d1

Method BLASTN
NCBI GI g1707656
BLAST score 340
E value 0.0e+00
Match length 528
% identity 91

NCBI Description P.sativum mRNA for DnaJ-like protein

Seq. No. 27184

Contig ID 151521\_1.R1040

5'-most EST uC-gmrominsoy272a07b1

Method BLASTX
NCBI GI g3548808
BLAST score 307
E value 4.0e-28
Match length 118
% identity 46

NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 27185

Contig ID 151547\_1.R1040 5'-most EST jC-gmfl02220051h11a1

Method BLASTX
NCBI GI g4218014
BLAST score 544
E value 9.0e-56
Match length 114
% identity 50

NCBI Description (AC006135) putative spliceosomal protein (RNA binding

protein) [Arabidopsis thaliana]

Seq. No. 27186

Contig ID 151555\_1.R1040 5'-most EST epx701106345.h1

Seq. No. 27187

Contig ID 151575\_1.R1040 5'-most EST pcp700990059.h1

Seq. No. 27188

Contig ID 151593 1.R1040 5'-most EST leu701154615.h1

Seq. No. 27189

Contig ID 151599\_1.R1040

5'-most EST jC-gmst02400037c02a1

Method BLASTX
NCBI GI g1213629
BLAST score 334
E value 6.0e-31
Match length 88
% identity 64

NCBI Description (X95991) pectinesterase [Prunus persica]



Seq. No. 151617 1.R1040 Contig ID kl1701211922.hl 5'-most EST BLASTX Method g4371285 NCBI GI 554 BLAST score 5.0e-57 E value 137 Match length 73 % identity (AC006260) hypothetical protein [Arabidopsis thaliana] NCBI Description 27191 Seq. No. 151624 1.R1040 Contig ID vzy700755958.h1 5'-most EST 27192 Seq. No. 151640 1.R1040 Contig ID pcp700990163.hl 5'-most EST 27193 Seq. No. 151652 1.R1040 Contig ID 5'-most EST pcp700990187.hl Method BLASTX g2190557 NCBI GI 272 BLAST score 2.0e-24 E value 71 Match length % identity 68 (ACO01229) F5I14.11 [Arabidopsis thaliana] NCBI Description 27194 Seq. No. Contig ID 151658 1.R1040 5'-most EST pcp700990202.h1 27195 Seq. No. 151699 1.R1040 Contig ID pcp700990264.hl 5'-most EST BLASTX Method NCBI GI g2465925 345 BLAST score 1.0e-32 E value Match length 122 % identity (AF024649) receptor-like serine/threonine kinase NCBI Description [Arabidopsis thaliana] Seq. No. 27196

151711 1.R1040 Contig ID 5'-most EST  $leu701\overline{1}53711.h1$ 

27197 Seq. No.

Contig ID 151713 1.R1040 5'-most EST dpv701098422.h1

Seq. No. 27198

151714 1.R1040 Contig ID 5'-most EST hrw701060337.h1



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27199
Seq. No.
                   151716 1.R1040
Contig ID
                   jC-gmle01810048c02a1
5'-most EST
                   BLASTX
Method
                   g1853970
NCBI GI
                   445
BLAST score
                   3.0e-44
E value
                   139
Match length
                   60
% identity
                   (D88122) CPRD46 protein [Vigna unguiculata]
NCBI Description
                   27200
Seq. No.
                   151721 1.R1040
Contig ID
                   pcp700990308.h1
5'-most EST
Seq. No.
                   27201
                   151750 1.R1040
Contig ID
                   uC-gmrominsoy315a04b1
5'-most EST
                   27202
Seq. No.
                   151785_1.R1040
Contig ID
                   dpv701\overline{0}97505.h1
5'-most EST
                   BLASTN
Method
                   q2852444
NCBI GI
                   147
BLAST score
                   9.0e-77
E value
                   347
Match length
                   86
% identity
NCBI Description Salix bakko mRNA for SUI1 homolog, complete cds
Seq. No.
                   27203
                   151813 1.R1040
Contig ID
                   jC-gmro02910016h12d1
5'-most EST
Seq. No.
                   27204
                   151863 1.R1040
Contig ID
                   pcp700990506.h1
5'-most EST
                   27205
Seq. No.
                   151877 1.R1040
Contig ID
                   vzy700756003.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4218120
                   362
BLAST score
                   9.0e-35
E value
Match length
                   102
% identity
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
```

Seq. No. 27206

Contig ID 151894\_1.R1040 5'-most EST gsv701051906.h1

thaliana]

Method BLASTX NCBI GI g4001803 BLAST score 147



E value 3.0e-09 Match length 44 % identity 57

NCBI Description (AF041474) BAF53a [Homo sapiens] >gi\_4218064\_dbj\_BAA74577\_

(AB015907) actin-related protein [Homo sapiens]

Seq. No. 27207

Contig ID 151959 1.R1040 5'-most EST epx701106226.h1

Method BLASTX
NCBI GI g3176709
BLAST score 143
E value 4.0e-09
Match length 72
% identity 42

NCBI Description (AC002392) putative anthranilate

N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis

thaliana]

Seq. No. 27208

Contig ID 151960 1.R1040 5'-most EST pcp700990806.h1

Method BLASTX
NCBI GI g2827534
BLAST score 471
E value 2.0e-47
Match length 108
% identity 87

NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 27209

Contig ID 151980\_1.R1040 5'-most EST pcp700990828.h1

Seq. No. 27210

Contig ID 151983\_1.R1040 5'-most EST pcp700990835.h1

Seq. No. 27211

Contig ID 151984\_1.R1040 5'-most EST pcp700990837.h1

Seq. No. 27212

Contig ID 151985\_1.R1040 5'-most EST sat701011675.h1

Method BLASTX
NCBI GI g4218991
BLAST score 222
E value 8.0e-20
Match length 94
% identity 53

NCBI Description (AF098632) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 27213

Contig ID 151989\_1.R1040 5'-most EST pcp700990844.h1



Seq. No. 27214

Contig ID 152017\_1.R1040 5'-most EST pcp700990879.h1

Seq. No. 27215

Contig ID 152030\_1.R1040 5'-most EST gsv701049324.h1

Seq. No. 27216

Contig ID 152032\_1.R1040 5'-most EST pcp700990902.h1

Method BLASTX
NCBI GI g1582580
BLAST score 167
E value 5.0e-17
Match length 78
% identity 68

NCBI Description caffeic acid O-methyltransferase [Stylosanthes humilis]

Seq. No. 27217

Contig ID 152057 1.R1040 5'-most EST pcp700990933.h1

Seq. No. 27218

Contig ID 152077\_1.R1040 5'-most EST uC-gmropic065f04b1

Method BLASTX
NCBI GI g4567197
BLAST score 433
E value 9.0e-43
Match length 132
% identity 60

NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]

Seq. No. 27219

Contig ID 152080\_1.R1040 5'-most EST jex700907316.h1

Seq. No. 27220

Contig ID 152094\_1.R1040

5'-most EST jC-gmle01810092f08a1

Method BLASTX
NCBI GI g2781357
BLAST score 178
E value 6.0e-13
Match length 57
% identity 70

NCBI Description (AC003113) F2401.13 [Arabidopsis thaliana]

Seq. No. 27221

Contig ID 152171\_1.R1040 5'-most EST zsg701117338.h1

Method BLASTX
NCBI GI g4314365
BLAST score 204
E value 3.0e-16
Match length 105



% identity NCBI Description

(AC006340) putative copia-like retrotransposon Hopscotch [Arabidopsis thaliana]

Seq. No. 27222

Contig ID 152182 1.R1040 5'-most EST kl1701204629.h1

Method BLASTN
NCBI GI g3868723
BLAST score 73

E value 1.0e-32 Match length 412 % identity 84

NCBI Description Arabidopsis thaliana chromosome V map 60.5 cM, complete

sequence [Arabidopsis thaliana]

Seq. No. 27223

Contig ID 152226\_1.R1040 5'-most EST kl1701214119.h1

Seq. No. 27224

Contig ID 152229 1.R1040 5'-most EST pcp700991187.h1

Seq. No. 27225

Contig ID 152236\_1.R1040 5'-most EST pcp700991196.h1

Method BLASTX
NCBI GI g4218062
BLAST score 250
E value 1.0e-21
Match length 115
% identity 41

NCBI Description (AB015906) actin-related protein [Homo sapiens]

Seq. No. 27226

Contig ID 152238\_1.R1040 5'-most EST uC-gmropic036h09b1

Seq. No. 27227

Contig ID 152253\_1.R1040

5'-most EST jC-gmro02910029a02d1

Seq. No. 27228

Contig ID 152262 1.R1040

5'-most EST g4397342

Seq. No. 27229

Contig ID 152289\_1.R1040 5'-most EST pcp700991276.h1

Seq. No. 27230

Contig ID 152306\_1.R1040 5'-most EST zhf700961049.h1

Method BLASTX NCBI GI g3024426 BLAST score 143



E value 90 Match length 44 % identity

PYRUVATE, PHOSPHATE DIKINASE PRECURSOR NCBI Description

(PYRUVATE,ORTHOPHOSPHATE DIKINASE) >gi 1084302\_pir\_\_S55478 pyruvate, orthophosphate dikinase (EC 2.7.9.1) - common ice

plant >gi 854265 emb CAA57872\_ (X82489)

pyruvate, orthophosphate dikinase [Mesembryanthemum

crystallinum]

27231 Seq. No.

152323 1.R1040 Contig ID leu701149479.h1 5'-most EST

BLASTX Method g4455299 NCBI GI BLAST score 264 3.0e-23 E value 73 Match length 75 % identity

(AL035528) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 27232

152332 1.R1040 Contig ID 5'-most EST epx701108066.hl

27233 Seq. No.

152345 1.R1040 Contig ID zhf700954390.h1 5'-most EST

27234 Seq. No.

152397 1.R1040 Contig ID 5'-most EST pcp700991432.h1

Method BLASTX g2865433 NCBI GI 142 BLAST score 7.0e-09 E value 81 Match length 37 % identity

(AF039374) chromomethylase [Arabidopsis suecica] NCBI Description

27235 Seq. No.

152399 1.R1040 Contig ID 5'-most EST jC-gmle01810047e05a1

BLASTX Method NCBI GI q541816 BLAST score 1689 0.0e + 00E value Match length 398 % identity 81

protein kinase - common ice plant >qi 457689 emb CAA82990 NCBI Description

(Z30329) protein kinase [Mesembryanthemum crystallinum]

27236 Seq. No.

152410 1.R1040 Contig ID 5'-most EST smc700746390.hl

Seq. No. 27237



Contig ID 152421\_1.R1040 5'-most EST rlr700896803.h1

Method BLASTX
NCBI GI g4309698
BLAST score 399
E value 1.0e-38
Match length 133
% identity 65

NCBI Description (AC006266) putative glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 27238

Contig ID 152428\_1.R1040 5'-most EST dpv701102248.h1

Seq. No. 27239

Contig ID 152430\_1.R1040 5'-most EST pcp700991510.h1

Seq. No. 27240

Contig ID 152435\_1.R1040 5'-most EST eep700866705.h1

Method BLASTX
NCBI GI g3702332
BLAST score 141
E value 1.0e-15
Match length 85
% identity 45

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.

Contig ID 152449\_1.R1040 5'-most EST pcp700991553.h1

27241

Method BLASTX
NCBI GI g4220514
BLAST score 376
E value 4.0e-36
Match length 142
% identity 57

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 27242

Contig ID 152456\_1.R1040 5'-most EST pmv700892711.h1

Seq. No. 27243

Contig ID 152459\_1.R1040 5'-most EST pcp700991575.h1

Method BLASTX
NCBI GI g1854386
BLAST score 236
E value 5.0e-20
Match length 56
% identity 73

NCBI Description (AB001375) similar to soluble NSF attachment protein [Vitis

vinifera]



Seq. No. 27244

Contig ID 152480 1.R1040

5'-most EST jC-gmro02910016d02a1

Method BLASTX
NCBI GI g2262107
BLAST score 820
E value 5.0e-88
Match length 196
% identity 81

NCBI Description (AC002343) Ser/Thr protein kinase isolog [Arabidopsis

thaliana]

Seq. No. 27245

Contig ID 152518\_1.R1040 5'-most EST pcp700991671.h1

Seq. No. 27246

Contig ID 152529\_1.R1040

 5'-most EST
 g4289922

 Method
 BLASTX

 NCBI GI
 g3033384

 BLAST score
 502

 E value
 6.0e-51

 Match length
 137

% identity 67

NCBI Description (AC004238) putative CTP synthase [Arabidopsis thaliana]

Seq. No. 27247

Contig ID 152534\_1.R1040 5'-most EST pcp700991688.h1

Method BLASTX
NCBI GI g4512657
BLAST score 155
E value 2.0e-10
Match length 103
% identity 33

NCBI Description (AC006931) putative APG protein [Arabidopsis thaliana] >gi 4544463 gb AAD22370.1 AC006580 2 (AC006580) putative

APG isolog protein [Arabidopsis thaliana]

Seq. No. 27248

Contig ID 152537\_1.R1040 5'-most EST jsh701068142.h1

Method BLASTX
NCBI GI g3769472
BLAST score 272
E value 5.0e-24
Match length 79
% identity 66

NCBI Description (AF064732) putative phospholipase A2 [Dianthus

caryophyllus]

Seq. No. 27249

Contig ID 152547\_1.R1040 5'-most EST pcp700991707.h1

Method BLASTX NCBI GI 94512705



BLAST score 353 E value 3.0e-44 Match length 136 % identity 67

NCBI Description (AC006569) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 27250

Contig ID 152601\_1.R1040 5'-most EST pcp700991775.h1

Seq. No. 27251

Contig ID 152625\_1.R1040

5'-most EST jC-gmst02400053f11d1

Seq. No. 27252

Contig ID 152638\_1.R1040

5'-most EST  $jC-gmf\overline{10}2220064f05a1$ 

Method BLASTX
NCBI GI g4508083
BLAST score 225
E value 2.0e-18
Match length 67
% identity 73

NCBI Description (AC005882) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 27253

Contig ID 152645\_1.R1040

5'-most EST jC-gmro02910074g05d1

Seq. No. 27254

Contig ID 152659\_1.R1040 5'-most EST pcp700991863.h1

Method BLASTX
NCBI GI g1001263
BLAST score 497
E value 3.0e-51
Match length 177
% identity 59

NCBI Description (D64003) hypothetical protein [Synechocystis sp.]

Seq. No. 27255

Contig ID 152686\_1.R1040 5'-most EST 2hf700957194.h1

Method BLASTX
NCBI GI 94415931
BLAST score 564
E value 3.0e-58
Match length 137
% identity 76

NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

>gi\_4559393\_gb\_AAD23053.1\_AC006526\_18 (AC006526) unknown

protein [Arabidopsis thaliana]

Seq. No. 27256

Contig ID 152695\_1.R1040 5'-most EST pcp700991916.h1



Seq. No. 27257

Contig ID 152698\_1.R1040 5'-most EST pmv700892414.h1

Method BLASTX
NCBI GI g3879119
BLAST score 162
E value 2.0e-11
Match length 65
% identity 48

NCBI Description (Z70310) similar to Glutathione S-transferases.

[Caenorhabditis elegans]

Seq. No. 27258

Contig ID 152715\_1.R1040 5'-most EST fua701039413.h1

Seq. No. 27259

Contig ID 152717\_1.R1040 5'-most EST sat701004613.h1

Seq. No. 27260

Contig ID 152747\_1.R1040 5'-most EST gsv701056878.h1

Seq. No. 27261

Contig ID 152768\_1.R1040 5'-most EST pcp700992052.h1

Method BLASTX
NCBI GI g1076427
BLAST score 174
E value 3.0e-24
Match length 70
% identity 83

NCBI Description ubiquitin--protein ligase (EC 6.3.2.19) - Arabidopsis

thaliana

Seq. No. 27262

Contig ID 152770\_1.R1040 5'-most EST kl1701204316.h2

Seq. No. 27263

Contig ID 152790\_1.R1040 5'-most EST fde700870510.h1

Method BLASTX
NCBI GI g2398853
BLAST score 227
E value 4.0e-19
Match length 69
% identity 61

NCBI Description (AB004822) plastid RNA polymerase sigma-subunit

[Arabidopsis thaliana]

Seq. No. 27264

Contig ID 152793\_1.R1040 5'-most EST fC-gmle700559592g3

Method BLASTX



NCBI GI g3169171 BLAST score 887 E value 2.0e-95 Match length 340 % identity 51

NCBI Description (AC004401) putative serine carboxypeptidase I [Arabidopsis

thaliana] >gi\_3445213 (AC004786) putative serine

carboxypeptidase I [Arabidopsis thaliana]

 Seq. No.
 27265

 Contig ID
 152800\_1.R1040

 5'-most EST
 pcp700992101.h1

 Method
 BLASTX

Method BLASTX
NCBI GI g3080436
BLAST score 94
E value 2.0e-09
Match length 77

% identity 53

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 27266

Contig ID 152833\_1.R1040 5'-most EST rca700997618.h1

Method BLASTN
NCBI GI g3985955
BLAST score 67
E value 8.0e-29
Match length 271
% identity 81

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTH16, complete sequence [Arabidopsis thaliana]

Seq. No. 27267

Contig ID 152879\_1.R1040 5'-most EST pcp700992237.h1

Method BLASTX
NCBI GI g3881189
BLAST score 185
E value 6.0e-14
Match length 76
% identity 49

NCBI Description (Z99281) similar to ADP-ribosylation factor; cDNA EST

EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4

Seq. No. 27268

Contig ID 152882\_1.R1040

5'-most EST jC-gmfl02220073d01a1

Method BLASTX
NCBI GI g3135269
BLAST score 316
E value 4.0e-29
Match length 111
% identity 59

NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                   152908 1.R1040
Contig ID
                   pcp700992291.h1
5'-most EST
                   27270
Seq. No.
                   152910 1.R1040
Contig ID
                   pcp700992296.h1
5'-most EST
                   BLASTX
Method
                   g2826900
NCBI GI
                   \bar{4}46
BLAST score
                   2.0e-44
E value
Match length
                   135
                   59
% identity
                   (AB004461) DNA polymerase alpha catalytic subunit [Oryza
NCBI Description
                   sativa]
                   27271
Seq. No.
                   152911 1.R1040
Contig ID
                   jC-gmle01810084g05a1
5'-most EST
Method
                   BLASTX
                   g2245095
NCBI GI
BLAST score
                   209
E value
                   1.0e-16
Match length
                   66
% identity
                   58
                   (Z97343) formyltransferase purU homolog [Arabidopsis
NCBI Description
                   thaliana]
                   27272
Seq. No.
                   152930 1.R1040
Contig ID
                   pcp700992322.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4490316
                   595
BLAST score
                   1.0e-61
E value
                   156
Match length
                   64
% identity
                  (AL035678) nucellin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   27273
                   152979 1.R1040
Contig ID
5'-most EST
                   pcp700992394.hl
Seq. No.
                   27274
                   152982 1.R1040
Contig ID
                   uC-gmflminsoy077g08b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4567250
                   275
BLAST score
```

3.0e-24E value

Match length 83 58 % identity

(AC007070) hypothetical protein [Arabidopsis thaliana] NCBI Description

27275 Seq. No.

Contig ID 152987 1.R1040 5'-most EST qsv701046566.hl



```
BLASTX
Method
                  q3868800
NCBI GI
                   340
BLAST score
                   4.0e-32
E value
                   107
Match length
% identity
                   60
                   (AB013603) topoisomerase III beta [Mus musculus]
NCBI Description
                   27276
Seq. No.
                   153000 1.R1040
Contig ID
5'-most EST
                   pxt700945348.h1
Method
                   BLASTX
                   q2809246
NCBI GI
BLAST score
                   284
                   4.0e-25
E value
Match length
                   68
% identity
                   76
                   (AC002560) F2401.15 [Arabidopsis thaliana]
NCBI Description
                   27277
Seq. No.
                   153000 4.R1040
Contig ID
5'-most EST
                   sat701007226.h2
Seq. No.
                   27278
                   153040 1.R1040
Contig ID
                   pcp700992508.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2760172
BLAST score
                   39
                   1.0e-12
E value
Match length
                   135
                   82
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUB3, complete sequence [Arabidopsis thaliana]
                   27279
Seq. No.
                   153067 1.R1040
Contig ID
5'-most EST
                   pcp700992566.hl
Seq. No.
                   27280
                   153084 1.R1040
Contig ID
5'-most EST
                   pcp700992605.hl
                   BLASTX
Method
NCBI GI
                   g2244806
BLAST score
                   144
                   2.0e-09
E value
Match length
                   76
                   32
% identity
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   27281
Seq. No.
Contig ID
                   153103 1.R1040
```

5'-most EST pcp700992649.h1

Method BLASTX
NCBI GI g3135693
BLAST score 232
E value 1.0e-19



Match length 49 % identity

(AF064201) glutathione S-transferase [Gossypium hirsutum] NCBI Description

27282 Seq. No.

153127 1.R1040 Contig ID jC-gmle01810020d10a1 5'-most EST

27283 Seq. No.

153150 1.R1040 Contig ID xpa700798018.hl 5'-most EST

Seq. No. 27284

153188 1.R1040 Contig ID 5'-most EST pcp700992794.hl

Seq. No. 27285

153207 1.R1040 Contig ID pcp700992831.hl 5'-most EST

27286 Seq. No.

Contig ID 153246 1.R1040

5'-most EST uC-gmrominsoy154d12b1

Method BLASTX g3695406 NCBI GI 580 BLAST score 4.0e-60 E value Match length 139 80 % identity

(AF096373) similar to isoleucyl-tRNA synthetases NCBI Description

[Arabidopsis thaliana]

Seq. No. 27287

153249 1.R1040 Contig ID

jC-gmle01810051e08a1 5'-most EST

BLASTX Method g3269292 NCBI GI BLAST score 164 E value 4.0e-11 50 Match length % identity

(AL030978) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 27288

153250 1.R1040 Contig ID  $sat701\overline{0}15386.h1$ 5'-most EST

BLASTX Method q3548810 NCBI GI 273 BLAST score 4.0e-24 E value 99 Match length 51 % identity

(AC005313) putative chloroplast nucleoid DNA binding NCBI Description

protein [Arabidopsis thaliana]

Seq. No. 27289

153265 1.R1040 Contig ID



5'-most EST g5058090
Method BLASTX
NCBI GI g3941289
BLAST score 354
E value 2.0e-33
Match length 82
% identity 76
NCBI Description (AF018093

NCBI Description (AF018093) similarity to SCAMP37 [Pisum sativum]

Seq. No. 27290

Contig ID 153268\_1.R1040 5'-most EST gsv701046031.h1

Method BLASTX
NCBI GI g3861199
BLAST score 224
E value 6.0e-22
Match length 124
% identity 46

NCBI Description (AJ235272) 50S RIBOSOMAL PROTEIN L3 (rplC) [Rickettsia

prowazekii]

Seq. No. 27291

Contig ID 153280\_1.R1040 5'-most EST pcp700993176.h1

Seq. No. 27292

Contig ID 153307\_1.R1040 5'-most EST sat701010787.h1

Seq. No. 27293

Contig ID 153307 2.R1040 5'-most EST kl1701206563.h1

Seq. No. 27294

Contig ID 153310\_1.R1040 5'-most EST pcp700993030.h1

Seq. No. 27295

Contig ID 153326 1.R1040 5'-most EST zhf700963321.h1

Method BLASTX
NCBI GI g3023928
BLAST score 133
E value 4.0e-12
Match length 49
% identity 67

NCBI Description PROBABLE HISTONE DEACETYLASE 1-2 (HD1) (RPD3 HOMOLOG)

>gi\_2444430 (AF020658) deacetylase [Xenopus laevis]

Seq. No. 27296

Contig ID 153333\_1.R1040

5'-most EST uC-gmrominsoy033c05b1

Seq. No. 27297

Contig ID 153344\_1.R1040

5'-most EST  $g56067\overline{33}$ 



Seq. No. 27298

Contig ID 153374 1.R1040 5'-most EST jex700908896.h1

Seq. No. 27299

Contig ID 153384\_1.R1040

5'-most EST jC-gmle01810092b12a1

Seq. No. 27300

Contig ID 153402 1.R1040

5'-most EST uC-gmflminsoy053c07b1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 47
% identity 66

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 27301

Contig ID 153442\_1.R1040 5'-most EST jsh701064316.h1

Method BLASTX
NCBI GI g3790587
BLAST score 222
E value 2.0e-18
Match length 92
% identity 57

NCBI Description (AF079182) RING-H2 finger protein RHF2a [Arabidopsis

thaliana]

Seq. No. 27302

Contig ID 153447 1.R1040 5'-most EST pcp700993261.h1

Method BLASTX
NCBI GI g3834307
BLAST score 378
E value 3.0e-36
Match length 100
% identity 69

NCBI Description (AC005679) Strong similarity to gene T10I14.120 gi\_2832679

putative protein from Arabidopsis thaliana BAC gb\_AL021712.

ESTs gb\_N65887 and gb\_N65627 come from this gene.

[Arabidopsis thaliana]

Seq. No. 27303

Contig ID 153451\_1.R1040 5'-most EST jex700907782.h1

Seq. No. 27304

Contig ID 153473\_1.R1040

5'-most EST  $g42916\overline{8}8$ 

Seq. No. 27305

Contig ID 153481\_1.R1040 5'-most EST pcp700993321.h1



Seq. No. 27306

Contig ID 153504\_1.R1040 5'-most EST pmv700894323.h1

Seq. No. 27307

Contig ID 153543\_1.R1040 5'-most EST pcp700993431.h1

Seq. No. 27308

Contig ID 153552\_1.R1040 5'-most EST pcp700993446.h1

Seq. No. 27309

Contig ID 153564 1.R1040

5'-most EST uC-gmflminsoy098c05b1

Method BLASTX
NCBI GI g3746568
BLAST score 506
E value 4.0e-51
Match length 104
% identity 92

NCBI Description (AF061638) branched-chain alpha-keto acid decarboxylase E1

beta subunit [Arabidopsis thaliana]

Seq. No. 27310

Contig ID 153574\_1.R1040 5'-most EST pcp700993477.h1

Method BLASTX
NCBI GI g3075399
BLAST score 173
E value 1.0e-12
Match length 47
% identity 64

NCBI Description (AC004484) SF16-like protein [Arabidopsis thaliana]

Seq. No. 27311

Contig ID 153575\_1.R1040 5'-most EST gsv701047759.h1

Seq. No. 27312

Contig ID 153591\_1.R1040 5'-most EST zzp700831713.h1

Seq. No. 27313

Contig ID 153601\_1.R1040 5'-most EST bth700846617.h1

Seq. No. 27314

Contig ID 153621\_1.R1040 5'-most EST pcp700993572.h1

Method BLASTX
NCBI GI g2191175
BLAST score 223
E value 2.0e-18
Match length 103
% identity 50

NCBI Description (AF007270) A\_IG002P16.24 gene product [Arabidopsis



## thaliana]

 Seq. No.
 27315

 Contig ID
 153623 1.R1040

 5'-most EST
 jex700904779.h1

 Method
 BLASTX

 NCBI GI
 g3445209

BLAST score 266
E value 2.0e-23
Match length 65
% identity 69

NCBI Description (AC004786) putative serine carboxypeptidase I [Arabidopsis

thaliana]

Seq. No. 27316

Contig ID 153642\_1.R1040 5'-most EST rca700996494.h1

Seq. No. 27317

Contig ID 153649\_1.R1040 5'-most EST pcp700993619.h1

Method BLASTX
NCBI GI g3851584
BLAST score 227
E value 1.0e-18
Match length 58
% identity 76

NCBI Description (AF092563) chromosome-associated protein-E [Homo sapiens]

Seq. No. 27318

Contig ID 153653 1.R1040

5'-most EST uC-gmrominsoy122b10b1

Seq. No. 27319

Contig ID 153695\_1.R1040 5'-most EST uC-gmropic031f04b1

Seq. No. 27320

Contig ID 153713\_1.R1040 5'-most EST pcp700995761.h1

Method BLASTN
NCBI GI g2564336
BLAST score 120
E value 6.0e-61
Match length 264
% identity 86

NCBI Description Brassica campestris mRNA for Tat binding protein 1,

complete cds

Seq. No. 27321

Contig ID 153723\_1.R1040 5'-most EST pcp700993740.h1

Method BLASTX
NCBI GI g3688209
BLAST score 568
E value 2.0e-58
Match length 158

```
% identity
                   (AJ010093) MAP3K beta 1 protein kinase [Brassica napus]
NCBI Description
                   27322
Seq. No.
                   153754 1.R1040
Contig ID
                  pcp700993803.hl
5'-most EST
                   27323
Seq. No.
                   153816 1.R1040
Contig ID
                   asn701\overline{1}38734.h1
5'-most EST
                   BLASTX
Method
                   q4558462
NCBI GI
                   797
BLAST score
                   2.0e-85
E value
                   194
Match length
                   36
% identity
                   (AF079404) cell cycle switch protein [Medicago sativa
NCBI Description
                   subsp. X varia]
                   27324
Seq. No.
                   153820 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910040e02a1
                   27325
Seq. No.
                   153850 1.R1040
Contig ID
                   pxt700942373.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3860250
                   408
BLAST score
                   6.0e-40
E value
                   131
Match length
                   63
% identity
                   (AC005824) putative chloroplast prephenate dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                   27326
Seq. No.
                   153852 1.R1040
Contig ID
                   jC-gms\overline{t}02400040a05a1
5'-most EST
                   BLASTX
Method
                   g114276
NCBI GI
                   204
BLAST score
                   6.0e-23
E value
                   106
Match length
                   55
% identity
                   N4-(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR
NCBI Description
                   (GLYCOSYLASPARAGINASE) (ASPARTYLGLUCOSAMINIDASE)
                    (N4-(N-ACETYL-BETA-GLUCOSAMINYL)-L-ASPARAGINE AMIDASE)
                    (AGA) >gi 67759 pir MUHUGD
                   N4-(beta-\overline{N}-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26)
                   precursor - human >gi 28534 emb CAA39029 (X55330)
```

Seq. No. 27327

sapiens] >gi 34760 emb CAA39288 (X55762)

aspartylglucosaminidase precursor

sapiens] >qi 4557273 ref NP 000018.1 pAGA

N4-(beta-N-acetylglucosaminyl)-L- asparaginase [Homo

glycosylasparaginase precursor (AA -23 to 323) [Homo



Contig ID	153861 1.R1040
5'-most EST	$pcp700\overline{9}93951.h1$

Seq. No. 27328

Contig ID 153867\_1.R1040 5'-most EST zhf700958665.h1

Seq. No. 27329

Contig ID 153873\_1.R1040 5'-most EST pcp700993969.h1

Seq. No. 27330

Contig ID 153879\_1.R1040 5'-most EST pcp700993978.h1

Seq. No. 27331

Contig ID 153895\_1.R1040 5'-most EST pcp700994004.h1

Seq. No. 27332

Contig ID 153919\_1.R1040

5'-most EST uC-gmrominsoy300g11b1

Seq. No. 27333

Contig ID 153935\_1.R1040 5'-most EST rca700999021.h1

Method BLASTX
NCBI GI g3924613
BLAST score 227
E value 5.0e-27
Match length 147
% identity 54

NCBI Description (AF069442) hypothetical protein [Arabidopsis thaliana]

>gi\_4263512\_gb\_AAD15338\_ (AC004044) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 27334

Contig ID 153935\_2.R1040 5'-most EST fC-gmro700864959d3

Seq. No. 27335

Contig ID 153938\_1.R1040 5'-most EST pmv700888824.h1

Seq. No. 27336

Contig ID 153941\_1.R1040

5'-most EST uC-gmrominsoy304h12b1

Seq. No. 27337

Contig ID 153941\_2.R1040

5'-most EST jC-gmf102220113e06d1

Seq. No. 27338

Contig ID 153943\_1.R1040

5'-most EST uC-gmflminsoy010d11b1

Seq. No. 27339



```
Contig ID
                   153958 1.R1040
5'-most EST
                   pcp700994093.h1
Seq. No.
                   27340
Contig ID
                   153988 1.R1040
5'-most EST
                   jC-qmst02400041b03a1
Method
                   BLASTX
NCBI GI
                   q640021
BLAST score
                   689
E value
                   7.0e-73
Match length
                   144
% identity
                   95
NCBI Description
                   (X83695) gamma-tubulin 1 [Zea mays]
Seq. No.
                   27341
Contig ID
                   154029 1.R1040
5'-most EST
                   smw700646254.h1
Method
                   BLASTX
NCBI GI
                   g4455226
BLAST score
                   286
E value
                   4.0e-42
Match length
                   129
% identity
NCBI Description
                   (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                   27342
Contig ID
                   154036 1.R1040
                   bth700847334.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4454006
BLAST score
                   263
E value
                   2.0e-22
Match length
                   181
% identity
                   31
                   (AL035396) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   27343
Contig ID
                   154045 1.R1040
5'-most EST
                   pcp700994234.h1
Seq. No.
                   27344
Contig ID
                   154060 1.R1040
5'-most EST
                   dpv701100937.h1
Method
                   BLASTX
NCBI GI
                   g3924603
BLAST score
                   247
E value
                   4.0e-27
Match length
                  99
% identity
NCBI Description
                   (AF069442) putative WD-repeat protein [Arabidopsis
                  thaliana]
Seq. No.
                  27345
Contig ID
                  154068 1.R1040
5'-most EST
                  pcp700994270.h1
Method
```

4255

BLASTX

q1399828

NCBI GI



```
BLAST score 157
E value 1.0e-10
Match length 111
% identity 39
```

NCBI Description (U59235) unknown [Synechococcus PCC7942]

Seq. No. 27346

Contig ID 154071\_1.R1040 5'-most EST pcp700994273.h1

Seq. No. 27347

Contig ID 154073\_1.R1040 5'-most EST epx701107468.h1

Method BLASTX
NCBI GI g3329368
BLAST score 261
E value 7.0e-23
Match length 110
% identity 60

NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 27348

Contig ID 154081\_1.R1040 5'-most EST pcp700994285.h1

Method BLASTN
NCBI GI g2262200
BLAST score 505
E value 0.0e+00
Match length 819
% identity 93

NCBI Description Phaseolus vulgaris gibberellin 20-oxidase mRNA, complete

cds

Seq. No. 27349

Contig ID 154089\_1.R1040 5'-most EST zhf700962711.h1

Method BLASTX
NCBI GI g3080414
BLAST score 476
E value 1.0e-47
Match length 120
% identity 78

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 27350

Contig ID 154097\_1.R1040 5'-most EST sat701008351.h1

Method BLASTX
NCBI GI g3549626
BLAST score 228
E value 6.0e-19
Match length 106
% identity 45

NCBI Description (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

Seq. No. 27351

Contig ID 154100\_1.R1040



```
pcp700994314.h1
5'-most EST
                  27352
Seq. No.
                  154104 1.R1040
Contig ID
                  pcp700994319.hl
5'-most EST
Method
                  BLASTX
                   g3860251
NCBI GI
                   310
BLAST score
                   9.0e-29
E value
Match length
                   90
% identity
                   69
                   (AC005824) putative permease [Arabidopsis thaliana]
NCBI Description
                   27353
Seq. No.
                   154108 1.R1040
Contig ID
5'-most EST
                   fC-gmle7000741294a1
                   BLASTX
Method
NCBI GI
                   g3021270
BLAST score
                   687
                   2.0e-72
E value
                   191
Match length
                   69
% identity
                   (AL022347) serine/threonine kinase -like protein
NCBI Description
                   [Arabidopsis thaliana]
                   27354
Seq. No.
                   154128 1.R1040
Contig ID
5'-most EST
                   pcp700994357.hl
                   27355
Seq. No.
                   154143 1.R1040
Contig ID
                   uC-gmrominsoy125f07b1
5'-most EST
Method
                   BLASTX
                   g2160694
NCBI GI
                   927
BLAST score
                   1.0e-100
E value
                   231
Match length
                   74
% identity
                   (U73528) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                   thaliana]
                   27356
Seq. No.
                   154158 1.R1040
Contig ID
                   pcp700994392.h1
5'-most EST
Seq. No.
                   27357
                   154165 1.R1040
Contig ID
                   pcp700994404.h1
 5'-most EST
                   BLASTX
Method
                   q3183077
NCBI GI
                   227
BLAST score
                   4.0e-28
E value
                   156
Match length
                   48
 % identity
                   PROBABLE 1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE
 NCBI Description
```

(DHNA-OCTAPRENYLTRANSFERASE) >gi\_1653114\_dbj\_BAA18030\_ (D90911) menaquinone biosynthesis protein [Synechocystis



```
27358
Seq. No.
Contig ID
                  154211 1.R1040
                  pcp700994466.hl
5'-most EST
                  BLASTX
Method
                  g4115938
NCBI GI
                  830
BLAST score
                   4.0e-89
E value
                  225
Match length
                  74
% identity
                   (AF118223) contains similarity several bacterial
NCBI Description
                   glutathione-regulated potassium efflux system proteins
                   [Arabidopsis thaliana]
                   27359
Seq. No.
```

 Seq. No.
 27359

 Contig ID
 154239\_1.R1040

 5'-most EST
 leu701152401.h1

 Method
 BLASTX

 NCBI GI
 g1076580

 RLAST score
 242

BLAST score 242
E value 1.0e-20
Match length 72
% identity 61

NCBI Description alcohol dehydrogenase homolog ADH3b - tomato

>gi\_913446\_bbs\_160508 (S75487) alcohol dehydrogenase ADH
{EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red
cherry, Peptide, 390 aa] [Lycopersicon esculentum]

Seq. No. 27360

Contig ID 154260\_1.R1040 5'-most EST pmv700893490.h1

Method BLASTX
NCBI GI g3947613
BLAST score 205
E value 2.0e-16
Match length 82
% identity 46

NCBI Description (AL023828) cDNA EST EMBL:M89008 comes from this gene; cDNA EST yk282d3.5 comes from this gene [Caenorhabditis elegans]

Seq. No. 27361

Contig ID 154271\_1.R1040 5'-most EST pcp700994568.h2

Seq. No. 27362

Contig ID 154327\_1.R1040 5'-most EST fua701037573.h1

Method BLASTX
NCBI GI g3688173
BLAST score 461
E value 4.0e-46
Match length 121
% identity 65

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 27363



Contig ID 154332\_1.R1040 5'-most EST zhf700960473.h1

Method BLASTN
NCBI GI g4417264
BLAST score 39
E value 1.0e-12
Match length 87
% identity 86

NCBI Description Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 27364

Contig ID 154344\_1.R1040 5'-most EST pcp700994703.h1

Method BLASTX
NCBI GI g2109293
BLAST score 450
E value 4.0e-45
Match length 103
% identity 81

NCBI Description (U97568) serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No. 27365

Contig ID 154349\_1.R1040 5'-most EST pcp700994708.h1

Seq. No. 27366

Contig ID 154358\_1.R1040 5'-most EST pcp700994724.h1

Seq. No. 27367

Contig ID 154376\_1.R1040 5'-most EST pcp700994752.h1

Seq. No. 27368

Contig ID 154382\_1.R1040 5'-most EST pcp700994763.h1

Method BLASTX
NCBI GI g3004564
BLAST score 377
E value 4.0e-36
Match length 150
% identity 46

NCBI Description (AC003673) putative receptor Ser/Thr protein kinase

[Arabidopsis thaliana]

Seq. No. 27369

Contig ID 154389\_1.R1040 5'-most EST pcp700994778.h1

Method BLASTX
NCBI GI g1172633
BLAST score 420
E value 1.0e-41
Match length 101
% identity 80

NCBI Description PROLIFERA PROTEIN >gi\_675491 (L39954) contains MCM2/3/5



family signature; PROSITE; PS00847; disruption leads to early lethal phenotype; similar to MCM2/3/5 family, most similar to YBR1441 [Arabidopsis thaliana]

Seq. No. 27370

Contig ID 154397 1.R1040 5'-most EST zhf700951878.h1

Seq. No. 27371

Contig ID 154398 1.R1040 5'-most EST pxt700943565.h1

Seq. No. 27372

Contig ID 154403\_1.R1040 5'-most EST rca700999409.h1

Method BLASTX
NCBI GI g4539343
BLAST score 255
E value 6.0e-22
Match length 94
% identity 57

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 27373

Contig ID 154436\_1.R1040 5'-most EST xpa700796580.h1

Method BLASTX
NCBI GI g3820614
BLAST score 333
E value 3.0e-31
Match length 110
% identity 59

NCBI Description (AF094516) E1-like protein [Homo sapiens]

Seq. No. 27374

Contig ID 154450\_1.R1040 5'-most EST dpv701097012.h1

Seq. No. 27375

Contig ID 154496\_1.R1040 5'-most EST uC-gmronoir036c08b1

Seq. No. 27376

Contig ID 154499\_1.R1040 5'-most EST pcp700994952.h1

Method BLASTX
NCBI GI g1170619
BLAST score 149
E value 5.0e-20
Match length 138
% identity 44

NCBI Description KINESIN-LIKE PROTEIN A >gi\_479594\_pir\_\_S34830

kinesin-related protein katA - Arabidopsis thaliana >gi\_303502\_dbj\_BAA01972\_ (D11371) kinesin-like motor

protein heavy chain [Arabidopsis thaliana]

>gi\_2911084\_emb\_CAA17546\_ (AL021960) kinesin-related

protein katA [Arabidopsis thaliana]



```
Seq. No.
                   27377
Contig ID
                   154509 1.R1040
5'-most EST
                   kmv700741667.h1
Seq. No.
                   27378
Contig ID
                   154517 1.R1040
5'-most EST
                   jex700903173.h1
Seq. No.
                   27379
Contig ID
                   154524 1.R1040
5'-most EST
                   uC-gmropic016c08b1
Method
                   BLASTX
NCBI GI
                   g733554
BLAST score
                   156
E value
                   1.0e-10
Match length
                   58
% identity
                   48
NCBI Description
                   (U23450) similar to RNA-binding protein [Caenorhabditis
                   elegans]
Seq. No.
                   27380
Contig ID
                   154524 2.R1040
5'-most EST
                   vzy700755643.h1
Seq. No.
                   27381
Contig ID
                   154530 1.R1040
5'-most EST
                   uC-gmflminsoy100g09b1
Seq. No.
                   27382
Contig ID
                   154530 2.R1040
5'-most EST
                   jC-gmro02910056f04a1
Seq. No.
                   27383
Contig ID
                   154539 1.R1040
5'-most EST
                   sat701005972.h1
Method
                   BLASTX
NCBI GI
                   g1001135
BLAST score
                   273
E value
                   3.0e-24
Match length
                   104
% identity
                   52
NCBI Description
                  (D64001) acetolactate synthase [Synechocystis sp.]
Seq. No.
                   27384
Contig ID
                  154545_1.R1040
5'-most EST
                  uC-gmflminsoy075c04b1
Method
                  BLASTX
NCBI GI
                  g4512704
BLAST score
                  146
                  3.0e-09
E value
Match length
                  117
% identity
                  29
```

NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27385 Contig ID 154557\_1.R1040

4261



```
jC-gmle01810055c05a1
5'-most EST
Seq. No.
                   27386
                   154558 1.R1040
Contig ID
5'-most EST
                   kmv700737854.h1
Method
                   BLASTX
                   q4239696
NCBI GI
                   266
BLAST score
                   3.0e-23
E value
                   63
Match length
% identity
                   (AJ132767) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   27387
Seq. No.
                   154562 1.R1040
Contig ID
                   epx701110279.hl
5'-most EST
                   27388
Seq. No.
                   154564 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir014g04b1
Method
                   BLASTX
                   q4539009
NCBI GI
                   525
BLAST score
                   3.0e-53
E value
Match length
                   169
                   58
% identity
                   (AL049481) putative protein [Arabidopsis thaliana]
NCBI Description
                   27389
Seq. No.
Contig ID
                   154569 1.R1040
5'-most EST
                   jC-qmf102220148h03a1
                   BLASTX
Method
NCBI GI
                   q4454011
BLAST score
                   195
E value
                   8.0e-15
Match length
                   85
                   51
% identity
                   (AL035396) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   27390
                   154588 1.R1040
Contig ID
5'-most EST
                   zhf700963125.h1
                   27391
Seq. No.
                   154595 1.R1040
Contig ID
5'-most EST
                   pcp700995152.hl
                   BLASTX
Method
                   g3025189
NCBI GI
                   147
BLAST score
                   5.0e-09
E value
                   57
Match length
                   42
% identity
                   HYPOTHETICAL 67.1 KD PROTEIN SLL1770
NCBI Description
                   >qi 1652753 dbj BAA17672 (D90908) ABC1-like [Synechocystis
                   sp.]
```

4262

27392

Seq. No.



154597 1.R1040 Contig ID jC-gmst02400014d10d1 5'-most EST 27393 Seq. No. 154610 1.R1040 Contig ID 5'-most EST pcp700995171.hl 27394 Seq. No. 154619\_1.R1040 Contig ID 5'-most EST pmv700892329.hl

Seq. No. 27395 154634 1.R1040 Contig ID jC-gmle01810059f08a1 5'-most EST BLASTX Method

NCBI GI g1362781 BLAST score 154 E value 1.0e-09 121 Match length 20 % identity

cytokine inducible nuclear protein C193 - human NCBI Description >gi\_793841\_emb\_CAA58676\_ (X83703) nuclear protein [Homo

sapiens]

27396 Seq. No. 154635 1.R1040 Contig ID pcp700995205.h1 5'-most EST Method BLASTX

g3628757 NCBI GI 181 BLAST score 1.0e-13 E value 75 Match length % identity 44

(AF038007) FIC1 [Homo sapiens] NCBI Description

27397 Seq. No.

154638 1.R1040 Contig ID asn701136321.hl 5'-most EST

27398 Seq. No.

154708 1.R1040 Contig ID pcp700995314.h1 5'-most EST

BLASTXMethod NCBI GI q3599489 1859 BLAST score 0.0e + 00E value 491 Match length 74 % identity

(AF085148) 3-oxoacyl-[acyl-carrier-protein] synthase NCBI Description

[Capsicum chinense]

Seq. No. 27399

154708 2.R1040 Contig ID leu701154660.h1 5'-most EST

Seq. No. 27400

154731 1.R1040 Contig ID



5'-most EST qsv701045552.h1 BLASTX Method NCBI GI g2245115 BLAST score 208 2.0e-16 E value Match length 126 % identity 39 (Z97343) unnamed protein product [Arabidopsis thaliana] NCBI Description 27401 Seq. No. 154732 1.R1040 Contig ID pcp700995353.hl 5'-most EST Seq. No. 27402 154732 2.R1040 Contig ID  $asn701\overline{1}35077.h1$ 5'-most EST 27403 Seq. No. 154736 1.R1040 Contig ID 5'-most EST pcp700995357.h1 27404 Seq. No. 154754 1.R1040 Contig ID epx701108951.hl 5'-most EST BLASTX Method NCBI GI g3327389 BLAST score 665 5.0e-70 E value 145 Match length 81 % identity (AC004483) putative DNA replication licensing factor, mcm5 NCBI Description [Arabidopsis thaliana] 27405 Seq. No. 154770 1.R1040 Contig ID 5'-most EST uC-gmronoir019f07b1 BLASTX Method NCBI GI g421980 BLAST score 363 1.0e-34 E value Match length 87 76 % identity NCBI Description transforming protein (myb3) - barley >gi 19059 emb\_CAA50223\_ (X70878) MybHv33 [Hordeum vulgare] Seq. No. 27406 154789 1.R1040 Contig ID 5'-most EST pcp700995433.h1

27407 Seq. No.

Contig ID 154801 1.R1040

uC-gmflminsoy118d08b1 5'-most EST

BLASTX Method g4530126 NCBI GI 413 BLAST score E value 2.0e-43 Match length 157



% identity 57

NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1

[Phaseolus vulgaris]

Seq. No. 27408

Contig ID 154812\_1.R1040 5'-most EST gsf700698449.h1

Seq. No. 27409

Contig ID 154816\_1.R1040 5'-most EST pcp700995472.h1

Method BLASTX
NCBI GI g3785977
BLAST score 357
E value 5.0e-34
Match length 120
% identity 53

NCBI Description (AC005560) putative growth regulator protein [Arabidopsis

thaliana]

Seq. No. 27410

Contig ID 154822\_1.R1040 5'-most EST sat701004175.h1

Method BLASTX
NCBI GI g3250675
BLAST score 754
E value 5.0e-80
Match length 342
% identity 51

NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 27411

Contig ID 154833 1.R1040 5'-most EST jex700905056.h1

Seq. No. 27412

Contig ID 154836\_1.R1040 5'-most EST uC-gmropic063d08b1

Seq. No. 27413

Contig ID 154848 1.R1040 5'-most EST smw700646161.h1

Seq. No. 27414

Contig ID 154848\_2.R1040 5'-most EST pcp700995515.h1

Seq. No. 27415

Contig ID 154849\_1.R1040

5'-most EST g4303828
Method BLASTX
NCBI GI g4455369
BLAST score 284
E value 6.0e-25
Match length 85
% identity 71

NCBI Description (AL035524) hypothetical protein [Arabidopsis thaliana]



```
27416
Seq. No.
                  154849 2.R1040
Contig ID
5'-most EST
                  fC-gmro700564066z3
                  BLASTX
Method
                  g4455369
NCBI GI
                  646
BLAST score
                  2.0e-67
E value
                  170
Match length
                  74
% identity
NCBI Description (AL035524) hypothetical protein [Arabidopsis thaliana]
                  27417
Seq. No.
                  154866 1.R1040
Contig ID
                  uC-gmflminsoy077a09b1
5'-most EST
                  BLASTN
Method
                  g2760172
NCBI GI
BLAST score
                  41
                   1.0e-13
E value
                   158
Match length
                   87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUB3, complete sequence [Arabidopsis thaliana]
                   27418
Seq. No.
                   154874 1.R1040
Contig ID
                   jC-qmle01810073e12a1
5'-most EST
                   BLASTN
Method
                   g1707656
NCBI GI
                   53
BLAST score
                   7.0e-21
E value
                   125
Match length
% identity
                   86
NCBI Description P.sativum mRNA for DnaJ-like protein
                   27419
Seq. No.
                   154904 1.R1040
Contig ID
                   kmv700743355.h1
5'-most EST
                   27420
Seq. No.
                   154940 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}06705.h1
Seq. No.
                   27421
                   154955 1.R1040
Contig ID
                   jC-gmro02910074d04a1
5'-most EST
                   27422
Seq. No.
                   154980 1.R1040
Contig ID
                   hrw701061966.h1
5'-most EST
```

Seq. No. 27423

Contig ID 154995\_1.R1040 5'-most EST pcp700995712.h1

Method BLASTX NCBI GI g3176684 BLAST score 156



E value 1.0e-10
Match length 77
% identity 44

NCBI Description (AC003671) Contains similarity to equilibratiave nucleoside transporter 1 gb\_U81375 from Homo sapiens. ESTs gb\_N65317, gb\_T20785, gb\_AA586285 and gb\_AA712578 come from this gene.

[Arabidopsis thaliana]

Seq. No. 27424

Contig ID 155009\_1.R1040 5'-most EST zhf700962113.h1

Method BLASTN
NCBI GI g3116019
BLAST score 208
E value 1.0e-113
Match length 331

% identity 91

NCBI Description Pisum sativum mRNA for ftsZ gene

Seq. No. 27425

Contig ID 155013\_1.R1040 5'-most EST fC-gmse700842410f1

Method BLASTX
NCBI GI g2492515
BLAST score 148
E value 2.0e-09
Match length 39
% identity 79

NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR

>gi\_2129924\_pir\_\_S58298 ATPase - pepper (fragment)

>gi\_929013\_emb\_CAA62084\_ (X90472) ATPase [Capsicum annuum]

Seq. No. 27426

Contig ID 155014\_1.R1040 5'-most EST pcp700995734.h1

Seq. No. 27427

Contig ID 155027\_1.R1040 5'-most EST pcp700995753.h1

Method BLASTX
NCBI GI g2262116
BLAST score 155
E value 5.0e-10
Match length 131
% identity 30

NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No. 27428

Contig ID 155028\_1.R1040 5'-most EST gsv701050132.h1

Seq. No. 27429

Contig ID 155063\_1.R1040 5'-most EST pcp700995804.h1

Seq. No. 27430

Contig ID 155066\_1.R1040



```
pcp700995808.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3550982
BLAST score
                   568
                   1.0e-58
E value
                   127
Match length
                   80
% identity
NCBI Description (AB010690) mutM homologue-1 [Arabidopsis thaliana]
Seq. No.
                   27431
                   155084 1.R1040
Contig ID
                   jC-gmf102220132aa08a1
5'-most EST
                   BLASTX
Method
                   q3426037
NCBI GI
BLAST score
                   518
E value
                   1.0e-52
                   161
Match length
                   63
% identity
                   (AC005168) putative ABC transporter protein [Arabidopsis
NCBI Description
                   thaliana]
                   27432
Seq. No.
                   155141 1.R1040
Contig ID
                   kmv700737722.h1
5'-most EST
                   BLASTX
Method
                   q3776557
NCBI GI
BLAST score
                   319
                   2.0e-29
E value
                   112
Match length
                   54
% identity
                   (AC005388) Contains similarity to gi 2924495 hypothetical
NCBI Description
                   protein Rv1920 from Mycobacterium tuberculosis genome
                   gb AL022020. [Arabidopsis thaliana]
                   27433
Seq. No.
                   155145 1.R1040
Contig ID
                   kmv700739054.h1
5'-most EST
Seq. No.
                   27434
                   155146 1.R1040
Contig ID
5'-most EST
                   g43976<del>5</del>9
Seq. No.
                   27435
                   155156 1.R1040
Contig ID
5'-most EST
                   kmv700737739.h1
Seq. No.
                   27436
                   155165 1.R1040
Contig ID
```

5'-most EST gsv701046071.hl

BLASTX Method NCBI GI q3005590 BLAST score 215 E value 3.0e-17 Match length 50 % identity 78

(AF051326) rRNA methylase [Arabidopsis thaliana] NCBI Description



```
27437
Seq. No.
                   155167 1.R1040
Contig ID
                   k11701\overline{2}13878.h1
5'-most EST
                   27438
Seq. No.
                   155174 1.R1040
Contig ID
                   kmv700\overline{7}37763.h1
5'-most EST
Seq. No.
                   27439
                   155198 1.R1040
Contig ID
                   kmv700737793.h1
5'-most EST
                   BLASTX
Method
                   q3047111
NCBI GI
                   271
BLAST score
                   5.0e-35
E value
                   171
Match length
% identity
                   52
                   (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
                   27440
Seq. No.
                   155214 1.R1040
Contig ID
                   kmv700737815.h1
5'-most EST
                   27441
Seq. No.
                   155218 1.R1040
Contig ID
                   zpv700762681.h1
5'-most EST
                   27442
Seq. No.
                   155247 1.R1040
Contig ID
                   kmv700737967.h1
5'-most EST
                   BLASTX
Method
                   g3184061
NCBI GI
                   143
BLAST score
                   3.0e-09
E value
                   77
Match length
                    42
% identity
                    (AL023776) atp dependent helicase [Schizosaccharomyces
NCBI Description
                   pombe]
                    27443
Seq. No.
                    155267 1.R1040
Contig ID
                    sat701\overline{0}09238.h1
5'-most EST
                    BLASTX
Method
NCBI GI
                    q4388717
                    821
BLAST score
                    4.0e-88
E value
                    199
Match length
                    78
% identity
                    (AC006413) putative nuclear phosphoprotein (contains
NCBI Description
```

multiple TPR repeats prosite:QDOC50005) [Arabidopsis

thaliana]

27444 Seq. No.

155284 1.R1040 Contig ID 5'-most EST jsh701068504.hl

27445 Seq. No.



Contig ID 155297 1.R1040 5'-most EST kmv700737947.h1

Seq. No. 27446

Contig ID 155305\_1.R1040

5'-most EST jC-gmle01810082g07a1

Method BLASTX
NCBI GI g1172586
BLAST score 502
E value 4.0e-91
Match length 384
% identity 43

NCBI Description POLYPHENOL OXIDASE A1 PRECURSOR (PPO) (CATECHOL OXIDASE)

>gi 22029 emb\_CAA77764\_ (Z11702) polyphenol oxidase [Vicia

faba]

Seq. No. 27447

Contig ID 155318\_1.R1040 5'-most EST zsg701127589.h1

Seq. No. 27448

Contig ID 155318\_2.R1040 5'-most EST zzp700836030.h1

Seq. No. 27449

Contig ID 155334\_1.R1040 5'-most EST kmv700738015.h1

Seq. No. 27450

Contig ID 155340\_1.R1040 5'-most EST xpa700795933.h1

Seq. No. 27451

Contig ID 155347\_1.R1040 5'-most EST zhf700962131.h1

Seq. No. 27452

Contig ID 155347\_2.R1040 5'-most EST kl1701215047.h1

Seq. No. 27453

Contig ID 155351\_1.R1040 5'-most EST kmv700738039.h1

Method BLASTX
NCBI GI g416651
BLAST score 328
E value 7.0e-31
Match length 93
% identity 71

NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN

PCNT103) >gi\_100301\_pir\_\_S16269 auxin-induced protein (clone pCNT103) - common tobacco >gi\_19791\_emb\_CAA39704\_

(X56263) auxin-induced protein [Nicotiana tabacum]

Seq. No. 27454

Contig ID 155406 1.R1040 5'-most EST kmv700738134.h1



```
BLASTX
Method
                  q3293547
NCBI GI
                  159
BLAST score
                  1.0e-10
E value
                  120
Match length
                  33
% identity
                  (AF072709) putative oxidoreductase [Streptomyces lividans]
NCBI Description
                  27455
Seq. No.
                  155415 1.R1040
Contig ID
                  g5607167
5'-most EST
                  BLASTX
Method
                  g3738298
NCBI GI
                   440
BLAST score
                   6.0e-43
E value
                   346
Match length
% identity
                   34
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4249394 (AC006072) unknown protein [Arabidopsis
                   thaliana]
                   27456
Seq. No.
                   155437 1.R1040
Contig ID
                   zhf700964234.hl
5'-most EST
                   27457
Seq. No. -
                   155438 1.R1040
Contig ID
                   kmv700738178.h1
5'-most EST
                   BLASTX
Method
                   g3176726
NCBI GI
BLAST score
                   243
                   5.0e-21
E value
                   73
Match length
                   68
% identity
                   (AC002392) putative serine proteinase [Arabidopsis
NCBI Description
                   thaliana]
                   27458
Seq. No.
                   155458 1.R1040
Contig ID
                   kmv700738215.h1
5'-most EST
                   BLASTX
Method
                   g4559332
NCBI GI
BLAST score
                   198
                   3.0e-15
E value
Match length
                   44
                   91
% identity
                   (AC007087) putative phosphoenolpyruvate carboxylase
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 27459

Contig ID 155462\_1.R1040 5'-most EST kmv700738220.h1

Method BLASTX
NCBI GI g4006868
BLAST score 330
E value 3.0e-31
Match length 80



% identity 76
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 27460

Contig ID 155479\_1.R1040

5'-most EST jC-gmro02910034d07a1

Method BLASTX
NCBI GI g1652280
BLAST score 293
E value 2.0e-26
Match length 143
% identity 44

NCBI Description (D90904) ribonuclease II [Synechocystis sp.]

Seq. No. 27461

Contig ID 155489\_1.R1040 5'-most EST zsg701130346.h1

Seq. No. 27462

Contig ID 155508\_1.R1040 5'-most EST kmv700738303.h1

Seq. No. 27463

Contig ID 155526\_1.R1040 5'-most EST kmv700740217.h1

Seq. No. 27464

Contig ID 155552\_1.R1040 5'-most EST zhf700962503.h1

Seq. No. 27465

Contig ID 155557\_1.R1040 5'-most EST kmv700738379.h1

Seq. No. 27466

Contig ID 155560\_1.R1040 5'-most EST kl1701215236.h1

Seq. No. 27467

Contig ID 155560\_2.R1040 5'-most EST jC-gmle01810028f10a1

Method BLASTX
NCBI GI g2828290
BLAST score 313
E value 1.0e-28
Match length 116
% identity 63

NCBI Description (AL021687) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 27468

Contig ID 155564 1.R1040 5'-most EST pmv700888237.h1

Method BLASTX
NCBI GI g1171577
BLAST score 296
E value 6.0e-40
Match length 120

4272



% identity 68

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No.

Contig ID 5'-most EST 27469 155584 1.R1040 kmv700738433.h1

Seq. No.

Contig ID 5'-most EST 27470 155593\_1.R1040 kmv700738455.h1

Seq. No. 27471

Contig ID 155608 1.R1040 5'-most EST kmv700739961.h1

Seq. No. Contig ID

No. 27472 g ID 155667\_1.R1040

5'-most EST jC-gmle01810091f05a1

Method BLASTX
NCBI GI 94508076
BLAST score 168
E value 8.0e-12
Match length 100

% identity 33

NCBI Description (AC005882) 55659 [Arabidopsis thaliana]

Seq. No. 27473

Contig ID 155687\_1.R1040 5'-most EST jsh701068458.h1

Seq. No. 27474

Contig ID 155706\_1.R1040 5'-most EST kmv700738615.h1

Seq. No. 27475

Contig ID 155720\_1.R1040 5'-most EST fua701039127.h1

Seq. No. 27476

Contig ID 155750 1.R1040 5'-most EST kl1701214463.h1

Method BLASTX
NCBI GI g1546694
BLAST score 528
E value 8.0e-54
Match length 144
% identity 69

NCBI Description (X98806) peroxidase ATP20a [Arabidopsis thaliana]

Seq. No. 27477

Contig ID 155815\_1.R1040 5'-most EST kmv700738766.h1

Seq. No. 27478

Contig ID 155874\_1.R1040 5'-most EST kmv700738846.h1



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27479
Seq. No.
                  155883 1.R1040
Contig ID
5'-most EST
                  epx701107287.h1
Method
                  BLASTX
NCBI GI
                  q3135611
BLAST score
                  221
                  5.0e-18
E value
Match length
                  119
% identity
                  44
                  (AF062485) cellulose synthase [Arabidopsis thaliana]
NCBI Description
                  27480
Seq. No.
Contig ID
                  155897_1.R1040
                  kmv700738875.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3367519
BLAST score
                  463
E value
                  3.0e-46
Match length
                  139
                  63
% identity
                  (AC004392) Contains similarity to gb U51898
NCBI Description
                  Ca2+-independent phospholipase A2 from Rattus norvegicus.
                  [Arabidopsis thaliana]
                  27481
Seq. No.
                  155911 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy174a06b1
Method
                  BLASTX
NCBI GI
                  g3859112
                  247
BLAST score
E value
                  3.0e-22
Match length
                  88
% identity
                  60
                  (AF031607) male sterility MS5 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  27482
Contig ID
                  155924 1.R1040
                  uC-gmronoir051d06b1
5'-most EST
Seq. No.
                  27483
Contig ID
                  155994 1.R1040
5'-most EST
                  kmv700739006.h1
Method
                  BLASTX
NCBI GI
                  q2244912
BLAST score
                  265
E value
                  2.0e-29
Match length
                  142
% identity
                  54
                 (Z97339) similar to transketolase [Arabidopsis thaliana]
NCBI Description
                  27484
Seq. No.
```

155996 1.R1040 Contig ID 5'-most EST kmv700739008.h1 Method BLASTX

NCBI GI g3859944 BLAST score 172 E value 4.0e-12



Match length % identity 70 NCBI Description

(AF084570) FKBP12 interacting protein [Arabidopsis

thaliana]

Seq. No. Contig ID 5'-most EST 27485 155996 2.R1040 smc700746270.hl

Seq. No.

27486 Contig ID 5'-most EST

156013 1.R1040  $gsv701\overline{0}46457.h1$ 

Seq. No.

Contig ID 5'-most EST Method

156019 1.R1040 fC-qmle700739040a1 BLASTX

NCBI GI g3450842 612 BLAST score 1.0e-63 E value 128 Match length % identity

(AF080436) mitogen activated protein kinase kinase [Oryza NCBI Description

27487

Seq. No.

Contig ID 5'-most EST 27488 156091 1.R1040

fC-gmle700739163a1 BLASTX

Method NCBI GI g3122671 702 BLAST score E value 2.0e-74 145 Match length % identity 86

NCBI Description

HYPOTHETICAL RAE1-LIKE PROTEIN >gi\_2129676\_pir\_\_S71241 probable export protein - Arabidopsis thaliana >gi\_1297188 (U53501) Theoretical protein with similarity to Swiss-Prot Accession Number P41838 poly A+ RNA export protein

[Arabidopsis thaliana]

27489 Seq. No.

Contig ID 5'-most EST 156136 1.R1040 pxt700940920.hl

Seq. No. Contig ID

27490

156216 1.R1040 kmv700739404.h1

Seq. No. Contig ID

5'-most EST

27491

5'-most EST

156217 1.R1040 kmv700739405.h1

BLASTX Method g2262158 NCBI GI 408 BLAST score 6.0e-40 E value 114 Match length 66 % identity



(AC002329) putative mitochondrial phosphate translocator protein [Arabidopsis thaliana]

27492 Seq. No. 156223 1.R1040 Contig ID awf700840272.hl 5'-most EST

27493 Seq. No.

NCBI Description

156256 1.R1040 Contig ID kmv700741147.hl 5'-most EST

27494 Seq. No.

156259 1.R1040 Contig ID kmv700739469.hl 5'-most EST BLASTX Method

q4510389 NCBI GI 479 BLAST score 2.0e-48 E value 128 Match length % identity

(AC007017) putative solute carrier protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 27495

156263 1.R1040 Contig ID rca700998391.hl 5'-most EST

BLASTX Method q3334667 NCBI GI BLAST score 138 E value 1.0e-08 36 Match length 75 % identity

(Y10493) putative cytochrome P450 [Glycine max] NCBI Description

27496 Seq. No.

156267 1.R1040 Contig ID fde700875994.hl 5'-most EST

27497 Seq. No.

156267 2.R1040 Contig ID fC-gmle700739489a1 5'-most EST

27498 Seq. No.

156285 1.R1040 Contig ID awf700836661.hl 5'-most EST

BLASTX Method g1076318 NCBI GI 219 BLAST score 3.0e-18 E value 78 Match length 41 % identity

dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) NCBI Description

precursor - Arabidopsis thaliana (fragment)

>gi 559395 emb CAA86300 (Z46230) dihydrolipoamide acetyltransferase (E2) subunit of PDC [Arabidopsis

thaliana]



```
27499
Seq. No.
                  156287 1.R1040
Contig ID
                  kmv700739545.h1
5'-most EST
                  BLASTX
Method
                  g3377803
NCBI GI
                  191
BLAST score
                   3.0e-14
E value
                   51
Match length
% identity
                   (AF075597) Similar to (p)ppGpp synthetase; T2H3.9
NCBI Description
                   [Arabidopsis thaliana]
                   27500
Seq. No.
                   156292 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy198c07b1
                   BLASTX
Method
                   g3935168
NCBI GI
                   1100
BLAST score
                   1.0e-120
E value
                   281
Match length
% identity
                   (AC004557) F17L21.11 [Arabidopsis thaliana]
NCBI Description
                   27501
Seq. No.
                   156301 1.R1040
Contig ID
                   q5677515
5'-most EST
                   BLASTX
Method
                   g3236235
NCBI GI
                   302
BLAST score
                   3.0e-27
E value
                   88
Match length
                   68
% identity
                   (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4056501 (AC005896) unknown protein [Arabidopsis
                   thalianal
                   27502
Seq. No.
                   156305 1.R1040
Contig ID
                   leu701145416.h1
5'-most EST
                   27503
Seq. No.
                   156309 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810009h02a1
                   BLASTX
Method
                   q1184075
NCBI GI
                   715
BLAST score
                   2.0e-75
E value
                   349
Match length
 % identity
                   (U42444) Cf-2.1 [Lycopersicon pimpinellifolium]
NCBI Description
                   >gi 1587673 prf__2207203A Cf-2 gene [Lycopersicon
```

esculentum]

Seq. No. 27504

Contig ID 156316\_1.R1040 5'-most EST kmv700739687.h1

Method BLASTX



q3402689 NCBI GI 303 BLAST score 6.0e-28 E value 81 Match length 73 % identity (AC004697) unknown protein [Arabidopsis thaliana] NCBI Description

27505 Seq. No. 156338 1.R1040 Contig ID 5'-most EST leu701154128.hl

Seq. No. 27506 156345 1.R1040 Contig ID 5'-most EST g5605837

27507 Seq. No. 156351 1.R1040 Contig ID

kmv700739670.h1 5'-most EST

27508 Seq. No. 156375 1.R1040 Contig ID kmv700739711.h1 5'-most EST

27509 Seq. No. 156391 1.R1040 Contig ID kmv700739779.h1 5'-most EST

Seq. No. 27510 156393\_1.R1040 Contig ID fC-gmse7000754533f1

5'-most EST BLASTX Method g3367568 NCBI GI BLAST score 643 3.0e-67 E value 174 Match length 68 % identity

(AL031135) protein kinase - like protein [Arabidopsis NCBI Description thaliana]

Seq. No. 156412 1.R1040 Contig ID

uC-gmrominsoy169b01b1 5'-most EST

27511

27512 Seq. No.

156412 2.R1040 Contig ID bth700848345.hl 5'-most EST

27513 Seq. No.

156425 1.R1040 Contig ID kmv700741476.hl 5'-most EST

Seq. No. 27514

156447 1.R1040 Contig ID fC-qmle700739836a1 5'-most EST

Method BLASTN NCBI GI q495658 BLAST score 161



4.0e-85 E value 377 Match length 86 % identity Pisum sativum aspartate carbamoyltransferase (pyrB1) mRNA, NCBI Description complete cds 27515 Seq. No. 156448 1.R1040 Contig ID jC-gmf102220077f06d1 5'-most EST BLASTX Method q2804280 NCBI GI 198 BLAST score 3.0e-15 E value 63 Match length 57 % identity (AB003687) 6-4 photolyase [Arabidopsis thaliana] NCBI Description >gi\_3929918\_dbj\_BAA34711\_ (AB017331) 6-4 photolyase [Arabidopsis thaliana] 27516 Seq. No. 156458 1.R1040 Contig ID kmv700739866.h1 5'-most EST Seq. No. 27517 156473 1.R1040 Contig ID eep700867371.hl 5'-most EST BLASTX Method g4455363 NCBI GI 313 BLAST score 2.0e-28 E value 142 Match length 40 % identity (AL035524) Medicago nodulin N21-like protein [Arabidopsis NCBI Description thaliana] 27518 Seq. No. 156506 1.R1040 Contig ID q5666770 5'-most EST BLASTX Method g4490316 NCBI GI 212 BLAST score 5.0e-17 E value 96 Match length 55 % identity (AL035678) nucellin-like protein [Arabidopsis thaliana] NCBI Description 27519 Seq. No. 156520 1.R1040 Contig ID

fC-gmle700739977a1 5'-most EST

BLASTX Method g2997593 NCBI GI BLAST score 259 9.0e-23 E value 89 Match length % identity

(AF020816) glucose-6-phosphate/phosphate-translocator NCBI Description

precursor [Solanum tuberosum]



Seq. No. 27520

Contig ID 156551\_1.R1040

5'-most EST jC-gmle01810009a03d1

Method BLASTX
NCBI GI g3080402
BLAST score 175
E value 1.0e-12
Match length 44
% identity 75

NCBI Description (AL022603) putative NADPH quinone oxidoreductase

[Arabidopsis thaliana] >gi\_4455266\_emb\_CAB36802.1\_(AL035527) putative NADPH quinone oxidoreductase

[Arabidopsis thaliana]

Seq. No. 27521

Contig ID 156581\_1.R1040 5'-most EST kmv700740079.h1

Seq. No. 27522

Contig ID 156588\_1.R1040 5'-most EST kmv700740093.h1

Seq. No. 27523

Contig ID 156593\_1.R1040 5'-most EST sat701003618.h1

Method BLASTX
NCBI GI g2832649
BLAST score 406
E value 6.0e-40
Match length 101
% identity 73

NCBI Description (AL021710) adenylosuccinate lyase - like protein

[Arabidopsis thaliana]

Seq. No. 27524

Contig ID 156634\_1.R1040

5'-most EST jC-gmro02910024d03a1

Seq. No. 27525

Contig ID 156651\_1.R1040 5'-most EST fC-gmle700740186a1

Method BLASTX
NCBI GI g4510406
BLAST score 475
E value 2.0e-47
Match length 147
% identity 65

NCBI Description (AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No. 27526

Contig ID 156665\_1.R1040 5'-most EST eep700865943.h1

Seq. No. 27527

Contig ID 156692\_1.R1040

5'-most EST jC-gmst02400057f01d1



27528 Seq. No. 156708 1.R1040 Contig ID fua701039591.h1 5'-most EST 27529 Seq. No. 156728 1.R1040 Contig ID kmv700740492.h1 5'-most EST

27530 Seq. No. 156800 1.R1040 Contig ID kmv700740391.h15'-most EST

27531 Seq. No. 156869 1.R1040 Contig ID kmv700740491.hl 5'-most EST

Method BLASTX NCBI GI q4218126 283 BLAST score 2.0e-25 E value 88 Match length 55 % identity

NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 156872 1.R1040 Contig ID kmv700740494.hl 5'-most EST

27533 Seq. No. 156877 1.R1040 Contig ID zhf700956784.h1 5'-most EST

27534 Seq. No. 156880 1.R1040 Contig ID asn701140433.hl 5'-most EST BLASTX Method

g4522004 NCBI GI 204 BLAST score 3.0e-16 E value 86 Match length 50 % identity

(AC007069) putative histidine kinase, sensory transduction NCBI Description

[Arabidopsis thaliana]

27535 Seq. No. 156898 1.R1040 Contig ID bth700848106.hl 5'-most EST

27536 Seq. No. 156905 1.R1040 Contig ID zhf700953760.h1 5'-most EST

27537 Seq. No. 156909 1.R1040 Contig ID 5'-most EST kmv700740557.hl

27538 Seq. No.



Contig ID 156939\_1.R1040 5'-most EST kmv700740625.h1

Seq. No. 27539

Contig ID 156942\_1.R1040 5'-most EST kmv700740628.h1

Method BLASTX
NCBI GI g3894172
BLAST score 532
E value 3.0e-54
Match length 194
% identity 48

NCBI Description (AC005312) putative cinnamoyl-CoA reductase [Arabidopsis

thalianal

Seq. No. 27540

Contig ID 156969 1.R1040 5'-most EST kmv700740688.h1

Seq. No. 27541

Contig ID 156974\_1.R1040 5'-most EST bth700849423.h1

Method BLASTX
NCBI GI g1296805
BLAST score 428
E value 2.0e-42
Match length 117
% identity 70

NCBI Description (X90929) C-terminal peptidase of the D1 protein [Hordeum

vulgare]

Seq. No. 27542

Contig ID 156980 1.R1040 5'-most EST leu701153567.h1

Seq. No. 27543

Contig ID 157021 1.R1040

5'-most EST g5607109

Seq. No. 27544

Contig ID 157046\_1.R1040 5'-most EST kmv700740817.h1

Seq. No. 27545

Contig ID 157070\_1.R1040 5'-most EST kmv700740864.h1

Method BLASTX
NCBI GI g2244910
BLAST score 176
E value 1.0e-12
Match length 85
% identity 44

NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No. 27546

Contig ID 157075\_1.R1040 5'-most EST jsh701064103.h1



Method BLASTX
NCBI GI g4115914
BLAST score 508
E value 9.0e-67
Match length 214
% identity 60

(AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85, N=1) [Arabidopsis thaliana] >gi\_4539410\_emb\_CAB40043.1\_(AL049524) putative Fe(II)/ascorbate oxidase [Arabidopsis

thaliana]

Seq. No. 27547

NCBI Description

Contig ID 157088\_1.R1040 5'-most EST kmv700743634.h1

Seq. No. 27548

Contig ID 157090\_1.R1040 5'-most EST leu701147124.h1

Seq. No. 27549

Contig ID 157095\_1.R1040 5'-most EST zpv700760606.h1

Method BLASTX
NCBI GI g2213597
BLAST score 607
E value 4.0e-63
Match length 170
% identity 63

NCBI Description (AC000348) T7N9.17 [Arabidopsis thaliana]

Seq. No. 27550

Contig ID 157123\_1.R1040 5'-most EST fC-gmle700741352a1

Seq. No. 27551

Contig ID 157158\_1.R1040 5'-most EST kmv700740995.h1

Seq. No. 27552

Contig ID 157181\_1.R1040 5'-most EST gsv701052712.h1

Seq. No. 27553

Contig ID 157191\_1.R1040

5'-most EST jC-gmle01810071e10a1

Seq. No. 27554

Contig ID 157215\_1.R1040 5'-most EST kmv700741072.h1

Method BLASTX
NCBI GI g3786011
BLAST score 177
E value 2.0e-23
Match length 69
% identity 86

NCBI Description (AC005499) putative elongation factor [Arabidopsis



## thaliana]

```
27555
Seq. No.
                   157220 1.R1040
Contig ID
                  hrw701061188.hl
5'-most EST
                   27556
Seq. No.
                   157221 1.R1040
Contig ID
                   rca700997763.hl
5'-most EST
                   BLASTX
Method
                   q3319713
NCBI GI
BLAST score
                   1046
                   1.0e-114
E value
                   272
Match length
                   71
% identity
NCBI Description (AJ006992) chitinase precursor [Canavalia ensiformis]
                   27557
Seq. No.
                   157237 1.R1040
Contig ID
                   kmv700741105.h1
5'-most EST
                   27558
Seq. No.
                   157244 1.R1040
Contig ID
                   kmv700741112.h1
5'-most EST
                   27559
Seq. No.
                   157324 1.R1040
Contig ID
                   uC-gmf\overline{l}minsoy099b09b1
5'-most EST
                   27560
Seq. No.
                   157332 1.R1040
Contig ID
                   bnu700\overline{9}67559.h1
5'-most EST
                   27561
Seq. No.
                   157336 1.R1040
Contig ID
                   smc700747435.h1
 5'-most EST
                   BLASTX
Method
                   q2501296
NCBI GI
                   217
BLAST score
                    6.0e-18
E value
                    87
Match length
                    49
 % identity
                   DNA GYRASE SUBUNIT B >gi_1652801_dbj_BAA17720_ (D90908) DNA
 NCBI Description
                    gyrase B subunit [Synechocystis sp.]
                    27562
 Seq. No.
                    157345 1.R1040
 Contig ID
                    kmv700741250.h1
 5'-most EST
                    BLASTX
 Method
                    q3493253
 NCBI GI
                    159
 BLAST score
                    3.0e-11
 E value
 Match length
                    64
                    50
```

27563 Seq. No.

% identity

NCBI Description (AF076156) catechol-O-methyltransferase [Mus musculus]



157355 1.R1040 Contig ID kmv700741261.h15'-most EST BLASTN Method q510546 NCBI GI BLAST score 324 0.0e + 00E value 589 Match length 89 % identity NCBI Description P.sativum mRNA for starch branching enzyme II 27564 Seq. No. 157442 1.R1040 Contig ID smc700749730.h1 5'-most EST BLASTX Method q4204311 NCBI GI 181 BLAST score 1.0e-13 E value Match length 65 % identity (AC003027) 1cl prt seq No definition line found NCBI Description [Arabidopsis thaliana] 27565 Seq. No. 157495 1.R1040 Contig ID kmv700741453.h1 5'-most EST 27566 Seq. No. 157496 1.R1040 Contig ID zsg701123053.h1 5'-most EST 27567 Seq. No. 157496 2.R1040 Contig ID fde700875595.h1 5'-most EST 27568 Seq. No. 157516 1.R1040 Contig ID kmv700741487.h1 5'-most EST BLASTX Method q404688 NCBI GI 266 BLAST score 1.0e-23 E value 97 Match length % identity (L19074) cytochrome P450 [Catharanthus roseus] NCBI Description 27569 Seq. No. 157539 1.R1040 Contig ID kmv700741519.h1 5'-most EST BLASTX Method q1708972 NCBI GI 333 BLAST score E value 8.0e-31

158 Match length 42 % identity

(R)-MANDELONITRILE LYASE ISOFORM 3 PRECURSOR NCBI Description

(HYDROXYNITRILE LYASE 3) ((R)-OXYNITRILASE 3) >gi\_1262279

(U51562) (R)-(+)-mandelonitrile lyase isoform  $MDL\overline{3}$ 



precursor [Prunus serotina] >gi\_2343181 (AF013161)
(R)-(+)-mandelonitrile lyase isoform MDL3 precursor [Prunus serotina]

Seq. No. 27570

Contig ID 157541\_1.R1040 5'-most EST kmv700741521.h1

Seq. No. 27571

Contig ID 157557 1.R1040 5'-most EST pmv700894256.h1

Seq. No. 27572

Contig ID 157585\_1.R1040 5'-most EST gsv701045237.h1

Seq. No. 27573

Contig ID 157633 1.R1040 5'-most EST kmv700741674.h1

Method BLASTX
NCBI GI g4539369
BLAST score 182
E value 1.0e-23
Match length 88
% identity 60

NCBI Description (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 27574

Contig ID 157640\_1.R1040 5'-most EST bth700844817.h1

Seq. No. 27575

Contig ID 157651 1.R1040 5'-most EST zpv700761954.h1

Seq. No. 27576

Contig ID 157651 2.R1040 5'-most EST kmv700741709.h1

Seq. No. 27577

Contig ID 157686\_1.R1040 5'-most EST kmv700741760.h1

Method BLASTX
NCBI GI g4539343
BLAST score 231
E value 3.0e-19
Match length 121
% identity 48

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 27578

Contig ID 157688\_1.R1040 5'-most EST sat701011341.h1

Seq. No. 27579

Contig ID 157700 1.R1040

5'-most EST jC-gmle01810057d04d1



```
27580
Seq. No.
                  157712 1.R1040
Contig ID
                  jC-gmst02400049h05d1
5'-most EST
                  27581
Seq. No.
                  157713 1.R1040
Contig ID
                  kmv700743793.h1
5'-most EST
                  BLASTX
Method
                  q3775987
NCBI GI
                   173
BLAST score
                   7.0e-13
E value
                   51
Match length
                   65
% identity
                   (AJ010457) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   27582
Seq. No.
                   157728 1.R1040
Contig ID
                   kmv700741821.hl
5'-most EST
                   BLASTN
Method
                   q4519184
NCBI GI
BLAST score
                   53
                   4.0e-21
E value
                   117
Match length
                   86
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K15F13, complete sequence
                   27583
Seq. No.
                   157739 1.R1040
Contig ID
                   xzm700763715.hl
5'-most EST
Seq. No.
                   27584
                   157754 2.R1040
Contig ID
                   cle700967748.h1
5'-most EST
                   BLASTX
Method
                   g3063455
NCBI GI
                   313
BLAST score
                   6.0e-29
E value
                   72
Match length
                   76
% identity
                   (AC003981) F22013.17 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   27585
                   157782 1.R1040
Contig ID
                   smc700748556.h1
5'-most EST
                   27586
Seq. No.
                   157783 1.R1040
Contig ID
                   jC-gmro02910038f02a1
 5'-most EST
                   BLASTX
Method
NCBI GI
                   q3080401
```

Method BLASIA NCBI GI g308040: BLAST score 337 E value 1.0e-31 Match length 95 % identity 67

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]



>gi\_4455265\_emb\_CAB36801.1\_ (AL035527) putative protein
[Arabidopsis thaliana]

 Seq. No.
 27587

 Contig ID
 157801 1.R1040

 5'-most EST
 kmv700741935.h1

Seq. No. 27588

Contig ID 157830\_1.R1040

5'-most EST jC-gmro02800031e05a1

Seq. No. 27589

Contig ID 157843 1.R1040 5'-most EST kmv700742008.h1

Seq. No. 27590

Contig ID 157865\_1.R1040 5'-most EST kmv700742049.h1

Method BLASTN
NCBI GI g510545
BLAST score 157
E value 6.0e-83
Match length 285
% identity 89

NCBI Description P.sativum mRNA for starch branching enzyme I

Seq. No. 27591

Contig ID 157870\_1.R1040 5'-most EST smc700747937.h1

Method BLASTX
NCBI GI g2388561
BLAST score 543
E value 1.0e-55
Match length 165
% identity 66

NCBI Description (AC000098) Similar to Arabidopsis hypothetical protein

PID:e326839 (gb\_Z97337). [Arabidopsis thaliana]

Seq. No. 27592

Contig ID 157913 1.R1040 5'-most EST kmv700742131.h1

Seq. No. 27593

Contig ID 157920\_1.R1040 5'-most EST kmv700742139.h1

Method BLASTX
NCBI GI g1168235
BLAST score 185
E value 2.0e-14
Match length 41
% identity 88

NCBI Description 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING

>gi\_1073800\_pir\_\_C64077 6-phosphogluconate dehydrogenase,
decarboxylating (gnd) homolog - Haemophilus influenzae
(strain Rd KW20) >gi\_1573539 (U32737) 6-phosphogluconate

dehydrogenase, decarboxylating (gnd) [Haemophilus

influenzae Rd]



Seq. No. 27594

Contig ID 157926\_1.R1040 5'-most EST kmv700742157.h1

Seq. No. 27595

Contig ID 157941\_1.R1040 5'-most EST jC-gmf102220127h11a1

Seq. No. 27596

Contig ID 157973\_1.R1040 5'-most EST pmv700890770.h1

Method BLASTX
NCBI GI g537404
BLAST score 335
E value 1.0e-31
Match length 66
% identity 89

NCBI Description (D26537) WSI76 protein induced by water stress [Oryza

sativa]

Seq. No. 27597

Contig ID 157991\_1.R1040 5'-most EST pxt700945008.h1

Method BLASTX
NCBI GI g3402687
BLAST score 394
E value 6.0e-38
Match length 151
% identity 53

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 27598

Contig ID 158003\_1.R1040 5'-most EST fC-gmle700742323a1

Method BLASTX
NCBI GI g126334
BLAST score 168
E value 1.0e-11
Match length 177
% identity 33

NCBI Description LIPASE PRECURSOR (TRIACYLGLYCEROL LIPASE)

>gi\_79925\_pir\_\_A24075 lipase precursor - Staphylococcus

hyicus  $>gi_47\overline{13}6$  emb\_CAA26602\_ (X02844) precursor

[Staphylococcus hyicus]

Seq. No. 27599

Contig ID 158036\_1.R1040 5'-most EST zhf700960242.h1

Method BLASTN
NCBI GI g1694899
BLAST score 103
E value 6.0e-51
Match length 271
% identity 85

NCBI Description P.sativum mRNA for Cop1 protein



Seq. No. 27600

Contig ID 158066 1.R1040

5'-most EST jC-gmle01810044h01d1

Seq. No. 27601

Contig ID 158088 1.R1040 5'-most EST kmv700742511.h1

Method BLASTX
NCBI GI g401213
BLAST score 376
E value 3.0e-36
Match length 127
% identity 64

NCBI Description ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PRECURSOR >gi\_166792

(M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana] >gi\_445600\_prf\_\_1909347A phosphoribosylanthranilate transferase [Arabidopsis

thaliana]

Seq. No. 27602

Contig ID 158097\_1.R1040 5'-most EST vzy700751779.h1

Seq. No. 27603

Contig ID 158122\_1.R1040 5'-most EST kmv700742589.h1

Seq. No. 27604

Contig ID 158141\_1.R1040

5'-most EST g5753461

Seq. No. 27605

Contig ID 158162 1.R1040 5'-most EST kmv700742669.h1

Seq. No. 27606

Contig ID 158207\_1.R1040

Method BLASTX
NCBI GI g2245095
BLAST score 446
E value 8.0e-57
Match length 143
% identity 81

NCBI Description (297343) formyltransferase purU homolog [Arabidopsis

thaliana]

Seq. No. 27607

Contig ID 158255\_1.R1040 5'-most EST jex700904465.h1

Seq. No. 27608

Contig ID 158289\_1.R1040 5'-most EST pmv700891478.h1

Seq. No. 27609

Contig ID 158291\_1.R1040



5'-most EST jC-gmle01810084f03a1

Method BLASTX
NCBI GI g3377517
BLAST score 670
E value 2.0e-70
Match length 208
% identity 64

NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No. 27610

Contig ID 158355\_1.R1040 5'-most EST kmv700743045.h1

Seq. No. 27611

Contig ID 158379 1.R1040 5'-most EST gsv701049990.h1

Method BLASTX
NCBI GI g3201635
BLAST score 296
E value 4.0e-27
Match length 75
% identity 76

NCBI Description (AC004669) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27612

Contig ID 158407\_1.R1040 5'-most EST kmv700743124.h1

Seq. No. 27613

Contig ID 158438\_1.R1040 5'-most EST rlr700895959.h1

Method BLASTX
NCBI GI g2827661
BLAST score 244
E value 3.0e-21
Match length 59
% identity 75

NCBI Description (AL021637) hyuC-like protein [Arabidopsis thaliana]

Seq. No. 27614

Contig ID 158440\_1.R1040

5'-most EST uC-gmflminsoy044b10b1

Seq. No. 27615

Contig ID 158473\_1.R1040 5'-most EST kmv700743250.h1

Seq. No. 27616

Contig ID 158558\_1.R1040 5'-most EST kmv700743410.h1

Seq. No. 27617

Contig ID 158571\_1.R1040 5'-most EST fde700874744.h1

Method BLASTX NCBI GI g3510254 BLAST score 260



5.0e-23 E value 67 Match length 75 % identity (AC005310) putative zinc transporter [Arabidopsis thaliana] NCBI Description 27618 Seq. No. 158599 1.R1040 Contig ID fC-gmle700743470a1 5'-most EST BLASTX Method g4102600 NCBI GI 544 BLAST score E value 6.0e-56 123 Match length 80 % identity (AF013467) ARF6 [Arabidopsis thaliana] NCBI Description Seq. No. 27619 158627 1.R1040 Contig ID uC-gmrominsoy030c01b1 5'-most EST Seq. No. 27620 158667 1.R1040 Contig ID 5'-most EST rca700997551.hl Method BLASTX g2347199 NCBI GI 30 BLAST score 522 7.0e-53 E value Match length 225 49 % identity (AC002338) protein kinase isolog [Arabidopsis thaliana] NCBI Description 27621 Seq. No. 158695 1.R1040 Contig ID leu701150633.h1 5'-most EST 27622 Seq. No. 158727 2.R1040 Contig ID jC-gmst02400049e02d1 5'-most EST 27623 Seq. No. 158736 1.R1040 Contig ID jC-gmst02400066b05a2 5'-most EST BLASTX Method g2088658 NCBI GI BLAST score 366 6.0e-35 E value 120 Match length 21 % identity (AF002109) unknown protein [Arabidopsis thaliana] NCBI Description 27624 Seq. No. 158751 1.R1040 Contig ID

Contig ID 158/51\_1
5'-most EST g5605744
Method BLASTX
NCBI GI g4567247
BLAST score 454

E value 4.0e-45



Match length 62 % identity

(AC007070) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 27625

158768\_1.R1040 Contig ID zhf700960112.h1 5'-most EST

Seq. No. 27626

158804 1.R1040 Contig ID kmv700743942.h1 5'-most EST

BLASTX Method q1903360 NCBI GI 188 BLAST score 4.0e-14 E value 123 Match length % identity 37

(AC000104) Similar to Arabidopsis 2A6 (gb X83096). EST NCBI Description

gb T76913 comes from this gene. [Arabidopsis thaliana]

27627 Seq. No.

158842 1.R1040 Contig ID kmv700744008.hl 5'-most EST

27628 Seq. No.

158954 1.R1040 Contig ID  $rca700\overline{9}96387.h1$ 5'-most EST

27629 Seq. No.

158989 1.R1040 Contig ID uC-gmronoir057f06b1 5'-most EST

27630 Seq. No.

158994 1.R1040 Contig ID leu701148728.h1 5'-most EST

27631 Seq. No.

158997 1.R1040 Contig ID smw700646229.hl 5'-most EST

27632 Seq. No.

159036 1.R1040 Contig ID ary700764309.hl 5'-most EST

BLASTX Method g3377803 NCBI GI BLAST score 601 2.0e-62 E value 200 Match length 61 % identity

(AF075597) Similar to (p)ppGpp synthetase; T2H3.9 NCBI Description

[Arabidopsis thaliana]

27633 Seq. No.

159055 1.R1040 Contig ID 5'-most EST smc700744206.h1

Method BLASTX NCBI GI q4263704



BLAST score 166
E value 3.0e-11
Match length 78
% identity 38

% identity 38
NCBI Description (AC006223) putative sugar starvation-induced protein

[Arabidopsis thaliana]

Seq. No. 27634

Contig ID 159080\_1.R1040 5'-most EST fC-gmro700744539a1

Seq. No. 27635

Contig ID 159153\_1.R1040 5'-most EST smc700744305.h1

Seq. No. 27636

Contig ID 159161\_1.R1040 5'-most EST smc700744314.h1

Method BLASTX
NCBI GI g2213594
BLAST score 219
E value 3.0e-19
Match length 84
% identity 56

NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No. 27637

Contig ID 159171\_1.R1040 5'-most EST smc700744327.h1

Seq. No. 27638

Contig ID 159179\_1.R1040 5'-most EST smc700747036.h1

Seq. No. 27639

Contig ID 159182 1.R1040

5'-most EST uC-gmrominsoy0001a08b1

Seq. No. 27640

Contig ID 159203 1.R1040 5'-most EST smc700747068.h1

Method BLASTN
NCBI GI g4519193
BLAST score 35
E value 2.0e-10
Match length 91
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC11, complete sequence

Seq. No. 27641

Contig ID 159274\_1.R1040 5'-most EST smc700744564.h1

Seq. No. 27642

Contig ID 159284\_1.R1040 5'-most EST pmv700888323.h1



Method BLASTX
NCBI GI g4455359
BLAST score 348
E value 4.0e-33
Match length 106
% identity 64

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 27643

Contig ID 159317\_1.R1040 5'-most EST smc700744707.h1

Method BLASTX
NCBI GI g2244763
BLAST score 339
E value 4.0e-37
Match length 104
% identity 72

NCBI Description (Z97335) A6 anther-specific protein [Arabidopsis thaliana]

Seq. No. 27644

Contig ID 159354\_1.R1040

5'-most EST uC-gmrominsoy050a03b1

Method BLASTX
NCBI GI g2827699
BLAST score 150
E value 2.0e-09
Match length 84
% identity 40

NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

Seq. No. 27645

Contig ID 159363\_1.R1040 5'-most EST jC-gmst02400027c08a1

Method BLASTX
NCBI GI g4467111
BLAST score 518
E value 2.0e-60
Match length 163
% identity 67

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 27646

Contig ID 159414 1.R1040 5'-most EST hrw701061205.h1

Seq. No. 27647

Contig ID 159468\_1.R1040 5'-most EST smc700745014.h1

Method BLASTX
NCBI GI 94433381
BLAST score 211
E value 3.0e-17
Match length 75
% identity 57

NCBI Description (D50034) 4-coumarate: CoA ligase [Nicotiana tabacum]

Seq. No. 27648



Contig ID 159475 1.R1040 5'-most EST smc700745049.h1

Seq. No. 27649

Contig ID 159490 1.R1040 5'-most EST kl1701210978.h1

Method BLASTX
NCBI GI g1931640
BLAST score 511
E value 4.0e-52
Match length 114
% identity 77

NCBI Description (U95973) Serine carboxypeptidase isolog [Arabidopsis

thaliana]

Seq. No. 27650

Contig ID 159500 1.R1040

5'-most EST uC-gmflminsoy001d04b1

Method BLASTX
NCBI GI g4038034
BLAST score 295
E value 2.0e-26
Match length 77
% identity 74

NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]

Seq. No. 27651

Contig ID 159536\_1.R1040 5'-most EST gsv701049536.h1

Method BLASTX
NCBI GI g4544412
BLAST score 150
E value 2.0e-09
Match length 101
% identity 32

NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27652

Contig ID 159606\_2.R1040 5'-most EST eep700866025.h1

Seq. No. 27653

Contig ID 159614\_1.R1040 5'-most EST pxt700946155.h1

Seq. No. 27654

Contig ID 159632\_1.R1040 5'-most EST smc700745377.h1

Method BLASTX
NCBI GI g3075398
BLAST score 576
E value 3.0e-59
Match length 199
% identity 55

NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]

Seq. No. 27655



```
Contig ID
                    159685 1.R1040
 5'-most EST
                    jex700\overline{9}09716.h1
Seq. No.
                    27656
Contig ID
                    159701 1.R1040
5'-most EST
                    pmv700891919.h1
Seq. No.
                    27657
Contig ID
                    159756 1.R1040
5'-most EST
                    uC-gmrominsoy230e08b1
Method
                    BLASTX
NCBI GI
                   q1946371
BLAST score
                   373
E value
                    9.0e-36
Match length
                   129
% identity
                   59
NCBI Description
                   (U93215) regulatory protein Viviparous-1 isolog
                    [Arabidopsis thaliana]
Seq. No.
                   27658
                   159823 1.R1040
Contig ID
5'-most EST
                   smc700745818.hl
Method
                   BLASTX
NCBI GI
                   g1086263
BLAST score
                   195
E value
                   7.0e-15
Match length
                   141
% identity
                   33
NCBI Description
                   TMV resistance protein N - tobacco (Nicotiana glutinosa)
                   >gi_558887 (U15605) N [Nicotiana glutinosa]
Seq. No.
                   27659
Contig ID
                   159837 1.R1040
5'-most EST
                   smc700745847.h1
Method
                   BLASTX
NCBI GI
                   g3367568
BLAST score
                   379
E value
                   2.0e-36
Match length
                   113
% identity
                   62
NCBI Description
                   (AL031135) protein kinase - like protein [Arabidopsis
                   thaliana]
Seq. No.
                   27660
Contig ID
                   159847 1.R1040
5'-most EST
                   smc700\overline{7}45871.h1
Seq. No.
                   27661
Contig ID
                   159851 1.R1040
5'-most EST
```

uC-gmrominsoy284d04b1

Seq. No. 27662

Contig ID 159884 1.R1040 5'-most EST smc700745936.h1

Method BLASTX NCBI GI g3776573 BLAST score 533



E value 2.0e-54 Match length 173 % identity 58

NCBI Description (AC005388) Similar to nodulins and lipase homolog F14J9.5

gi\_3482914 from Arabidopsis thaliana BAC gb\_AC003970. Alternate first exon from 72258 to 72509. [Arabidopsis

thaliana]

Seq. No. 27663

Contig ID 159920\_1.R1040 5'-most EST smc700746027.h1

Seq. No. 27664

Contig ID 159922 1.R1040 5'-most EST smc700746031.h1

Method BLASTX
NCBI GI g2129933
BLAST score 153
E value 2.0e-10
Match length 47
% identity 66

NCBI Description myb-related transcription factor TMH27 - tomato

>gi 1167484 emb CAA64614 (X95296) transcription factor

[Lycopersicon esculentum]

Seq. No. 27665

Contig ID 159925 1.R1040 5'-most EST leu701149294.h1

Seq. No. 27666

Contig ID 159930\_1.R1040 5'-most EST gsv701054304.h1

Method BLASTX
NCBI GI g3036840
BLAST score 232
E value 2.0e-19
Match length 91
% identity 51

NCBI Description (AJ222967) cystinosin [Homo sapiens]

>gi\_3036851\_emb\_CAA75882\_ (Y15924) cystinosin [Homo

sapiens]

Seq. No. 27667

Contig ID 159951 1.R1040 5'-most EST dpv701101389.h1

Seq. No. 27668

Contig ID 159970\_1.R1040 5'-most EST hrw701062059.h1

Seq. No. 27669

Contig ID 159984\_1.R1040 5'-most EST smc700747140.h1

Seq. No. 27670

Contig ID 159988\_1.R1040 5'-most EST asn701139351.h1



Method BLASTX
NCBI GI g3172025
BLAST score 210
E value 6.0e-17
Match length 70
% identity 66

NCBI Description (AB005805) aldehyde oxidase [Arabidopsis thaliana]

Seq. No. 27671

Contig ID 159993\_1.R1040 5'-most EST zhf700951771.h1

Seq. No. 27672

Contig ID 160011\_1.R1040 5'-most EST kl1701206372.h1

Method BLASTX
NCBI GI g3355464
BLAST score 246
E value 5.0e-21
Match length 118
% identity 47

NCBI Description (AC004218) putative ATP-binding-cassette protein, 3'

partial [Arabidopsis thaliana]

Seq. No. 27673

Contig ID 160016\_1.R1040 5'-most EST smc700746184.h1

Seq. No. 27674

Contig ID 160042 1.R1040 5'-most EST smc700746222.h1

Seq. No. 27675

Contig ID 160049\_1.R1040 5'-most EST smc700746233.h1

Seq. No. 27676

Contig ID 160064 1.R1040 5'-most EST smc700746265.h1

Seq. No. 27677

Contig ID 160071\_1.R1040

5'-most EST g5753341
Method BLASTX
NCBI GI g2288982
BLAST score 357
E value 8.0e-34
Match length 111
% identity 68

NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27678

Contig ID 160071\_2.R1040 5'-most EST jex700908256.h1

Seq. No. 27679

Contig ID 160087 1.R1040



5'-most EST jC-qmro02800042a02a1 Method BLASTX NCBI GI q4097522 BLAST score 689 E value 2.0e-72 Match length 213 % identity 66 (U63534) cinnamyl alcohol dehydrogenase [Fragaria x NCBI Description ananassa] 27680 Seq. No. 160087 2.R1040 Contig ID 5'-most EST fC-gmro700749247a2 BLASTX Method NCBI GI q4097522 598 BLAST score 4.0e-62 E value Match length 170 % identity 66 NCBI Description (U63534) cinnamyl alcohol dehydrogenase [Fragaria x ananassa] Seq. No. 27681 160101 1.R1040 Contig ID 5'-most EST jC-qmst02400016d01d1 27682 Seq. No. 160103 1.R1040 Contig ID 5'-most EST epx701105621.h1 Method BLASTX NCBI GI g3661610 BLAST score 711 2.0e-75 E value Match length 145 % identity 93 NCBI Description (AF092565) splicing factor Prp8 [Homo sapiens] Seq. No. 27683 Contig ID 160104 1.R1040 5'-most EST jC-gmf102220081e06a1 Method BLASTX NCBI GI g4539314 BLAST score 238 E value 1.0e-19 Match length 282 % identity 34 (AL035679) kinesin like protein [Arabidopsis thaliana] NCBI Description Seq. No. 27684 160104 2.R1040 Contig ID 5'-most EST uC-gmflminsoy082c05b1 Method BLASTX NCBI GI g4539314

Method BLASTX
NCBI GI g4539314
BLAST score 160
E value 7.0e-11
Match length 132
% identity 38



NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 27685

Contig ID 160107\_1.R1040 5'-most EST zzp700833586.h1

Seq. No. 27686

Contig ID 160111 1.R1040

5'-most EST jC-gmro02800035c06a1

Method BLASTX
NCBI GI g4467125
BLAST score 604
E value 3.0e-81
Match length 200
% identity 73

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 27687

Contig ID 160129 1.R1040 5'-most EST pmv700889726.h1

Method BLASTX
NCBI GI g4426611
BLAST score 156
E value 2.0e-10
Match length 106
% identity 32

NCBI Description (AF096897) pushover [Drosophila melanogaster]

Seq. No. 27688

Contig ID 160141\_1.R1040 5'-most EST smc700746360.h1

Seq. No. 27689

Contig ID 160148\_1.R1040 5'-most EST smc700746369.h1

Seq. No. 27690

Contig ID 160156\_1.R1040 5'-most EST dpv701099069.h1

Method BLASTN
NCBI GI g218261
BLAST score 92
E value 2.0e-44
Match length 180
% identity 88

NCBI Description Soybean mRNA for early nodulin

Seq. No. 27691

Contig ID 160163 1.R1040 5'-most EST zpv700759810.h1

Method BLASTX
NCBI GI g3193310
BLAST score 356
E value 1.0e-33
Match length 130
% identity 52

NCBI Description (AF069300) contains similarity to Nicotiana tabacum hin1



## (GB:Y07563) [Arabidopsis thaliana]

```
27692
Seq. No.
                  160174 1.R1040
Contig ID
                  jC-gmst02400076g03a1
5'-most EST
                  27693
Seq. No.
                  160179 1.R1040
Contig ID
                   jex700\overline{9}08178.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4490937
BLAST score
                   299
E value
                   7.0e-27
Match length
                   192
% identity
                   (AJ132261) hypothetical helicase K12H4.8-like protein [Homo
NCBI Description
                   sapiens]
                   27694
Seq. No.
                   160195 1.R1040
Contig ID
                   smc700746437.h1
5'-most EST
                   27695
Seq. No.
                   160197 1.R1040
Contig ID
                   jC-gmro02910016h01a1
5'-most EST
                   BLASTX
Method
                   q2980798
NCBI GI
                   258
BLAST score
E value
                   4.0e-22
                   101
Match length
% identity
                   (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                   27696
Seq. No.
                   160204 1.R1040
Contig ID
                   jC-gmro02910011d08d1
5'-most EST
                   BLASTX
Method
                   q4580463
NCBI GI
                   157
BLAST score
                   3.0e-10
E value
                   47
Match length
                   60
% identity
                   (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                   27697
Seq. No.
                   160232 1.R1040
Contig ID
                   zhf700952347.h1
5'-most EST
                   BLASTX
Method
                   g2132842
NCBI GI
                   128
BLAST score
                   3.0e-16
E value
                   105
Match length
                   42
 % identity
                   probable membrane protein YOL077c - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >gi 1419909_emb_CAA99087_ (Z74819) ORF YOL077c
```

[Saccharomyces cerevisiae]



```
Seq. No.
                   160238 1.R1040
Contig ID
                   uC-gmflminsoy026d11b1
5'-most EST
                   BLASTX
Method
                   g2769642
NCBI GI
                   429
BLAST score
                   3.0e-42
E value
                   150
Match length
                   61
% identity
                   (Z97215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon
NCBI Description
                   esculentum]
                   27699
Seq. No.
                   160252 1.R1040
Contig ID
                   smc700\overline{7}46519.h1
5'-most EST
                   27700
Seq. No.
                   160260 1.R1040
Contig ID
                   gsv701048360.hl
5'-most EST
                   BLASTX
Method
                   g4455175
NCBI GI
                   143
BLAST score
E value
                   6.0e-09
Match length
                   81
                   37
% identity
                   (AL035521) putative protein [Arabidopsis thaliana]
NCBI Description
                   27701
Seq. No.
                   160276 1.R1040
Contig ID
                   jsh701066720.hl
5'-most EST
                   BLASTX
Method
                    g4263704
NCBI GI
BLAST score
                    207
                    1.0e-16
E value
Match length
                    65
                    55
 % identity
                    (AC006223) putative sugar starvation-induced protein
NCBI Description
                    [Arabidopsis thaliana]
                    27702
 Seq. No.
                    160287 1.R1040
 Contig ID
                    smc700\overline{7}46568.h1
 5'-most EST
                    27703
 Seq. No.
                    160287 2.R1040
 Contig ID
                    zzp700831088.hl
 5'-most EST
                    27704
 Seq. No.
                    160297 1.R1040
 Contig ID
                    smc700746585.h1
 5'-most EST
```

Method BLASTX
NCBI GI g3980412
BLAST score 428
E value 1.0e-42
Match length 95
% identity 24

NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]



Seq. No. 27705

Contig ID 160303\_1.R1040 5'-most EST smc700746593.h1

Method BLASTX
NCBI GI g2244990
BLAST score 482
E value 7.0e-49
Match length 105
% identity 95

NCBI Description (297340) similarity to LIM homeobox protein -

Caenorhabditis [Arabidopsis thaliana]

Seq. No. 27706

Contig ID 160330 1.R1040 5'-most EST smc700746653.h1

Method BLASTN
NCBI GI g4151924
BLAST score 40
E value 4.0e-13
Match length 72
% identity 89

NCBI Description Arabidopsis thaliana CYT1 protein (cyt1) mRNA, complete cds

Seq. No. 27707

Contig ID 160356\_1.R1040

5'-most EST  $g43964\overline{18}$  Method BLASTX NCBI GI g4539383 BLAST score 622 E value 2.0e-64 Match length 232 % identity 51

NCBI Description (AL035526) putative protein (fragment) [Arabidopsis

thaliana]

Seq. No. 27708

Contig ID 160379\_1.R1040 5'-most EST dpv701100411.h1

Seq. No. 27709

Contig ID 160399\_1.R1040 5'-most EST uC-gmropic009d01b1

Method BLASTX
NCBI GI g4567194
BLAST score 262
E value 1.0e-22
Match length 75
% identity 61

NCBI Description (AC007168) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No. 27710

Contig ID 160478\_1.R1040 5'-most EST smc700746889.h1

Seq. No. 27711

Contig ID 160496 1.R1040

4304



zlv700807562.h1 5'-most EST 27712 Seq. No. 160508 2.R1040 Contig ID smc700746930.hl 5'-most EST Seq. No. 27713 160511 1.R1040 Contig ID jC-gmle01810023c12a1 5'-most EST BLASTX Method NCBI GI q2829864 BLAST score 298 E value 8.0e-48221 Match length 48 % identity (AC002396) similar to zinc metalloproteinases [Arabidopsis NCBI Description thaliana] 27714 Seq. No. 160516 1.R1040 Contig ID  $jC-gms\overline{t}02400030c03a1$ 5'-most EST BLASTX Method NCBI GI q4539324 BLAST score 979 1.0e-106 E value 355 Match length % identity 62 (AL035679) kinesin like protein [Arabidopsis thaliana] NCBI Description 27715 Seq. No. 160520 1.R1040 Contig ID 5'-most EST zsg701125310.h1 Method BLASTX g1345571 NCBI GI BLAST score 407 1.0e-39 E value 115 Match length 68 % identity (X80010) starch branching enzyme II [Pisum sativum] NCBI Description 27716 Seq. No. 160524 1.R1040 Contig ID smc700747747.hl 5'-most EST BLASTX Method NCBI GI

g3482978 289 BLAST score 3.0e-26 E value 77 Match length 75 % identity

(AL031369) putative protein [Arabidopsis thaliana] NCBI Description

27717 Seq. No.

160541 1.R1040 Contig ID zzp700835619.h1 5'-most EST

Seq. No. 27718

Contig ID 160563 1.R1040



5'-most EST smc700748250.h1

Seq. No. 27719

Contig ID 160702\_1.R1040 5'-most EST sat701010058.h2

Method BLASTX
NCBI GI g3128210
BLAST score 483
E value 7.0e-49
Match length 111

% identity 81
NCBI Description (AC004077) putative cytochrome P450 protein [Arabidopsis thaliana] >gi 3337378 (AC004481) putative cytochrome P450

protein [Arabidopsis thaliana]

Seq. No. 27720

Contig ID 160703\_1.R1040 5'-most EST smc700747185.h1

Seq. No. 27721

Contig ID 160709\_1.R1040 5'-most EST smc700747193.h1

Seq. No. 27722

Contig ID 160712 1.R1040 5'-most EST awf700840345.h1

Seq. No. 27723

Contig ID 160723\_1.R1040 5'-most EST asn701139051.h1

Seq. No. 27724

Contig ID 160746\_1.R1040 5'-most EST smc700747234.h1

Seq. No. 27725

Contig ID 160765\_1.R1040 5'-most EST smc700747259.h1

Seq. No. 27726

Contig ID 160808\_1.R1040 5'-most EST uC-gmropic045e04b1 Method BLASTX

Method BLASTX
NCBI GI 94490319
BLAST score 161
E value 1.0e-10
Match length 141
% identity 33

NCBI Description (AL035678) metal-transporting P-type ATPase [Arabidopsis

thaliana]

Seq. No. 27727

Contig ID 160818\_1.R1040 5'-most EST pmv700893763.h1

Method BLASTX NCBI GI g285741 BLAST score 148



3.0e-09 E value 136 Match length 35 % identity

(D14550) EDGP precursor [Daucus carota] NCBI Description

Seq. No.

27728 160823 1.R1040 Contig ID smc700747335.h1 5'-most EST

Seq. No. Contig ID 27729 160837 1.R1040

uC-gmrominsoy120h03b1 5'-most EST

27731

27730 Seq. No.

160844 1.R1040 Contig ID smc700747364.hl 5'-most EST

Seq. No.

160860\_1.R1040 Contig ID smc700747387.h1 5'-most EST

BLASTX Method g2494898 NCBI GI 235 BLAST score 9.0e-20 E value 115 Match length 40 % identity

PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG >gi\_1545982 (U53346) NCBI Description

PWP2H protein [Homo sapiens] >gi\_1737066 (U56085) periodic tryptophan protein 2 [Homo sapiens] >gi 1737072 (U56089)

periodic tryptophan protein 2 [Homo sapiens]

Seq. No. 27732

160874 1.R1040 Contig ID zhf700963734.h1 5'-most EST

27733 Seq. No.

160918 1.R1040 Contig ID smc700747781.hl 5'-most EST

27734 Seq. No.

160950 1.R1040 Contig ID smc700749017.h1 5'-most EST

27735 Seq. No.

160950 2.R1040 Contig ID

uC-gmrominsoy032a05b1 5'-most EST

27736 Seq. No.

160972 1.R1040 Contig ID pmv700893606.h1 5'-most EST

BLASTX Method NCBI GI q2245069 BLAST score 575 2.0e-59 E value Match length 147 % identity

NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]



```
27737
Seq. No.
                  160983 1.R1040
Contig ID
                  smc700747596.h1
5'-most EST
                  BLASTX
Method
                  g1752734
NCBI GI
BLAST score
                  218
                  5.0e-18
E value
                  85
Match length
                  49
% identity
                  (D78510) beta-glucan-elicitor receptor [Glycine max]
NCBI Description
                  27738
Seq. No.
                  160985 1.R1040
Contig ID
                  uC-gmrominsoy320g06b1
5'-most EST
                  27739
Seq. No.
                  160992 1.R1040
Contig ID
                   smc700747620.hl
5'-most EST
                   27740
Seq. No.
                   161005_1.R1040
Contig ID
                   fde700871538.hl
5'-most EST
                   27741
Seq. No.
                   161006 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910007d03d1
                   27742
Seq. No.
                   161056 1.R1040
Contig ID
                   uC-gmropic008f11b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2088651
                   349
BLAST score
                   6.0e-33
E value
                   121
Match length
                   55
% identity
                   (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   27743
Seq. No.
                   161065 1.R1040
Contig ID
                   zsg701128088.h1
5'-most EST
                   BLASTX
Method
                   g3550588
NCBI GI
                   277
BLAST score
                   2.0e-24
E value
Match length
                   143
                   49
% identity
                   (AJ010643) heat shock transcription factor (HSFA) [Pisum
NCBI Description
                   sativum]
```

27744 Seq. No.

161165 1.R1040 Contig ID 5'-most EST kl1701210268.h1

Method BLASTX NCBI GI q3135265

4308



BLAST score 216
E value 6.0e-24
Match length 114
% identity 50
NCRI Description (ACO030

NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 27745

Contig ID 161172\_1.R1040 5'-most EST rca700998634.h1

Seq. No. 27746

Contig ID 161183\_1.R1040 5'-most EST zhf700957607.h1

Seq. No. 27747

Contig ID 161199\_1.R1040 5'-most EST smc700747996.h1

Method BLASTX
NCBI GI g4140691
BLAST score 174
E value 8.0e-13
Match length 69
% identity 55

NCBI Description (AF101972) zeatin O-glucosyltransferase [Phaseolus lunatus]

Seq. No. 27748

Contig ID 161214\_1.R1040 5'-most EST uC-gmropic102g11b1

Method BLASTX
NCBI GI g2129953
BLAST score 505
E value 3.0e-51
Match length 127
% identity 69

NCBI Description laccase (EC 1.10.3.2) - common tobacco >gi\_1685087 (U43542)

diphenol oxidase [Nicotiana tabacum]

Seq. No. 27749

Contig ID 161276\_1.R1040 5'-most EST rca700997496.h1

Seq. No. 27750

Contig ID 161302\_1.R1040 5'-most EST rca700998578.h1

Method BLASTX
NCBI GI g3319345
BLAST score 143
E value 3.0e-09
Match length 86
% identity 33

NCBI Description (AF077407) contains similarity to maize transposon MuDR

(GB:M76978) [Arabidopsis thaliana]

Seq. No. 27751

Contig ID 161313\_1.R1040 5'-most EST zsg701126738.h1

Method BLASTX



NCBI GI g2264380 BLAST score 391 E value 9.0e-38 Match length 89 % identity 88

NCBI Description (AC002354) NAD+ dependent isocitrate dehydrogenase subunit

2 [Arabidopsis thaliana]

Seq. No. 27752

Contig ID 161326\_1.R1040 5'-most EST smc700748137.h1

Method BLASTX
NCBI GI g2500547
BLAST score 298
E value 5.0e-30
Match length 184
% identity 45

NCBI Description DIS3 PROTEIN >gi\_2131990\_pir\_\_S66704 hypothetical protein

YOL021c - yeast (Saccharomyces cerevisiae)

>gi\_1419801\_emb\_CAA99021\_ (Z74763) ORF YOL021c
[Saccharomyces cerevisiae] >gi\_1754617\_dbj\_BAA11176\_
(D76430) DIS3 protein [Saccharomyces cerevisiae]

Seq. No. 27753

Contig ID 161340\_1.R1040 5'-most EST fC-gmro7000748156a1

Method BLASTX
NCBI GI g4539004
BLAST score 609
E value 2.0e-63
Match length 169
% identity 66

NCBI Description (AL049481) putative protein kinase [Arabidopsis thaliana]

Seq. No. 27754

Contig ID 161362 1.R1040 5'-most EST smc700748191.h1

Seq. No. 27755

Contig ID 161398\_1.R1040 5'-most EST smc700748247.h1

Method BLASTX
NCBI GI g3292821
BLAST score 146
E value 3.0e-09
Match length 67
% identity 54

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 27756

Contig ID 161431\_1.R1040 5'-most EST zpv700763075.h1

Seq. No. 27757

Contig ID 161435\_1.R1040

5'-most EST uC-gmflminsoy091e02b1

Method BLASTX



NCBI GI g4205079 BLAST score 204 E value 1.0e-15 Match length 150 % identity 24

NCBI Description (U70425) ankyrin repeat-containing protein 2 [Arabidopsis

thaliana]

Seq. No. 27758

Contig ID 161438\_1.R1040 5'-most EST smc700749922.h1

Seq. No. 27759

Contig ID 161443\_1.R1040 5'-most EST zhf700958132.h1

Seq. No. 27760

Contig ID 161460\_1.R1040 5'-most EST asn701133614.h2

Seq. No. 27761

Contig ID 161466\_1.R1040

5'-most EST jC-gmst02400055g07a1

Method BLASTX
NCBI GI g3033388
BLAST score 195
E value 8.0e-15
Match length 112
% identity 32

NCBI Description (AC004238) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27762

Contig ID 161488\_1.R1040 5'-most EST fua701040684.h1

Seq. No. 27763

Contig ID 161490 1.R1040 5'-most EST smc700748381.h1

Seq. No. 27764

Contig ID 161515\_1.R1040 5'-most EST fC-gmro7000748409f1

Method BLASTX
NCBI GI g2982431
BLAST score 199
E value 4.0e-15
Match length 155
% identity 4

NCBI Description (AL022224) leucine rich repeat-like protein [Arabidopsis

thaliana]

Seq. No. 27765

Contig ID 161531\_1.R1040 5'-most EST fC-gmro700847984r1

Method BLASTX NCBI GI g1236961 BLAST score 285



E value 2.0e-25 Match length 68

% identity 75

NCBI Description (U50201) prunasin hydrolase precursor [Prunus serotina]

Seq. No. 27766

Contig ID 161531 2.R1040 5'-most EST smc700748435.h1

Seq. No. 27767

Contig ID 161545\_1.R1040 5'-most EST asn701139424.h1

Method BLASTX
NCBI GI g2829887
BLAST score 306
E value 3.0e-28
Match length 93
% identity 70

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 27768

Contig ID 161550\_1.R1040 5'-most EST fC-gmro7000748459f1

Method BLASTX
NCBI GI g2760839
BLAST score 260
E value 2.0e-22
Match length 169
% identity 25

NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 27769

Contig ID 161570\_1.R1040 5'-most EST uC-gmronoir052g11b1

Method BLASTX
NCBI GI g3367578
BLAST score 464
E value 3.0e-46
Match length 120
% identity 69

NCBI Description (AL031135) protein kinase - like protein [Arabidopsis

thaliana]

Seq. No. 27770

Contig ID 161576 1.R1040

5'-most EST uC-gmrominsoy312h07b1

Method BLASTN
NCBI GI g3643588
BLAST score 52
E value 5.0e-20
Match length 116
% identity 86

NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 27771

Contig ID 161577 1.R1040



5'-most EST zhf700952184.h1 Method BLASTX

NCBI GI g4455307 BLAST score 542 E value 2.0e-55 Match length 106 % identity 91

NCBI Description (AL035528) methionyl-tRNA synthetase-like protein

[Arabidopsis thaliana]

Seq. No. 27772

Contig ID 161604\_1.R1040 5'-most EST fC-gmro700748540a2

Method BLASTX
NCBI GI g4539320
BLAST score 562
E value 6.0e-58
Match length 152
% identity 63

NCBI Description (AL035679) putative endo-1, 4-beta-glucanase [Arabidopsis

thaliana]

Seq. No. 27773

Contig ID 161607\_1.R1040 5'-most EST smc700748580.h1

Seq. No. 27774

Contig ID 161610\_1.R1040 5'-most EST smc700748551.h1

Seq. No. 27775

Contig ID 161650\_1.R1040 5'-most EST smc700748596.h1

Seq. No. 27776

Contig ID 161667\_1.R1040 5'-most EST smc700748623.h1

Seq. No. 27777

Contig ID 161727\_1.R1040 5'-most EST bth700847982.h1

Method BLASTX
NCBI GI g112947
BLAST score 202
E value 8.0e-16
Match length 88
% identity 31

NCBI Description AAC-RICH MRNA CLONE AAC3 PROTEIN >gi 84121 pir S05357

hypothetical protein (clone AAC3) - slime mold

(Dictyostelium discoideum) (fragment)

>gi\_7176\_emb\_CAA34531\_ (X16524) coding region (AA 1 - 437)

[Dictyostelium discoideum]

Seq. No. 27778

Contig ID 161758\_1.R1040 5'-most EST smc700748749.h1



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Seq. No.
                  161780 1.R1040
Contig ID
                  smc700748780.hl
5'-most EST
                  27780
Seq. No.
                  161788 1.R1040
Contig ID
                  uC-gmropic016b02b1
5'-most EST
                  27781
Seq. No.
                  161836 1.R1040
Contig ID
                  jC-gmf102220108c08a1
5'-most EST
Method
                  BLASTX
                  g3850585
NCBI GI
                  191
BLAST score
                  2.0e-14
E value
Match length
                  52
                  71
% identity
                  (AC005278) ESTs gb_H36966, gb_R65511, gb_T42324 and
NCBI Description
                  gb_T20569 come from this gene. [Arabidopsis thaliana]
                  27782
Seq. No.
                  161836 2.R1040
Contig ID
5'-most EST
                  gsv701050118.h1
Method
                  BLASTX
                  q3850585
NCBI GI
                  191
BLAST score
                  2.0e-14
E value
Match length
                  52
% identity
                  71
                  (AC005278) ESTs gb_H36966, gb_R65511, gb_T42324 and
NCBI Description
                  gb_T20569 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  27783
                  161836 3.R1040
Contig ID
                   jsh701066140.h1
5'-most EST
                  BLASTX
Method
                  q3850585
NCBI GI
BLAST score
                  172
                  2.0e-12
E value
                   43
Match length
                  77
% identity
                  (AC005278) ESTs gb H36966, gb_R65511, gb_T42324 and
NCBI Description
                  gb T20569 come from this gene. [Arabidopsis thaliana]
                   27784
Seq. No.
                  161856 1.R1040
Contig ID
5'-most EST
                  smc700748885.hl
                  BLASTX
Method
```

NCBI GI q2213592 BLAST score 211 E value 3.0e-17 85 Match length 27 % identity

(AC000348) T7N9.12 [Arabidopsis thaliana] NCBI Description

27785 Seq. No.

161859\_1.R1040 Contig ID



5'-most EST smc700748888.h1
Method BLASTX
NCBI GI g3786009
BLAST score 379

E value 7.0e-37 Match length 87 % identity 82

NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 27786

Contig ID 161865\_1.R1040 5'-most EST gsv701047952.h1

Seq. No. 27787

Contig ID 161881\_1.R1040 5'-most EST fC-gmro7000748929a1

Method BLASTX
NCBI GI g2760836
BLAST score 202
E value 2.0e-15
Match length 111
% identity 40

NCBI Description (AC003105) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 27788

Contig ID 161885\_1.R1040 5'-most EST zlv700807563.h1

Seq. No. 27789

Contig ID 161912\_1.R1040 5'-most EST smc700749012.h1

Seq. No. 27790

Contig ID 161913\_1.R1040 5'-most EST smc700749013.h1

Seq. No. 27791

Contig ID 161922\_1.R1040 5'-most EST smc700749027.h1

Method BLASTX
NCBI GI g995714
BLAST score 231
E value 3.0e-23
Match length 129
% identity 44

NCBI Description (X91258) L3177 [Saccharomyces cerevisiae]

Seq. No.

Contig ID 162005\_1.R1040 5'-most EST jsh701066291.h1

27792

Seq. No. 27793

Contig ID 162025 1.R1040 5'-most EST smc700749221.h1

Method BLASTX NCBI GI g4249402



BLAST score 219 E value 1.0e-17 Match length 153 % identity 39

NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 27794

Contig ID 162054\_1.R1040 5'-most EST hrw701062841.h1

Method BLASTX
NCBI GI g2388689
BLAST score 328
E value 2.0e-35
Match length 94
% identity 83

NCBI Description (AF016633) GH1 protein [Glycine max]

Seq. No. 27795

Contig ID 162064\_1.R1040 5'-most EST pmv700895230.h1

Method BLASTX
NCBI GI g1076498
BLAST score 170
E value 6.0e-12
Match length 70
% identity 49

NCBI Description zinc-finger protein (C-terminal) - soybean

>gi\_558543\_emb\_CAA85320\_ (Z36749) C-terminal zinc-finger

[Glycine max]

Seq. No. 27796

Contig ID 162154\_1.R1040 5'-most EST uC-gmronoir000h01b1

Seq. No. 27797

Contig ID 162179 1.R1040 5'-most EST smc700749541.h1

Seq. No. 27798

Contig ID 162187\_1.R1040 5'-most EST smc700749560.h1

Seq. No. 27799

Contig ID 162206 1.R1040 5'-most EST gsv701050671.h1

Method BLASTX
NCBI GI g3393062
BLAST score 338
E value 6.0e-32
Match length 80
% identity 74

NCBI Description (Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No. 27800

Contig ID 162214 1.R1040

5'-most EST jC-gmst02400057g05a1

Method BLASTX



NCBI GI g2739379
BLAST score 165
E value 2.0e-11
Match length 107
% identity 54

NCBI Description (AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27801

Contig ID 162269\_1.R1040 5'-most EST smc700749733.h1

Method BLASTN
NCBI GI g3882144
BLAST score 172
E value 3.0e-92
Match length 223
% identity 95

NCBI Description Homo sapiens mRNA for KIAA0712 protein, complete cds

Seq. No. 27802

Contig ID 162278\_1.R1040 5'-most EST jC-gmro02910030a07a1

Method BLASTX
NCBI GI g3335357
BLAST score 597
E value 5.0e-62
Match length 123
% identity 85

NCBI Description (AC003028) putative diphenol oxidase [Arabidopsis thaliana]

Seq. No. 27803

Contig ID 162307\_1.R1040 5'-most EST eep700864855.h1

Seq. No. 27804

Contig ID 162329 1.R1040

5'-most EST jC-gmro02910039g11a1

Seq. No. 27805

Contig ID 162329\_2.R1040 5'-most EST zhf700962763.h1

Seq. No. 27806

Contig ID 162333\_1.R1040 5'-most EST kl1701202535.h1

Seq. No. 27807

Contig ID 162346\_1.R1040 5'-most EST smc700749796.h1

Method BLASTN
NCBI GI g3309572
BLAST score 182
E value 5.0e-98
Match length 227
% identity 98

NCBI Description Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA,

complete cds >gi\_4505460\_ref\_NM\_003633.1\_NRPB\_ Homo sapiens nuclear restricted protein, BTB domain-like (brain) (NRPB)



## mRNA, and translated products

Seq. No. 27808

Contig ID 162360\_1.R1040 5'-most EST smc700749822.h1

Method BLASTX
NCBI GI g3172025
BLAST score 559
E value 1.0e-57
Match length 140
% identity 75

NCBI Description (AB005805) aldehyde oxidase [Arabidopsis thaliana]

Seq. No. 27809

Contig ID 162361\_1.R1040 5'-most EST uC-gmronoir049h07b1

Seq. No. 27810

Contig ID 162414\_1.R1040 5'-most EST uC-gmropic019e08b1

Seq. No. 27811

Contig ID 162419 1.R1040 5'-most EST pmv700893728.h1

Method BLASTX
NCBI GI 94510377
BLAST score 146
E value 2.0e-09
Match length 76
% identity 36

NCBI Description (AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No. 27812

Contig ID 162420\_1.R1040 5'-most EST dpv701101092.h1

Seq. No. 27813

Contig ID 162447 1.R1040 5'-most EST smc700749945.h1

Seq. No. 27814

Contig ID 162452\_1.R1040 5'-most EST smc700749951.h1

Method BLASTX
NCBI GI g3413700
BLAST score 388
E value 1.0e-37
Match length 118
% identity 63

NCBI Description (AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No. 27815

Contig ID 162457\_1.R1040 5'-most EST smc700749958.h1

Seq. No. 27816

Contig ID 162466\_1.R1040



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5'-most EST
                   smc700749970.h1
Seq. No.
                   27817
Contig ID
                   162487 1.R1040
5'-most EST
                   smc700750012.h1
                   27818
Seq. No.
Contig ID
                   162502 1.R1040
                   fC-gmro700750041a2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4138209
BLAST score
                   309
E value
                   3.0e-28
Match length
                   140
% identity
                   43
```

NCBI Description (AJ223071) serine/threonine kinase protein MSTK2L,long-form [Mus musculus]

Seq. No. 27819 Contig ID 162513 1.R1040 5'-most EST uC-gmropic108f03b1 BLASTXMethod NCBI GI

g1946367 330 BLAST score E value 3.0e-30 176 Match length 39 % identity

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 27820

Contig ID 162513 2.R1040 uC-gmropic037c12b1 5'-most EST

Method BLASTX NCBI GI a3738298 BLAST score 157 E value 9.0e-16 Match length 77 % identity 56

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

>gi\_4249394 (AC006072) unknown protein [Arabidopsis

thaliana]

Seq. No. 27821

Contig ID 162514 1.R1040

5'-most EST uC-gmrominsoy128d07b1

Seq. No. 27822

Contig ID 162530 1.R1040 5'-most EST uC-gmropic106c05b1

Seq. No. 27823

Contig ID 162532 1.R1040 5'-most EST kl1701214995.h1

Method BLASTX NCBI GI q3063451 BLAST score 182 3.0e-28 E value



Match length % identity

NCBI Description (AC003981) F22013.13 [Arabidopsis thaliana]

Seq. No. 27824

Contig ID 162540 1.R1040

5'-most EST uC-gmflminsoy065h02b1

Seq. No. 27825

Contig ID 162543 1.R1040

5'-most EST uC-gmrominsoy138e10b1

Seq. No. 27826

Contig ID 162562 1.R1040 5'-most EST fC-gmro700750148a2

Method BLASTX NCBI GI q2935300 BLAST score 602 1.0e-62 E value Match length 135 % identity

(AF038046) 3-hydroxy-3-methylglutaryl-coenzyme A reductase NCBI Description

2 [Gossypium hirsutum]

Seq. No. 27827

Contig ID 162574 1.R1040 5'-most EST rca700998968.h1

27828 Seq. No.

Contig ID 162582 1.R1040 5'-most EST crh700851350.hl

Seq. No. 27829

Contig ID 162624 1.R1040 5'-most EST smc700750249.h1

Seq. No. 27830

Contig ID 162632 1.R1040 5'-most EST sat701009548.h1

Seq. No. 27831

Contig ID 162649 1.R1040 5'-most EST fC-qmro700750285a2

Method BLASTX NCBI GI q1888357 BLAST score 624 7.0e-65 E value Match length 227 % identity 57

(X98130) alpha-mannosidase [Arabidopsis thaliana] NCBI Description >gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. Contig ID 162661 1.R1040

5'-most EST k11701212328.h1

27832



Contig ID 162672 1.R1040

5'-most EST  $jC-gmf\overline{1}02220141e11a1$ 

Seq. No. 27834

Contig ID 162680 1.R1040

5'-most EST jC-gmf102220085h08a1

Method BLASTX
NCBI GI g3402677
BLAST score 176
E value 1.0e-12
Match length 77

Match length 77 % identity 49

NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27835

Contig ID 162703\_1.R1040 5'-most EST smc700750385.h1

Seq. No. 27836

Contig ID 162723\_1.R1040 5'-most EST smc700750417.h1

Seq. No. 27837

Contig ID 162762\_2.R1040 5'-most EST pmv700890418.h1

Method BLASTX
NCBI GI g2588895
BLAST score 216
E value 1.0e-17
Match length 91
% identity 41

NCBI Description (AB008515) RanBPM [Homo sapiens]

Seq. No. 27838

Contig ID 162775\_1.R1040 5'-most EST tku700646303.h1

Seq. No. 27839

Contig ID 162783\_1.R1040 5'-most EST sat701011406.h1

Seq. No. 27840

Contig ID 162784 1.R1040 5'-most EST rca701000069.h1

Method BLASTX
NCBI GI g2654868
BLAST score 461
E value 4.0e-46
Match length 125
% identity 66

NCBI Description (AF015301) RbohAp108 [Arabidopsis thaliana]

Seq. No. 27841

Contig ID 162807 1.R1040

5'-most EST uC-gmrominsoy125h06b1

Method BLASTX



NCBI GI q3335060 BLAST score 632 E value 6.0e-66 170 Match length % identity 70

NCBI Description (AF025842) plasma membrane-type calcium ATPase [Arabidopsis

thaliana] >gi\_4468989\_emb\_CAB38303 (AL035605) plasma

membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

27842 Seq. No.

162810 1.R1040 Contig ID tku700646344.h1 5'-most EST

Seq. No. 27843

162838 1.R1040 Contig ID  $fua701\overline{0}41113.h1$ 5'-most EST

Seq. No. 27844

162841 1.R1040 Contig ID 5'-most EST  $k11701\overline{2}07057.h1$ 

27845 Seq. No.

162858 1.R1040 Contig ID 5'-most EST awf700841108.h1

27846 Seq. No.

162885 1.R1040 Contig ID 5'-most EST pxt700945733.h1

Method BLASTX NCBI GI q3377802 BLAST score 449 8.0e-45 E value Match length 122 % identity 65

(AF075597) Similar to sucrose synthase; T2H3.8 [Arabidopsis NCBI Description

thaliana]

Seq. No. 27847

Contig ID 162943 1.R1040 5'-most EST  $ujr700\overline{646531.h1}$ 

Seq. No. 27848

Contig ID 162946 1.R1040

5'-most EST jC-qmst02400072d11a1

Method BLASTX NCBI GI q1946367 BLAST score 328 2.0e-30 E value Match length 86 % identity 70

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 27849

162954 1.R1040 Contig ID 5'-most EST qsv701047970.h1

Method BLASTX NCBI GI q134889



BLAST score 249 E value 4.0e-21 Match length 165 % identity 35

NCBI Description SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68)

>gi\_108065\_pir\_\_S12981 68K protein - gray wolf

>gi\_227342\_prf\_\_1702226A SRP68 protein [Canis familiaris]

Seq. No. 27850

Contig ID 162964\_1.R1040 5'-most EST hrw701062474.h1

Seq. No. 27851

Contig ID 162965\_1.R1040 5'-most EST pxt700945737.h1

Seq. No. 27852

Contig ID 162980\_1.R1040 5'-most EST jsh701068517.h1

Seq. No. 27853

Contig ID 162987\_1.R1040 5'-most EST zhf700963936.h1

Seq. No. 27854

Contig ID 162991\_1.R1040 5'-most EST uC-gmropic021g10b1

Method BLASTX
NCBI GI g1419036
BLAST score 438
E value 2.0e-43
Match length 116
% identity 78

NCBI Description (X98421) delta-1-pyrroline-5-carboxylate synthase [Medicago

sativa]

Seq. No. 27855

Contig ID 162991 2.R1040

5'-most EST jC-gmro02910066g03a1

Method BLASTX
NCBI GI g1709534
BLAST score 460
E value 4.0e-46
Match length 140
% identity 69

NCBI Description DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE A (P5CS A)

[CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);

GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)

(GLUTAMYL-GAMMA-SEMIALDE... >gi\_2129572\_pir\_\_S66637 delta-1-pyrroline-5-carboxylate synthetase - Arabidopsis

thaliana >gi\_829100\_emb\_CAA60740\_ (X87330)

pyrroline-5-carboxylate synthetase [Arabidopsis thaliana] >gi\_870866\_emb\_CAA60446\_ (X86777) pyrroline-5-carboxylate

synthetase A [Arabidopsis thaliana]

>gi\_1041248\_emb\_CAA61593\_ (X89414) pyrroline-5-carboxylate

synthase [Arabidopsis thaliana] >gi 2642162 (AC003000)



delta-1-pyrroline 5-carboxylase synthetase, P5C1 [Arabidopsis thaliana]

 Seq. No.
 27856

 Contig ID
 163015 1.R1040

 5'-most EST
 ujr700646622.h1

Seq. No. 27857

Contig ID 163018\_1.R1040

5'-most EST uC-gmrominsoy155b12b1

Seq. No. 27858

Contig ID 163055\_1.R1040 5'-most EST ujr700646676.h1

Seq. No. 27859

Contig ID 163069\_1.R1040 5'-most EST bth700844272.h1

Seq. No. 27860

Contig ID 163071\_1.R1040

5'-most EST jC-gmr002910062c04a1

Seq. No. 27861

Contig ID 163080\_1.R1040 5'-most EST vzy700750670.h1

Method BLASTN
NCBI GI g1947070
BLAST score 229
E value 1.0e-126
Match length 245
% identity 98

NCBI Description Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene,

complete cds

Seq. No. 27862

Contig ID 163094 1.R1040

5'-most EST g5057812
Method BLASTX
NCBI GI g3643082
BLAST score 348
E value 2.0e-32
Match length 100
% identity 64

NCBI Description (AF075579) protein phosphatase-2C; PP2C [Mesembryanthemum

crystallinum]

Seq. No. 27863

Contig ID 163101\_1.R1040 5'-most EST vzy700750543.h1

Method BLASTX
NCBI GI g282881
BLAST score 237
E value 3.0e-20
Match length 82
% identity 56

NCBI Description receptor-like protein kinase precursor - Arabidopsis



thaliana >gi\_166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 27864

Contig ID 163102 1.R1040

5'-most EST uC-gmflminsoy030a08b1

Seq. No. 27865

Contig ID 163147\_1.R1040 5'-most EST vzy700750613.h1

Method BLASTX
NCBI GI g4455171
BLAST score 185
E value 5.0e-14
Match length 73
% identity 62

NCBI Description (AL035521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27866

Contig ID 163148\_1.R1040 5'-most EST zsg701120644.h1

Method BLASTX
NCBI GI g3047111
BLAST score 536
E value 5.0e-55
Match length 125
% identity 71

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 27867

Contig ID 163154 1.R1040 5'-most EST zhf700952519.h1

Seq. No. 27868

Contig ID 163165\_1.R1040 5'-most EST vzy700750638.h1

Seq. No. 27869

Contig ID 163168\_1.R1040 5'-most EST vzy700750650.h1

Seq. No. 27870

Contig ID 163175\_1.R1040 5'-most EST fC-gmse7000751147f1

Method BLASTX
NCBI GI g120745
BLAST score 893
E value 2.0e-96
Match length 229
% identity 76

NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (PHOSPHOGLUCOSE

ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI)
>gi\_68450\_pir\_\_NUBY glucose-6-phosphate isomerase (EC

5.3.1.9) - yeast (Saccharomyces cerevisiae)

>gi\_4135\_emb\_CAA32158\_ (X13977) phosphoglucose isomerase (AA 1-554) [Saccharomyces cerevisiae] >gi\_172142 (M37267) phosphoglucose isomerase (EC 5.3.1.9) [Saccharomyces

4325



cerevisiae] >gi\_172225 (M21696) phosophoglucoisomerase (EC
5.3.1.9) [Saccharomyces cerevisiae]
>gi\_311672\_emb\_CAA79683\_ (Z21487) glycolytic enzyme
phosphoglucoisomerase [Saccharomyces cerevisiae]
>gi\_536565\_emb\_CAA85158\_ (Z36065) ORF YBR196c
[Saccharomyces cerevisiae]

 Seq. No.
 27871

 Contig ID
 163178\_1.R1040

 5'-most EST
 zhf700955950.h1

Seq. No. 27872

Contig ID 163179 1.R1040 5'-most EST zsg701126321.h1

Seq. No. 27873

Contig ID 163195\_1.R1040 5'-most EST zzp700831750.h1 Method BLASTN

Method BLASTN
NCBI GI g871468
BLAST score 142
E value 4.0e-74
Match length 280
% identity 90

NCBI Description H.annuus mitochondrion genes trnH and trnE

Seq. No. 27874

Contig ID 163205\_1.R1040 5'-most EST vzy700750716.h1

Seq. No. 27875

Contig ID 163225\_1.R1040 5'-most EST awf700837938.h1

Seq. No. 27876

Contig ID 163241 1.R1040

5'-most EST uC-gmflminsoy117a12b1

Seq. No. 27877

Contig ID 163271\_1.R1040 5'-most EST vzy700750891.h1

Seq. No. 27878

Contig ID 163277\_1.R1040 5'-most EST vzy700750823.h1

Seq. No. 27879

Contig ID 163292\_1.R1040 5'-most EST zhf700955919.h1

Seq. No. 27880

Contig ID 163294 1.R1040 5'-most EST vzy700750849.h1

Seq. No. 27881

Contig ID 163301\_1.R1040 5'-most EST rca700996549.h1



Method BLASTX
NCBI GI g4176531
BLAST score 260
E value 1.0e-22
Match length 95
% identity 47

NCBI Description (AL035263) weak similarity to chick phosphatidylcholine-ste rol acetyltransferase [Schizosaccharomyces pombe]

Seq. No. 27882

Contig ID 163328\_1.R1040 5'-most EST zzp700833379.h1

Seq. No. 27883

Contig ID 163340\_1.R1040

5'-most EST uC-gmrominsoy097a01b1

Seq. No. 27884

Contig ID 163362\_1.R1040

5'-most EST jC-gmf $\overline{1}$ 022220141e03a1

Seq. No. 27885

Contig ID 163376\_1.R1040 5'-most EST epx701106687.h1

Method BLASTN NCBI GI g2218149

BLAST score 94

E value 2.0e-45 Match length 218 % identity 86

NCBI Description Vigna unguiculata type IIIa membrane protein cp-wap11 mRNA,

complete cds

Seq. No. 27886

Contig ID 163387\_1.R1040 5'-most EST vzy700750993.h1

Seq. No. 27887

Contig ID 163395\_1.R1040 5'-most EST fde700876383.h1

Seq. No. 27888

Contig ID 163406\_1.R1040 5'-most EST vzy700751028.h1

Seq. No. 27889

Contig ID 163415\_1.R1040 5'-most EST zhf700953130.h1

Seq. No. 27890

Contig ID 163463 1.R1040 5'-most EST vzy700751115.h1 Method BLASTX

Method BLASTX
NCBI GI g4115371
BLAST score 601
E value 4.0e-62
Match length 218



% identity 58
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 27891

Contig ID 163471 1.R1040 5'-most EST vzy700751131.h1

Seq. No. 27892

Contig ID 163487\_1.R1040 5'-most EST vzy700751154.h1

Method BLASTN
NCBI GI g340697
BLAST score 331
E value 0.0e+00
Match length 375
% identity 84

NCBI Description Soybean chloroplast 16S/23S ribosomal intergenic spacer DNA

Seq. No. 27893

Contig ID 163491\_1.R1040 5'-most EST vzy700751160.h1

Seq. No. 27894

Contig ID 163497\_1.R1040 5'-most EST vzy700751180.h1

Method BLASTN
NCBI GI g392991
BLAST score 143
E value 9.0e-75
Match length 287
% identity 90

NCBI Description Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete

cds

Seq. No. 27895

Contig ID 163508\_1.R1040 5'-most EST vzy700751201.h1

Seq. No. 27896

Contig ID 163514\_1.R1040 5'-most EST vzy700751208.h1

Method BLASTX
NCBI GI g2388574
BLAST score 276
E value 4.0e-24
Match length 83
% identity 75

NCBI Description (AC000098) Strong similarity to Phalaenopsis homeobox

protein (gb\_U34743). [Arabidopsis thaliana]

Seq. No. 27897

Contig ID 163557\_1.R1040 5'-most EST vzy700751274.h1

Method BLASTX
NCBI GI g2655008
BLAST score 150
E value 4.0e-10



Match length 52 % identity 46

NCBI Description (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon

esculentum]

Seq. No. 27898

Contig ID 163558\_1.R1040 5'-most EST pmv700894549.h1

Seq. No. 27899

Contig ID 163567\_1.R1040 5'-most EST bth700846161.h1

Seq. No. 27900

Contig ID 163587\_1.R1040 5'-most EST awf700843147.h1

Seq. No. 27901

Contig ID 163609\_1.R1040 5'-most EST pmv700888988.h1

Seq. No. 27902

Contig ID 163626\_1.R1040 5'-most EST vzy700751413.h1

Method BLASTX
NCBI GI g3281850
BLAST score 555
E value 3.0e-57
Match length 125
% identity 81

NCBI Description (AL031004) monogalactosyldiacylglycerol synthase - like

protein [Arabidopsis thaliana]

Seq. No. 27903

Contig ID 163633 1.R1040 5'-most EST vzy700751420.h1

Seq. No. 27904

Contig ID 163645\_1.R1040 5'-most EST vzy700751441.h1

Seq. No. 27905

Contig ID 163695\_1.R1040 5'-most EST vzy700751535.h1

Seq. No. 27906

Contig ID 163712\_1.R1040 5'-most EST vzy700751804.h1

Method BLASTX
NCBI GI g32709
BLAST score 288
E value 3.0e-26
Match length 81
% identity 64

NCBI Description (X62570) IFP53 [Homo sapiens]

Seq. No. 27907



Contig ID 163733\_1.R1040

5'-most EST uC-gmflminsoy076c09b1

Method BLASTX
NCBI GI g4193320
BLAST score 181
E value 6.0e-17
Match length 55
% identity 75

NCBI Description (AF045473) histone deacetylase [Zea mays]

Seq. No. 27908

Contig ID 163733\_2.R1040 5'-most EST awf700841470.h1

Method BLASTX
NCBI GI g3023947
BLAST score 202
E value 7.0e-16
Match length 45
% identity 76

NCBI Description PROBABLE HISTONE DEACETYLASE (RPD3 HOMOLOG) >gi\_2665840

(AF035815) putative histone deacetylase RPD3 [Zea mays]

Seq. No. 27909

Contig ID 163771 1.R1040 5'-most EST zzp700833196.h1

Seq. No. 27910

Contig ID 163782\_1.R1040 5'-most EST fC-gmse700752579a1

Method BLASTX
NCBI GI g4140255
BLAST score 455
E value 4.0e-45
Match length 160
% identity 59

NCBI Description (AJ009973) hexokinase [Aspergillus niger]

Seq. No. 27911

Contig ID 163811\_1.R1040 5'-most EST jsh701069592.h1

Seq. No. 27912

Contig ID 163814\_1.R1040 5'-most EST leu701149792.h1

Seq. No. 27913

Contig ID 163830\_1.R1040 5'-most EST vzy700756824.h1

Seq. No. 27914

Contig ID 163831\_1.R1040 5'-most EST jC-qmst02400053f04a1

Method BLASTX
NCBI GI g4107099
BLAST score 465
E value 2.0e-46
Match length 154



% identity 58

NCBI Description (AB015141) AHP1 [Arabidopsis thaliana]

>gi\_4156245\_dbj\_BAA37112\_ (AB012570) ATHP3 [Arabidopsis

thaliana]

Seq. No. 27915

Contig ID 163866\_1.R1040 5'-most EST zsg701120567.h1

Seq. No. 27916

Contig ID 163877\_1.R1040

5'-most EST uC-gmflminsoy045e04b1

Method BLASTX
NCBI GI g4539359
BLAST score 236
E value 1.0e-19
Match length 131
% identity 39

NCBI Description (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 27917

Contig ID 163877 2.R1040

5'-most EST uC-gmflminsoy093b06b1

Method BLASTX
NCBI GI g2244949
BLAST score 206
E value 3.0e-16
Match length 98
% identity 48

NCBI Description (Z97339) similarity to ORF - Lilium longiflorum

[Arabidopsis thaliana]

Seq. No. 27918

Contig ID 163877\_3.R1040

5'-most EST uC-gmflminsoy063b02b1

Method BLASTX
NCBI GI g2244949
BLAST score 152
E value 5.0e-10
Match length 80
% identity 45

NCBI Description (Z97339) similarity to ORF - Lilium longiflorum

[Arabidopsis thaliana]

Seq. No. 27919

Contig ID 163883\_1.R1040 5'-most EST vzy700751835.h1

Method BLASTX
NCBI GI g2225877
BLAST score 201
E value 4.0e-16
Match length 81
% identity 50

NCBI Description (AB002406) TIP49 [Rattus norvegicus] >gi\_4106528 (AF100694)

Pontin52 [Mus musculus] >gi\_4521276\_dbj\_BAA76313.1\_

(AB001581) DNA helicase p50 [Rattus norvegicus]



Contig ID 163898\_1.R1040 5'-most EST vzy700751866.h1

Method BLASTX
NCBI GI g1778095
BLAST score 327
E value 3.0e-30
Match length 124
% identity 54

NCBI Description (U64903) putative sugar transporter; member of major

facilitative superfamily; integral membrane protein [Beta

vulgaris]

Seq. No. 27921

Contig ID 163906 1.R1040 5'-most EST leu701150641.h1

Seq. No. 27922

Contig ID 163909\_1.R1040 5'-most EST zzp700829891.h1

Method BLASTX
NCBI GI g4559327
BLAST score 236
E value 8.0e-20
Match length 109
% identity 50

NCBI Description (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27923

Contig ID 164014\_1.R1040 5'-most EST vzy700752066.h1

Seq. No. 27924

Contig ID 164056\_1.R1040 5'-most EST jC-gmle01810078f10a1

Method BLASTX
NCBI GI g1495259
BLAST score 490
E value 3.0e-49

Match length 204 % identity 46

NCBI Description (X97826) orf04 [Arabidopsis thaliana]

Seq. No. 27925

Contig ID 164102\_1.R1040

5'-most EST jC-gmfl02220052f06a1

Method BLASTX
NCBI GI g2492792
BLAST score 692
E value 6.0e-73
Match length 187
% identity 73

NCBI Description LATE NODULIN 56 (N-56) >gi\_532290\_dbj\_BAA07212\_ (D38015)

soybean late nodulin [Glycine max]

Seq. No. 27926

Contig ID 164102\_2.R1040



zpv700763092.h1 5'-most EST Method BLASTX g2492792 NCBI GI BLAST score 294 E value 2.0e-26 Match length 93 % identity 68 LATE NODULIN 56 (N-56) >gi 532290 dbj BAA07212 (D38015) NCBI Description soybean late nodulin [Glycine max] 27927 Seq. No. 164154 1.R1040 Contig ID 5'-most EST epx701105636.h1 Seq. No. 27928 164156 1.R1040 Contig ID 5'-most EST vzy700752270.h1 Method BLASTX NCBI GI g2668492 BLAST score 198 3.0e-15 E value Match length 151 % identity 36 NCBI Description (D89981) metal-transporting P-type ATPase [Arabidopsis thaliana] 27929 Seq. No. 164175 1.R1040 Contig ID 5'-most EST uC-gmropic035g09b1 Seq. No. 27930 Contig ID 164205 1.R1040 5'-most EST zhf700953905.h1 Seq. No. 27931 164230 1.R1040 Contig ID 5'-most EST epx701105604.hl Seq. No. 27932 164235 1.R1040 Contig ID 5'-most EST uC-gmrominsoy215c09b1 27933 Seq. No. 164269 1.R1040 Contig ID

5'-most EST jex700907685.h1

Method BLASTX g3342798 NCBI GI BLAST score 305 E value 8.0e-28 Match length 105 % identity

NCBI Description (AF061240) glutamine cyclotransferase precursor [Carica

papaya]

Seq. No. Contig ID 27934

5'-most EST

164269 2.R1040 fua701036923.h1



Method BLASTX
NCBI GI g3342798
BLAST score 199
E value 1.0e-15
Match length 49
% identity 78

NCBI Description (AF061240) glutamine cyclotransferase precursor [Carica

papaya]

Seq. No. 27935

Contig ID 164270\_1.R1040 5'-most EST pmv700893975.h1

Method BLASTX
NCBI GI g4220512
BLAST score 1125
E value 1.0e-123
Match length 258
% identity 79

NCBI Description (AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No. 27936

Contig ID 164277\_1.R1040

5'-most EST uC-gmrominsoy102h05b1

Seq. No. 27937

Contig ID 164278\_1.R1040 5'-most EST vzy700752453.h1

Method BLASTX
NCBI GI g3046815
BLAST score 214
E value 5.0e-18
Match length 130
% identity 41

NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 27938

Contig ID 164337 1.R1040 5'-most EST zhf700958489.h1

Seq. No. 27939

Contig ID 164425\_1.R1040 5'-most EST jC-gmfl02220093h03a1

Method BLASTX
NCBI GI g4220524
BLAST score 268
E value 2.0e-23
Match length 68
% identity 69

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 27940

Contig ID 164446\_1.R1040 5'-most EST vzy700752710.h1

Seq. No. 27941

Contig ID 164497 2.R1040 5'-most EST vzy700753311.h1



Seq. No. 27942 Contig ID 164507 1.R1040 5'-most EST jC-gmf\(\overline{1}\)02220071g03d1 BLASTX Method g2109293 NCBI GI BLAST score 237 9.0e-20 E value Match length 55 80 % identity (U97568) serine/threonine protein kinase [Arabidopsis NCBI Description thaliana] Seq. No. 27943 164524 1.R1040 vzy700752812.h1

Contig ID 5'-most EST Method BLASTX NCBI GI g2979562 BLAST score 194 E value 6.0e-15 Match length 88

% identity 49

(AC003680) unknown protein [Arabidopsis thaliana] NCBI Description >gi 3386623 (AC004665) unknown protein [Arabidopsis

thaliana]

27944 Seq. No.

Contig ID 164529 1.R1040 5'-most EST vzy700752822.h1

Seq. No. 27945

164541\_1.R1040 Contig ID 5'-most EST  $jC-gmf\overline{1}02220051c03a1$ 

Method BLASTX NCBI GI g1621465 BLAST score 172 E value 2.0e-12 Match length 109 % identity 39

NCBI Description (U73105) laccase [Liriodendron tulipifera]

Seq. No. 27946

164557 1.R1040 Contig ID 5'-most EST vzy700752856.hl

Seq. No. 27947

Contig ID 164563 1.R1040 5'-most EST vzy700752865.h1

Seq. No. 27948

Contig ID 164598 1.R1040 5'-most EST zzp700833255.h1

Method BLASTX NCBI GI g2651308 BLAST score 151 E value 8.0e-10 Match length 63



% identity

(AC002336) putative myosin heavy chain [Arabidopsis NCBI Description

thaliana]

Seq. No.

27949

Contig ID 5'-most EST

uC-gmrominsoy207f12b1

Seq. No.

27950

Contig ID 5'-most EST 164608 1.R1040 pmv700894015.h1

164602 1.R1040

Method NCBI GI BLASTX q3157949

BLAST score E value

860 9.0e-93

Match length % identity

189 84

NCBI Description

(AC002131) Similar to glucan endo-1,3-beta-D-glucosidase

precursor gb Z28697 from Nicotiana tabacum. ESTs gb Z18185 and gb  $AA605\overline{3}62$  come from this gene. [Arabidopsis thaliana]

Seq. No.

27951

Contig ID 5'-most EST

164614 1.R1040 uC-gmropic039d10b1

BLASTX

Method NCBI GI

a2196466

BLAST score E value

331 1.0e-30

Match length

115 62

% identity NCBI Description

(Y13673) TATA binding protein-associated factor

[Arabidopsis thaliana]

Seq. No.

27952

Contig ID 5'-most EST 164617 1.R1040 vzy700752953.h1

Method

BLASTX

NCBI GI

q2190547

BLAST score

661

E value

Match length

2.0e-69

197

% identity

59 (AC001229) ESTs

NCBI Description

gb\_T43256,gb\_46316,gb\_N64930,gb\_AA395255,gb\_AA404382 come

from this gene. [Arabidopsis thaliana]

Seq. No.

27953

Contig ID 5'-most EST

164655 1.R1040 leu701148730.h1

Seq. No.

Seq. No.

27954

Contig ID 5'-most EST

164655 2.R1040 vzy700753025.h1

27955

Contig ID

164664 1.R1040

5'-most EST

vzy700753040.h1



Contig ID 164683\_1.R1040 5'-most EST pmv700890195.h1

Method BLASTX
NCBI GI g2244792
BLAST score 529
E value 3.0e-54
Match length 109
% identity 86

NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No. 27957

Contig ID 164691\_1.R1040 5'-most EST leu701146647.h1

Seq. No. 27958

Contig ID 164693\_1.R1040 5'-most EST pmv700890724.h1

Method BLASTX
NCBI GI g4220529
BLAST score 349
E value 8.0e-57
Match length 144
% identity 73

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 27959

Contig ID 164705 1.R1040

5'-most EST uC-gmflminsoy034g04b1

Seq. No. 27960

Contig ID 164755\_1.R1040 5'-most EST fC-gmse700753182a1

Method BLASTX
NCBI GI g2833378
BLAST score 652
E value 2.0e-68
Match length 194
% identity 65

NCBI Description HEXOKINASE >gi\_619928 (U18754) hexokinase [Arabidopsis

thaliana] >gi\_1582383 prf\_\_2118367A hexokinase [Arabidopsis

thaliana]

Seq. No. 27961

Contig ID 164774\_1.R1040 5'-most EST uC-gmropic106g09b1

Method BLASTX
NCBI GI g4325342
BLAST score 354
E value 1.0e-33
Match length 121
% identity 63

NCBI Description (AF128393) No definition line found [Arabidopsis thaliana]

Seq. No. 27962

Contig ID 164816\_1.R1040



```
5'-most EST
                  pmv700889507.h1
Seq. No.
                   27963
                   164832 1.R1040
Contig ID
5'-most EST
                   fC-gmf1700902412f1
Method
                   BLASTX
NCBI GI
                   q4558591
BLAST score
                   1003
                   1.0e-109
E value
Match length
                   263
                   72
% identity
                   (AC006555) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                   thaliana]
                   27964
Seq. No.
                   164835 1.R1040
Contig ID
5'-most EST
                   epx701\overline{1}08908.h1
Seq. No.
                   27965
Contig ID
                   164844 1.R1040
5'-most EST
                   vzy700753308.hl
                   BLASTX
Method
NCBI GI
                   g3451071
BLAST score
                   622
                   1.0e-64
E value
Match length
                   151
                   86
% identity
                   (AL031326) beta adaptin - like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   27966
                   164848 1.R1040
Contig ID
                   vzy700753314.h1
5'-most EST
                   27967
Seq. No.
Contig ID
                   164859 1.R1040
5'-most EST
                   jC-qmro02910012d03a1
Method
                   BLASTX
NCBI GI
                   g3834323
BLAST score
                   361
E value
                   2.0e-34
                   100
Match length
% identity
                   63
                   (AC005679) F9K20.25 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   27968
Contig ID
                   164876 1.R1040
5'-most EST
                   fC-qmse700753353a2
Method
                   BLASTX
NCBI GI
                   g2832304
BLAST score
                   189
E value
                   9.0e-15
Match length
                   60
% identity
                   58
```

NCBI Description

(AF044489) receptor-like protein kinase [Oryza sativa]



```
164883 1.R1040
Contig ID
                  fC-gmse7000764856f1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3093294
BLAST score
                  909
                  2.0e-98
E value
                  227
Match length
                  33
% identity
NCBI Description (Y12782) putative villin [Arabidopsis thaliana]
                  27970
Seq. No.
                  164914 1.R1040
Contig ID
                  zsq701124756.h1
5'-most EST
Method
                  BLASTX
                  g4406820
NCBI GI
BLAST score
                  288
                  1.0e-28
E value
                  90
Match length
                  77
% identity
                   (AC006201) putative ras superfamily member [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  27971
                  164922 1.R1040
Contig ID
                  zhf700963488.hl
5'-most EST
                  BLASTX
Method
                  q3367534
NCBI GI
BLAST score
                  256
                  2.0e-22
E value
                  51
Match length
                   94
% identity
                   (AC004392) Strong similarity to coatamer alpha subunit
NCBI Description
                   (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis
                  thaliana]
                  27972
Seq. No.
                  164952 1.R1040
Contig ID
                  hrw701059334.h1
5'-most EST
                  27973
Seq. No.
                  164953 1.R1040
Contig ID
5'-most EST
                  vzy700753465.hl
Seq. No.
                  27974
                  164971 1.R1040
Contig ID
5'-most EST
                  gsv701047903.hl
Seq. No.
                  27975
                  164974 1.R1040
Contig ID
                  g4397649
5'-most EST
```

Contig ID 164979\_1.R1040

5'-most EST jC-gmle01810064a01a1

Seq. No. 27977

Contig ID 165063\_1.R1040

% identity

64



```
vzy700753634.h1
5'-most EST
                  27978
Seq. No.
                  165090 1.R1040
Contig ID
5'-most EST
                  fua701041406.hl
                  BLASTX
Method
                  g3540207
NCBI GI
BLAST score
                  240
                  2.0e-20
E value
Match length
                  64
                  75
% identity
                  (AC004260) Putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  27979
Seq. No.
                  165093 1.R1040
Contig ID
5'-most EST
                  vzy700756828.h1
                  27980
Seq. No.
                  165096 1.R1040
Contig ID
5'-most EST
                  vzy700753682.h1
Method
                  BLASTX
NCBI GI
                  q818849
BLAST score
                  356
                  4.0e-34
E value
Match length
                  89
                  67
% identity
                  (U25430) nucleotide pyrophosphatase precursor [Oryza
NCBI Description
                  27981
Seq. No.
                  165111 1.R1040
Contig ID
5'-most EST
                  vzy700753707.hl
Seq. No.
                  27982
                  165120 1.R1040
Contig ID
5'-most EST
                  vzy700753719.h1
                  BLASTX
Method
NCBI GI
                  q4102600
BLAST score
                  415
                  2.0e-40
E value
                  160
Match length
                   64
% identity
                  (AF013467) ARF6 [Arabidopsis thaliana]
NCBI Description
                  27983
Seq. No.
                  165121 1.R1040
Contig ID
5'-most EST
                  vzy700753721.hl
                  27984
Seq. No.
                  165146 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy261c08b1
                  BLASTX
Method
NCBI GI
                  g3582436
BLAST score
                   429
E value
                  3.0e-42
Match length
                  129
```



NCBI Description (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No. 27985

Contig ID 165155\_1.R1040

5'-most EST uC-gmrominsoy218h10b1

45

Method BLASTX
NCBI GI g3043529
BLAST score 194
E value 8.0e-15
Match length 82

NCBI Description (AJ002204) polyamine oxidase [Zea mays]

Seq. No. 27986

% identity

Contig ID 165155\_2.R1040 5'-most EST crh700853013.h1

Seq. No. 27987

Contig ID 165159\_1.R1040 5'-most EST vzy700753785.h1

Seq. No. 27988

Contig ID 165169\_1.R1040 5'-most EST vzy700755286.h1

Method BLASTX
NCBI GI g2924509
BLAST score 752
E value 6.0e-80
Match length 184
% identity 72

NCBI Description (AL022023) subtilisin proteinase - like [Arabidopsis

thaliana]

Seq. No. 27989

Contig ID 165175\_1.R1040 5'-most EST vzy700753812.h1

Seq. No. 27990

Contig ID 165186\_1.R1040 5'-most EST fC-gmse700753825a1

Method BLASTX
NCBI GI g1783355
BLAST score 581
E value 3.0e-60
Match length 139
% identity 72

NCBI Description (Y10421) delta-9 fatty acid desaturase [Cryptococcus

curvatus]

Seq. No. 27991

Contig ID 165193\_1.R1040 5'-most EST uC-gmropic101d11b1

Seq. No. 27992

Contig ID 165237\_1.R1040 5'-most EST vzy700753918.h1

Method BLASTX



NCBI GI g1173063 BLAST score 281 E value 2.0e-25 Match length 78 % identity 71

NCBI Description 60S RIBOSOMAL PROTEIN YL17-B >gi\_1071989\_pir\_\_S56960

ribosomal protein L17.e.B, cytosolic - yeast (Saccharomyces cerevisiae) >gi\_1008376\_emb\_CAA89472\_ (Z49452) ORF YJL177w

[Saccharomyces cerevisiae]

Seq. No. 27993

Contig ID 165255 1.R1040 5'-most EST vzy700755902.h1

Seq. No. 27994

Contig ID 165306 1.R1040 5'-most EST leu701151074.h1

Method BLASTX
NCBI GI g1916809
BLAST score 237
E value 4.0e-20
Match length 83
% identity 61

NCBI Description (U81163) auxin-binding protein [Prunus persica]

Seq. No. 27995

Contig ID 165353\_1.R1040 5'-most EST fC-gmse700754105a1

Method BLASTN
NCBI GI g517257
BLAST score 66
E value 2.0e-28
Match length 118
% identity 89

NCBI Description Z.mays MNBla mRNA for DNA-binding protein

Seq. No. 27996

Contig ID 165356\_1.R1040 5'-most EST jsh701066076.h1

Seq. No. 27997

Contig ID 165376\_1.R1040 5'-most EST dpv701103230.h1

Method BLASTX
NCBI GI g4063743
BLAST score 402
E value 6.0e-39
Match length 147
% identity 58

NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27998

Contig ID 165427\_1.R1040 5'-most EST sat701007081.h1

Seq. No. 27999

Contig ID 165432\_1.R1040



```
5'-most EST
                  vzy700756123.h1
Seq. No.
                  28000
Contig ID
                  165434 1.R1040
5'-most EST
                  fC-gmse700754216a2
Method
                  BLASTX
NCBI GI
                  g3928095
BLAST score
                  1029
                  1.0e-112
E value
Match length
                  258
                  74
% identity
NCBI Description
                  (AC005770) putative protein kinase [Arabidopsis thaliana]
                  28001
Seq. No.
                  165461 1.R1040
Contig ID
5'-most EST
                  sat701014070.h1
Method
                  BLASTX
NCBI GI
                  g3193306
BLAST score
                  381
E value
                  1.0e-36
Match length
                  120
                  67
% identity
NCBI Description
                  (AF069300) contains similarity to Arabidopsis
                  membrane-associated salt-inducible-like protein
                   (GB:AL021637) [Arabidopsis thaliana]
                  28002
Seq. No.
Contig ID
                  165468 1.R1040
5'-most EST
                  asn701141825.h1
Method
                  BLASTN
NCBI GI
                  g3600062
BLAST score
                  111
E value
                  2.0e-55
Match length
                  363
% identity
                  83
NCBI Description Arabidopsis thaliana BAC T25C13
Seq. No.
                  28003
Contig ID
                  165486 1.R1040
5'-most EST
                  bth700845218.h1
Method
                  BLASTX
NCBI GI
                  g3114658
BLAST score
                  234
E value
                  2.0e-19
Match length
                  108
% identity
                  42
```

(AF060871) hypothetical alcohol dehydrogenase [Rhodococcus NCBI Description

rhodochrous]

Seq. No. 28004

Contig ID 165486 2.R1040 5'-most EST vzy700754292.h1

Method BLASTN NCBI GI g2264306 BLAST score 44 E value 2.0e-15 Match length 203



```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBK5, complete sequence [Arabidopsis thaliana]
                  28005
Seq. No.
Contig ID
                  165495 1.R1040
                  hrw701\overline{0}58919.h1
5'-most EST
Seq. No.
                  28006
                  165531 1.R1040
Contig ID
5'-most EST
                  ary700764358.hl
Method
                  BLASTX
NCBI GI
                  q3885334
BLAST score
                  250
E value
                  2.0e-43
                  136
Match length
                  67
% identity
                  (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  28007
Contig ID
                  165551 1.R1040
5'-most EST
                  zsg701129794.h1
Method
                  BLASTX
NCBI GI
                  g3426038
BLAST score
                  404
                  2.0e-39
E value
                  127
Match length
                  70
% identity
NCBI Description
                  (AC005168) unknown protein [Arabidopsis thaliana]
                  28008
Seq. No.
                  165571 2.R1040
Contig ID
                  fde700872101.h1
5'-most EST
Seq. No.
                  28009
                  165591 1.R1040
Contig ID
                  vzy700754437.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2702273
BLAST score
                  324
E value
                  4.0e-30
Match length
                  114
% identity
                  60
NCBI Description
                  (AC003033) carrot B2 protein-like [Arabidopsis thaliana]
Seq. No.
                  28010
Contig ID
                  165599 1.R1040
5'-most EST
                  uC-gmflminsoy042e03b1
Method
                  BLASTX
```

NCBI GI q4558672 BLAST score 428 E value 4.0e-42 Match length 171 % identity

NCBI Description

(AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis

thaliana]

```
Seq. No. 28011
Contig ID 165619_1.R1040
5'-most EST uC-gmropic078b09b1
Seq. No. 28012
Contig ID 165630_1.R1040
5'-most EST kl1701210418.h1
```

 Seq. No.
 28013

 Contig ID
 165639\_1.R1040

 5'-most EST
 vzy700755930.h1

 Method
 BLASTX

NCBI GI g2145358
BLAST score 378
E value 9.0e-37
Match length 80
% identity 90

NCBI Description (Y10922) HD-Zip protein [Arabidopsis thaliana]

Seq. No. 28015

Contig ID 165705\_1.R1040 5'-most EST fC-gmse7000754553f1

Seq. No. 28016 Contig ID 165721

Contig ID 165721\_1.R1040 5'-most EST fC-gmse700754614a2

Method BLASTX
NCBI GI 94522003
BLAST score 294
E value 2.0e-26
Match length 107
% identity 22

NCBI Description (AC007069) putative protein kinase [Arabidopsis thaliana]

Seq. No. 28017

Contig ID 165731 1.R1040

5'-most EST uC-gmrominsoy084h10b1

Seq. No. 28018

Contig ID 165742\_1.R1040 5'-most EST kl1701204535.h2

Seq. No. 28019

Contig ID 165748\_1.R1040 5'-most EST zzp700836267.h1

Method BLASTX
NCBI GI g3367534
BLAST score 392
E value 4.0e-38
Match length 99
% identity 76

NCBI Description (AC004392) Strong similarity to coatamer alpha subunit



(HEPCOP) homolog gb\_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 28020

Contig ID 165758 1.R1040

5'-most EST uC-gmflminsoy091g09b1

Method BLASTN
NCBI GI g1638836
BLAST score 166
E value 3.0e-88
Match length 438
% identity 84

% identity 84
NCBI Description H.vulgare mRNA for alpha-tubulin

Seq. No. 28021

Contig ID 165763\_1.R1040

5'-most EST jC-gmfl02220077b10a1

Method BLASTX
NCBI GI g3548808
BLAST score 221
E value 8.0e-18
Match length 89
% identity 54

NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 28022

Contig ID 165777\_1.R1040 5'-most EST vzy700754713.h1

Seq. No. 28023

Contig ID 165788\_1.R1040 5'-most EST fC-gmse700754725a2

Method BLASTX
NCBI GI g584882
BLAST score 380
E value 1.0e-36
Match length 131
% identity 54

NCBI Description CYCLOARTENOL SYNTHASE (2,3-EPOXYSQUALENE--CYCLOARTENOL

CYCLASE) >gi\_452446 (U02555) cycloartenol synthase; (S)-2,3-epoxysqualene mutase [Arabidopsis thaliana]

Seq. No. 28024

Contig ID 165835\_1.R1040 5'-most EST asn701138122.h1

Seq. No. 28025

Contig ID 165850\_1.R1040 5'-most EST jC-gmle01810086f01a1

Seq. No. 28026

Contig ID 165853\_1.R1040 5'-most EST vzy700754816.h1

Method BLASTX
NCBI GI g3461848
BLAST score 231
E value 2.0e-19



Match length 87 % identity 60

NCBI Description (AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No. 28027

Contig ID 165854 1.R1040 5'-most EST vzy700754817.h1

Seq. No. 28028

Contig ID 165866 1.R1040 5'-most EST hrw701063185.h1

Seq. No. 28029

Contig ID 165914 1.R1040 5'-most EST vzy700754893.h1

Seq. No. 28030

Contig ID 165924\_1.R1040 5'-most EST fC-gmse700754910a2

Method BLASTX
NCBI GI g4204912
BLAST score 407
E value 6.0e-40
Match length 113
% identity 69

NCBI Description (U58918) MEK kinase [Arabidopsis thaliana]

Seq. No. 28031

Contig ID 165987\_1.R1040 5'-most EST pmv700892680.h1

Method BLASTX
NCBI GI g1352681
BLAST score 210
E value 6.0e-22
Match length 83
% identity 58

NCBI Description PROTEIN PHOSPHATASE 2C (PP2C) >gi\_1076391\_pir\_\_S55457

phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis

thaliana >gi\_633028\_dbj\_BAA07287\_ (D38109) protein

phosphatase 2C [Arabidopsis thaliana]

Seq. No. 28032

Contig ID 166019 1.R1040

5'-most EST g5342541

Method BLASTX

NCBI GI g4038036

BLAST score 323

E value 9.0e-30

Match length 101
% identity 63

NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]

Seq. No. 28033

Contig ID 166048\_1.R1040 5'-most EST jC-qmle01810044f05a1

Seq. No. 28034



Contig ID 166059\_1.R1040

5'-most EST uC-gmflminsoy028e09b1

Method BLASTX
NCBI GI g1263160
BLAST score 331
E value 2.0e-30
Match length 217
% identity 9

NCBI Description (X89226) leucine-rich repeat/receptor protein kinase [Oryza

sativa]

Seq. No. 28035

Contig ID 166125\_1.R1040 5'-most EST vzy700755190.h1

Seq. No. 28036

Contig ID 166176\_1.R1040 5'-most EST vzy700755267.h1

Method BLASTN
NCBI GI g1171481
BLAST score 104
E value 2.0e-51
Match length 260
% identity 85

NCBI Description Nicotiana tabacum mRNA for nitrilase, complete cds

Seq. No. 28037

Contig ID 166191\_1.R1040 5'-most EST fC-gmst700888672d3

Seq. No. 28038

Contig ID 166206\_1.R1040 5'-most EST fC-gmse7000755316a1

Method BLASTN
NCBI GI g3860320
BLAST score 215
E value 1.0e-117
Match length 475
% identity 86

NCBI Description Cicer arietinum mRNA for beta-galactosidase, clone

CanBGal-5

Seq. No. 28039

Contig ID 166216\_1.R1040

5'-most EST uC-gmrominsoy201h12b1

Method BLASTX
NCBI GI g1938424
BLAST score 190
E value 4.0e-14
Match length 97
% identity 49

NCBI Description (U97002) similar to acyl-CoA dehydrogenases and epoxide

hydrolases [Caenorhabditis elegans]

Seq. No. 28040

Contig ID 166229 1.R1040

5'-most EST uC-gmrominsoy106g01b1



Method BLASTX
NCBI GI g2864614
BLAST score 181
E value 3.0e-13
Match length 67
% identity 46

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 28041

Contig ID 166240 1.R1040

5'-most EST uC-gmrominsoy215h09b1

Method BLASTX
NCBI GI g3056591
BLAST score 234
E value 1.0e-19
Match length 87
% identity 48

NCBI Description (AC004255) T1F9.12 [Arabidopsis thaliana]

Seq. No. 28042

Contig ID 166259 1.R1040

5'-most EST uC-gmrominsoy260h09b1

Seq. No. 28043

Contig ID 166262 1.R1040

5'-most EST jC-gmro02910047f02a1

Seq. No. 28044

Contig ID 166298\_1.R1040 5'-most EST zzp700833791.h1

Seq. No. 28045

Contig ID 166352\_1.R1040 5'-most EST asj700967425.h1

Method BLASTX
NCBI GI g2460203
BLAST score 190
E value 1.0e-14
Match length 72
% identity 50

NCBI Description (AF021244) coronatine-induced protein 1 [Arabidopsis

thaliana]

Seq. No. 28046

Contig ID 166370\_1.R1040 5'-most EST gsv701054482.h1

Seq. No. 28047

Contig ID 166399\_1.R1040 5'-most EST lus701015762.h1

Seq. No. 28048

Contig ID 166427\_1.R1040 5'-most EST hrw701060518.h1

Seq. No. 28049

Contig ID 166428 1.R1040



5'-most EST vzy700755673.h1

Method BLASTX
NCBI GI g1652082
BLAST score 158
E value 1.0e-10
Match length 95
% identity 41

NCBI Description (D90902) UDP-3-0-acyl N-acetylglcosamine deacetylase

[Synechocystis sp.]

Seq. No. 28050

Contig ID 166428 2.R1040 5'-most EST vzy700756093.h1

Seq. No. 28051

Contig ID 166497\_1.R1040 5'-most EST vzy700755817.h1

Seq. No. 28052

Contig ID 166500\_1.R1040 5'-most EST pmv700891978.h1

Seq. No. 28053

Contig ID 166545\_1.R1040 5'-most EST fde700873207.h1

Seq. No. 28054

Contig ID 166567\_1.R1040 5'-most EST xpa700792682.h1

Seq. No. 28055

Contig ID 166579 1.R1040 5'-most EST xpa700798256.h1

Seq. No. 28056

Contig ID 166699 1.R1040 5'-most EST vzy700756121.h1

Seq. No. 28057

Contig ID 166735 1.R1040

5'-most EST g4290552

Seq. No. 28058

Contig ID 166742\_1.R1040 5'-most EST vzy700756182.h1

Seq. No. 28059

Contig ID 166759\_1.R1040 5'-most EST hrw701060431.h1

Method BLASTX
NCBI GI g4567311
BLAST score 176
E value 1.0e-12
Match length 43
% identity 41

NCBI Description (AC005956) putative protein kinase [Arabidopsis thaliana]



166790 1.R1040 Contig ID 5'-most EST fde700871081.h1

28061 Seq. No.

Contig ID 166806 1.R1040 5'-most EST fC-gmro700843710a3

BLASTX Method NCBI GI g2754825 BLAST score 439 4.0e-43E value 245 Match length 42 % identity

(AF033097) NPH1-2 [Avena sativa] NCBI Description

28062 Seq. No.

166839 1.R1040 Contig ID 5'-most EST vzy700756331.h1

28063 Seq. No.

Contig ID 166845 1.R1040

5'-most EST g4397586 Method BLASTX NCBI GI g2501182 BLAST score 695 2.0e-73 E value Match length 164 73 % identity

OSMOTIN-LIKE PROTEIN PRECURSOR >gi 2129934 pir JC5237 NCBI Description

osmotin-like protein - tomato >gi 1220537 (L76632) osmotin-like protein [Lycopersicon esculentum]

28064 Seq. No.

166851 1.R1040 Contig ID jC-gmst02400040h11a1 5'-most EST

Method BLASTX NCBI GI q4008006 175 BLAST score E value 9.0e-13 Match length 92

(AF084034) receptor-like protein kinase [Arabidopsis NCBI Description

thaliana]

28065 Seq. No.

% identity

Contig ID 166889 1.R1040 5'-most EST

jC-gmro02910068h05a1

43

Method BLASTX NCBI GI q4106395 BLAST score 166 E value 1.0e-18 Match length 100 % identity

NCBI Description (AF073744) raffinose synthase [Cucumis sativus]

28066 Seq. No.

Contig ID 166891 1.R1040



5'-most EST vzy700756410.h1

Seq. No. 28067

Contig ID 166900\_1.R1040 5'-most EST vzy700756421.h1

Seq. No. 28068

Contig ID 166905\_1.R1040 5'-most EST hrw701063660.h1

Seq. No. 28069

Contig ID 166907\_1.R1040 5'-most EST vzy700756429.h1

Method BLASTX
NCBI GI g1176658
BLAST score 270
E value 6.0e-24
Match length 105
% identity 52

NCBI Description HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II

>gi 726363 (U23168) No definition line found

[Caenorhabditis elegans]

Seq. No. 28070

Contig ID 166918 1.R1040

5'-most EST jC-gmf102220081b08a1

Seq. No. 28071

Contig ID 166923\_1.R1040

5'-most EST jC-gmst02400065a11d1

Seq. No. 28072

Contig ID 166927\_1.R1040 5'-most EST vzy700756461.h1

Seq. No. 28073

Contig ID 166960\_1.R1040 5'-most EST leu701147985.h1

Seq. No. 28074

Contig ID 166976\_1.R1040 5'-most EST zhf700955028.h1

Method BLASTX
NCBI GI g3482978
BLAST score 277
E value 8.0e-25
Match length 108
% identity 61

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 28075

Contig ID 167014\_1.R1040 5'-most EST fC-gmse7000756618f1

Method BLASTX
NCBI GI g4006924
BLAST score 1058
E value 1.0e-116



Match length 247 % identity 79

NCBI Description (Z99708) beta-galactosidase like protein [Arabidopsis

thaliana]

Seq. No. 28076

Contig ID 167017 1.R1040 5'-most EST sat701012712.h1

Method BLASTX
NCBI GI g4490303
BLAST score 306
E value 4.0e-28
Match length 94
% identity 63

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 28077

Contig ID 167039\_1.R1040 5'-most EST sat701004384.h1

Seq. No. 28078

Contig ID 167083 1.R1040 5'-most EST vzy700756695.h1

Seq. No. 28079

Contig ID 167086\_1.R1040 5'-most EST uC-gmropic057g02b1

Seq. No. 28080

Contig ID 167088\_1.R1040

5'-most EST jC-gmro02910006h02a1

Method BLASTX
NCBI GI g4538926
BLAST score 538
E value 8.0e-57
Match length 213

% identity 56

NCBI Description (AL049483) putative phosphatidylserine decarboxylase

[Arabidopsis thaliana]

Seq. No. 28081

Contig ID 167111\_1.R1040 5'-most EST fC-gmse7000756739a1

Method BLASTX
NCBI GI g461538
BLAST score 474
E value 1.0e-47
Match length 158
% identity 58

NCBI Description PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE,

PHENYLALANINE-INHIBITED (PHOSPHO-2-KETO-3-DEOXYHEPTONATE

ALDOLASE) (DAHP SYNTHETASE)

(3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE)

>gi 478311 pir JN0865

3-Deoxy-D-arabinoheptulosonate-7-phosphate synthase - yeast

(Candida albicans) >gi 410315 (L12217)

3-deoxy-D-arabinoheptulosonate-7-phosphate synthase



## [Candida albicans]

Seq. No. 28082

Contig ID 167113\_1.R1040 5'-most EST pmv700890784.h1

Seq. No. 28083

Contig ID 167116\_1.R1040 5'-most EST asn701135289.h1

Method BLASTX
NCBI GI g3600036
BLAST score 190
E value 3.0e-14
Match length 175
% identity 35

NCBI Description (AF080119) contains similarity to protein kinase domains (Pfam: pkinase.hmm, score: 227.04) [Arabidopsis thaliana]

Seq. No. 28084

Contig ID 167152 1.R1040 5'-most EST vzy700756817.h1

Seq. No. 28085

Contig ID 167172 1.R1040 5'-most EST zhf700960734.h1

Method BLASTX
NCBI GI g631069
BLAST score 152
E value 3.0e-10
Match length 83
% identity 13

NCBI Description AF-1p protein - human >gi\_470035 emb\_CAA82305\_ (Z29064)

Highly similar to murine eps 15 GB A.N. L221768 [Homo sapiens] >gi 4503593 ref NP 001972.1 pEPS15 epidermal

growth factor receptor pathway substrate

Seq. No. 28086

Contig ID 167175\_1.R1040 5'-most EST zhf700963525.h1

Method BLASTX
NCBI GI g3243033
BLAST score 162
E value 4.0e-11
Match length 85
% identity 36

NCBI Description (AF069765) signal recognition particle 72 [Homo sapiens]

>gi\_3335650 (AF077019) signal recognition particle 72 [Homo

sapiens]

Seq. No. 28087

Contig ID 167195\_1.R1040 5'-most EST fua701042252.h1

Method BLASTX
NCBI GI g2190419
BLAST score 233
E value 2.0e-19
Match length 77



% identity

(Y13632) dem [Lycopersicon esculentum] NCBI Description

Seq. No.

28088

Contig ID 5'-most EST 167215 1.R1040  $euj700\overline{6}97912.h1$ 

Seq. No.

28089

Contig ID 5'-most EST 167220 1.R1040 euj700697919.hl

Seq. No.

28090

Contig ID 5'-most EST 167233 1.R1040 zhf700957625.h1

Method NCBI GI BLASTX g4467108

BLAST score E value

141 9.0e-09

Match length % identity

46 61

NCBI Description

(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.

28091

Contig ID 5'-most EST 167238 1.R1040 euj700697955.hl

Seq. No.

28092

Contig ID 5'-most EST 167280 1.R1040 euj700698032.hl

Method NCBI GI

BLASTX g2244807

BLAST score E value Match length 175 7.0e-13

% identity

73 53

NCBI Description

(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.

28093

Contig ID

167287 1.R1040

5'-most EST

uC-gmrominsoy087b11b1

Method NCBI GI BLASTX g3953471

BLAST score

322

E value Match length 8.0e-30

% identity

122 52

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No.

28094

Contig ID 5'-most EST

167396 1.R1040 crh700851493.h1

Seq. No.

28095

Contig ID 5'-most EST 167406 1.R1040 zpv700757086.h1

Method NCBI GI BLASTX

q2507426

4355



BLAST score 438 E value 2.0e-43 Match length 110 % identity 78

NCBI Description ALANYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR

(ALANINE--TRNA LIGASE) (ALARS) >gi\_1673365\_emb\_CAA80380\_ (Z22673) mitochondrial tRNA-Ala synthetase [Arabidopsis

thaliana]

Seq. No. 28096

Contig ID 167461\_1.R1040 5'-most EST crh700851213.h1

Method BLASTX
NCBI GI g2459431
BLAST score 194
E value 7.0e-15
Match length 82
% identity 46

NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

Seq. No. 28097

Contig ID 167481\_1.R1040 5'-most EST dpv701097070.h1

Seq. No. 28098

Contig ID 167481 2.R1040

5'-most EST uC-gmrominsoy260b03b1

Seq. No. 28099

Contig ID 167498\_1.R1040 5'-most EST zpv700757247.h1

Seq. No. 28100

Contig ID 167518 1.R1040 5'-most EST zpv700757279.h1

Method BLASTN
NCBI GI g2264302
BLAST score 69
E value 3.0e-30
Match length 205
% identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAC12, complete sequence [Arabidopsis thaliana]

Seq. No. 28101

Contig ID 167545\_1.R1040 5'-most EST fC-gmse7000757329a1

Method BLASTX
NCBI GI g4567307
BLAST score 195
E value 7.0e-15
Match length 72
% identity 51

NCBI Description (AC005956) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 28102



```
167556 1.R1040
Contig ID
                  rlr700899695.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4572676
BLAST score
                   316
                   6.0e-29
E value
Match length
                   187
% identity
                   36
NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]
Seq. No.
                   28103
                   167611 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}09728.h1
Seq. No.
                   28104
                   167613 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir065c05b1
                   28105
Seq. No.
Contig ID
                   167641 1.R1040
5'-most EST
                   zpv700757524.h1
Seq. No.
                   28106
                   167673 1.R1040
Contig ID
5'-most EST
                   xpa700795867.hl
Seq. No.
                   28107
                   167692 1.R1040
Contig ID
5'-most EST
                   zpv700757614.h1
Method
                   BLASTX
NCBI GI
                   g3980413
BLAST score
                   364
                   4.0e-35
E value
Match length
                   94
                   16
% identity
NCBI Description
                  (AC004561) pumilio-like protein [Arabidopsis thaliana]
                   28108
Seq. No.
                   167727 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810087a02d1
                   28109
Seq. No.
Contig ID
                   167745 1.R1040
5'-most EST
                   jC-gmro02910072e07a1
Seq. No.
                   28110
Contig ID
                   167756 1.R1040
                   zpv700758462.hl
5'-most EST
                   BLASTX
Method
```

NCBI GI g1084950
BLAST score 195
E value 8.0e-15
Match length 143
% identity 29

NCBI Description probable membrane protein YPR029c - yeast (Saccharomyces cerevisiae) >gi\_809594\_emb\_CAA89283\_ (Z49274) unknown [Saccharomyces cerevisiae] >gi\_1314103 emb\_CAA95025





## (Z71255) unknown [Saccharomyces cerevisiae]

Seq. No. 28111

Contig ID 167774\_1.R1040 5'-most EST fC-gmse7000757783f1

Method BLASTX
NCBI GI g1076755
BLAST score 537
E value 8.0e-76
Match length 175
% identity 79

NCBI Description protein kinase - rice >gi\_450300 (L27821) protein kinase

[Oryza sativa]

Seq. No. 28112

Contig ID 167806\_1.R1040 5'-most EST zpv700757855.h1

Method BLASTX
NCBI GI g3212855
BLAST score 378
E value 5.0e-36
Match length 207
% identity 44

NCBI Description (AC004005) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28113

Contig ID 167840\_1.R1040 5'-most EST zhf700958356.h1

Method BLASTX
NCBI GI g3831452
BLAST score 189
E value 5.0e-14
Match length 171
% identity 27

NCBI Description (AC005700) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 28114

Contig ID 167854\_1.R1040 5'-most EST zhf700953487.h1

Seq. No. 28115

Contig ID 167860\_1.R1040 5'-most EST zpv700757966.h1

Method BLASTX
NCBI GI g4467158
BLAST score 169
E value 7.0e-12
Match length 108
% identity 55

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 28116

Contig ID 167944\_1.R1040 5'-most EST zpv700758128.h1

Seq. No. 28117

Contig ID 168079\_1.R1040



5'-most EST jC-gmle01810054d10a1

Seq. No. 28118

Contig ID 168102\_1.R1040 5'-most EST pmv700889065.h1

Seq. No. 28119

Contig ID 168114\_1.R1040 5'-most EST sat701002912.h1

Seq. No. 28120

Contig ID 168121\_1.R1040 5'-most EST zpv700758467.h1

Method BLASTN
NCBI GI g169972
BLAST score 199
E value 1.0e-108
Match length 259
% identity 94

NCBI Description Soybean glycinin A-la-B-x subunit mRNA, complete cds

Seq. No. 28121

Contig ID 168198\_1.R1040

5'-most EST jC-gmro02910071d07d1

Seq. No. 28122

Contig ID 168211\_1.R1040 5'-most EST zpv700758640.h1

Seq. No. 28123

Contig ID 168257\_1.R1040 5'-most EST zpv700758723.h1

Seq. No. 28124

Contig ID 168394\_1.R1040 5'-most EST zpv700759012.h1

Seq. No. 28125

Contig ID 168417\_1.R1040 5'-most EST zhf700955494.h1

Seq. No. 28126

Contig ID 168460\_1.R1040 5'-most EST zpv700759109.h1

Method BLASTX
NCBI GI g4006887
BLAST score 244
E value 7.0e-21
Match length 60
% identity 70

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 28127

Contig ID 168467\_1.R1040 5'-most EST leu701155432.h1

Method BLASTX NCBI GI g3548818



```
BLAST score
                  1.0e-15
E value
                  49
Match length
                  78
% identity
                  (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                  28128
Seq. No.
                  168505 1.R1040
Contig ID
                  rlr700896855.h1
5'-most EST
                  28129
Seq. No.
                  168538 1.R1040
Contig ID
                  pmv700890049.h1
5'-most EST
                   28130
Seq. No.
                   168594 1.R1040
Contig ID
                   zpv700759541.hl
5'-most EST
                  BLASTX
Method
                   g1906830
NCBI GI
                   662
BLAST score
                   1.0e-69
E value
Match length
                   168
                   76
% identity
                   (Y11829) heat shock protein [Arabidopsis thaliana]
NCBI Description
                   28131
Seq. No.
                   168598 1.R1040
Contig ID
                   sat701008969.hl
5'-most EST
                   28132
Seq. No.
                   168601 1.R1040
Contig ID
                   g4314150
5'-most EST
Method
                   BLASTX
                   g3257262
NCBI GI
                   162
BLAST score
                   4.0e-11
E value
                   66
Match length
                   52
% identity
                   (AP000003) 450aa long hypothetical fmu protein [Pyrococcus
NCBI Description
                   horikoshii]
                   28133
Seq. No.
                   168619 1.R1040
Contig ID
                   kl1701203142.h1
5'-most EST
                   28134
Seq. No.
                   168679 1.R1040
Contig ID
                   crh700853122.h1
5'-most EST
                   BLASTN
Method
```

g2605511 NCBI GI 168 BLAST score 2.0e-89 E value 389 Match length 86 % identity

Glycine max mRNA for beta subunit of beta conglycinin, NCBI Description

complete cds



Seq. No. 28135

Contig ID 168704\_1.R1040 5'-most EST zpv700759841.h1

Seq. No. 28136

Contig ID 168760\_1.R1040 5'-most EST zpv700760005.h1

Seq. No. 28137

Contig ID 168790\_1.R1040 5'-most EST zpv700760103.h1

Method BLASTX
NCBI GI g461753
BLAST score 178
E value 4.0e-13
Match length 56
% identity 64

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

PRECURSOR >gi\_419773\_pir\_\_S31164 ATP-dependent ClpB

proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi\_169128 (L09547) nuclear encoded precursor

to chloroplast protein [Pisum sativum]

Seq. No. 28138

Contig ID 168809 1.R1040

5'-most EST g4396542
Method BLASTX
NCBI GI g3377822
BLAST score 289
E value 6.0e-26
Match length 96
% identity 53

NCBI Description (AF076275) contains similarity to Caenorhabditis elegans

MEL-26 (GB:U67737) [Arabidopsis thaliana]

Seq. No. 28139

Contig ID 168851\_1.R1040

5'-most EST g5677098

Seq. No. 28140

Contig ID 168940\_1.R1040 5'-most EST zpv700760448.h1

Seq. No. 28141

Contig ID 168982\_1.R1040 5'-most EST zpv700760532.h1

Seq. No. 28142

Contig ID 168994\_1.R1040 5'-most EST zpv700760559.h1

Method BLASTX
NCBI GI g1001312
BLAST score 204
E value 7.0e-16
Match length 59
% identity 66

NCBI Description (D64006) hypothetical protein [Synechocystis sp.]



 Seq. No.
 28143

 Contig ID
 169024 1.R1040

 5'-most EST
 zhf700956343.h1

Method BLASTX
NCBI GI g4539321
BLAST score 166
E value 8.0e-12
Match length 58
% identity 52

NCBI Description (AL035679) putative protein [Arabidopsis thaliana]

Seq. No. 28144

Contig ID 169045\_1.R1040 5'-most EST zpv700763458.h1

Seq. No. 28145

Contig ID 169159 1.R1040

5'-most EST jC-gmf\(\bar{1}\)02220075a09d1

Seq. No. 28146

Contig ID 169260\_1.R1040 5'-most EST zpv700761194.h1

Seq. No. 28147

Contig ID 169354\_1.R1040 5'-most EST zpv700761405.h1

Seq. No. 28148

Contig ID 169360\_1.R1040 5'-most EST zpv700761423.h1

Seq. No. 28149

Contig ID 169365 1.R1040 5'-most EST sat701004686.h1

Seq. No. 28150

Contig ID 169429\_2.R1040 5'-most EST jC-gmst02400060a10a1

Seq. No. 28151

Contig ID 169443\_1.R1040 5'-most EST sat701004844.h1

Method BLASTX
NCBI GI g4559388
BLAST score 697
E value 2.0e-73
Match length 248
% identity 53

NCBI Description (AC006526) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28152

Contig ID 169450\_1.R1040 5'-most EST leu701145131.h1

Seq. No. 28153

Contig ID 169497\_1.R1040



5'-most EST zpv700761731.h1 Method BLASTX NCBI GI g3790677 BLAST score 143 E value 6.0e-09 Match length 103 % identity 33 (AF099002) similar to human 5'-nucleotidase (SW:P49902) NCBI Description [Caenorhabditis elegans] Seq. No. 28154 Contig ID 169560 1.R1040 5'-most EST uC-gmrominsoy029h01b1 Method BLASTN NCBI GI g2924733 BLAST score 41 E value 2.0e-13 Match length 61 92 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana] 28155 Seq. No. 169613 1.R1040 Contig ID 5'-most EST zpv700762023.h1 Method BLASTX NCBI GI q3372671 BLAST score 432 E value 6.0e-43 105 Match length % identity 83 NCBI Description (AF061286) gamma-adaptin 1 [Arabidopsis thaliana] Seq. No. 28156 Contig ID 169680 1.R1040 5'-most EST epx701110086.h1 Seq. No. 28157 169712 1.R1040 Contig ID 5'-most EST jC-gmf\(\bar{1}\)02220079g12a1 Seq. No. 28158 Contig ID 169719 1.R1040 5'-most EST uC-gmflminsoy046h06b1 Method BLASTN NCBI GI q975703 BLAST score 55 E value 6.0e-22 Match length 174 88 % identity NCBI Description P.sativum GR gene

Seq. No. 28159 Contig ID 169719

Contig ID 169719 2.R1040 5'-most EST epx701107025.h1

Method BLASTN NCBI GI g975703



BLAST score 43 E value 6.0e-15 Match length 91 % identity 87

NCBI Description P.sativum GR gene

Seq. No. 28160

Contig ID 169744\_1.R1040 5'-most EST pmv700889274.h1

Seq. No. 28161

Contig ID 169760\_1.R1040 5'-most EST zpv700762329.h1

Seq. No. 28162

Contig ID 169818\_1.R1040

5'-most EST jC-gmro02910033a10a1

Seq. No. 28163

Contig ID 169832\_1.R1040 5'-most EST fC-gmse7000762491f1

Method BLASTN
NCBI GI g1806143
BLAST score 287
E value 1.0e-160
Match length 519
% identity 89

NCBI Description M.sativa mRNA for cdc2 kinase homologue, cdc2MsE

Seq. No. 28164

Contig ID 169845\_1.R1040 5'-most EST zpv700762525.h1

Method BLASTX
NCBI GI g4097880
BLAST score 318
E value 8.0e-30
Match length 81
% identity 81

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 28165

Contig ID 169895\_1.R1040 5'-most EST zpv700762633.h1

Method BLASTX
NCBI GI g4249402
BLAST score 171
E value 2.0e-12
Match length 66
% identity 55

NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 28166

Contig ID 169896\_1.R1040 5'-most EST jC-gmle01810021b01d1

Method BLASTN NCBI GI g287567 BLAST score 47



```
E value 3.0e-17
Match length 75
% identity 91
```

NCBI Description Vigna radiata auxin-regulated mRNA

Seq. No. 28167

Contig ID 169917 1.R1040 5'-most EST bth700846108.h1

Seq. No. 28168

Contig ID 169926\_1.R1040 5'-most EST sat701005108.h1

Method BLASTN
NCBI GI g2760172
BLAST score 44
E value 1.0e-15
Match length 182

% identity 85 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUB3, complete sequence [Arabidopsis thaliana]

Seq. No. 28169

Contig ID 170013\_1.R1040 5'-most EST sat701008610.h1

Method BLASTX
NCBI GI g4262226
BLAST score 173
E value 2.0e-12
Match length 78
% identity 51

NCBI Description (AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No. 28170

Contig ID 170062 1.R1040 5'-most EST zpv700763005.h1

Seq. No. 28171

Contig ID 170091\_1.R1040 5'-most EST hrw701063395.h1

Method BLASTX
NCBI GI g123534
BLAST score 336
E value 1.0e-31
Match length 73
% identity 88

NCBI Description 17.3 KD CLASS I HEAT SHOCK PROTEIN (HSP 17.3)

>gi\_71493\_pir\_\_HHSY17 heat shock protein 17 - soybean
>gi\_18656\_emb\_CAA25578\_ (X01104) heat shock protein 6871
(aa 1-153) [Glycine max] >gi\_224205\_prf\_\_1012218B protein

6871, heat shock [Glycine max]

Seq. No. 28172

Contig ID 170100 1.R1040 5'-most EST zpv700763069.h1

Seq. No. 28173

Contig ID 170154\_1.R1040



5'-most EST jC-gmfl02220106g10a1

Seq. No. 28174

Contig ID 170195\_1.R1040 5'-most EST zpv700763257.h1

Method BLASTX
NCBI GI g3763916
BLAST score 532
E value 3.0e-54
Match length 190

% identity 54

NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

>gi\_4531439\_gb\_AAD22124.1\_AC006224\_6 (AC006224) unknown

protein [Arabidopsis thaliana]

Seq. No. 28175

Contig ID 170233\_1.R1040 5'-most EST jC-gmfl02220092a11a1

Seq. No. 28176

Contig ID 170309\_1.R1040 5'-most EST zpv700763470.h1

Seq. No. 28177

Contig ID 170397\_1.R1040 5'-most EST zpv700763625.h1

Seq. No. 28178

Contig ID 170449\_1.R1040 5'-most EST eep700863716.h1

Method BLASTX
NCBI GI g1710401
BLAST score 777
E value 5.0e-83
Match length 165
% identity 89

NCBI Description RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN

(RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)

>gi 1044912 emb\_CAA63194\_ (X92443) ribonucleotide reductase

R2 [Nicotiana tabacum]

Seq. No. 28179

Contig ID 170451\_1.R1040 5'-most EST jC-gmle01810094d11d1

Seq. No. 28180

Contig ID 170477 1.R1040 5'-most EST eep700863816.h1

Seq. No. 28181

Contig ID 170486\_1.R1040 5'-most EST fC-gmro700863840a3

Method BLASTX
NCBI GI g1743354
BLAST score 747
E value 1.0e-109
Match length 264



% identity (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum] NCBI Description 28182 Seq. No. 170486 2.R1040 Contig ID 5'-most EST dpv701099622.h1 Method BLASTX g4056462 NCBI GI 791 BLAST score E value 1.0e-137 320 Match length % identity 78 (AC005990) Strong similarity to gb Y09876 aldehyde NCBI Description dehydrogenase (NAD+) from Nicotiana tabacum and a member of the aldehyde dehydrogenase family PF\_00171. ESTs gb F15117, gb R83958 and gb 586262 come from this gene. [Arabidopsis thaliana] Seq. No. 28183 170490 1.R1040 Contig ID 5'-most EST eep700863849.hl Method BLASTX NCBI GI g2842478 220 BLAST score 3.0e-18 E value Match length 86 % identity 56 (AL021749) receptor protein kinase like protein NCBI Description [Arabidopsis thaliana] 28184 Seq. No. Contig ID 170520 1.R1040  $rca701\overline{0}00811.h1$ 5'-most EST Method BLASTX g1698548 NCBI GI 317 BLAST score 9.0e-29 E value Match length 135 47 % identity (U58971) calmodulin-binding protein [Nicotiana tabacum] NCBI Description

Seq. No. 28185

170574 1.R1040 Contig ID 5'-most EST pxt700942627.h1

Seq. No. 28186

170576 1.R1040 Contig ID 5'-most EST zhf700955167.h1

Method BLASTX q4558672 NCBI GI BLAST score 347 E value 9.0e-33 Match length 88 80 % identity

(AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis NCBI Description

thaliana]



 Seq. No.
 28187

 Contig ID
 170588\_1.R1040

 5'-most EST
 jC-gmst02400057h01a1

 Method
 BLASTX

 NCBI GI
 g1871185

NCBI GI g1871185
BLAST score 554
E value 9.0e-57
Match length 125
% identity 80

NCBI Description (U90439) seven in absentia isolog [Arabidopsis thaliana]

Seq. No. 28188

Contig ID 170647\_1.R1040 5'-most EST eep700864290.h1

Seq. No. 28189

Contig ID 170677\_1.R1040 5'-most EST eep700867106.h1

Seq. No. 28190

Contig ID 170695\_1.R1040 5'-most EST fC-gmro700864412a3

Method BLASTX
NCBI GI 94038030
BLAST score 419
E value 1.0e-40
Match length 196
% identity 45

NCBI Description (AC005936) putative protein kinase, 5' partial [Arabidopsis

thaliana]

Seq. No. 28191

Contig ID 170705\_1.R1040 5'-most EST eep700864431.h1

Seq. No. 28192

Contig ID 170730\_1.R1040 5'-most EST eep700864515.h1

Method BLASTX
NCBI GI g547706
BLAST score 233
E value 4.0e-19
Match length 190
% identity 32

NCBI Description INSULIN-DEGRADING ENZYME (INSULYSIN) (INSULINASE) (INSULIN

PROTEASE) >gi\_347022\_pir\_\_S29509 insulinase (EC 3.4.99.45) - rat >gi\_56492 emb CAA47689 (X67269) insulin-degrading

enzyme [Rattus norvegicus]

Seq. No. 28193

Contig ID 170743\_1.R1040 5'-most EST eep700864542.h1

Method BLASTX
NCBI GI g3540204
BLAST score 523
E value 3.0e-53
Match length 139



% identity

(AC004260) Hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

28194

Contig ID 5'-most EST 170763 1.R1040 yza700763910.h1

Method

BLASTX

NCBI GI

g1706956

BLAST score

181

E value Match length 3.0e-27

% identity

121 57

NCBI Description

(U58283) cellulose synthase [Gossypium hirsutum]

Seq. No.

28195

Contig ID

170766 1.R1040

5'-most EST

jC-gmst02400005d11d1

Seq. No.

28196

Contig ID 5'-most EST 170799 1.R1040

Method

eep700864693.h1

NCBI GI

BLASTX g3757822

BLAST score

212

E value

6.0e-17

Match length

117

% identity

41

NCBI Description

(AF044195) IkappaB kinase complex associated protein; IKAP

[Homo sapiens] >gi 4504629 ref NP 003631.1\_pIKBKAP inhibitor of kappa light polypeptide gene enhancer in

B-cells, kinase complex-associated protein; IKAP

Seq. No.

28197

Contig ID 5'-most EST 170816 1.R1040 dpv701098520.h1

Seq. No.

28198

Contig ID 5'-most EST 170823 1.R1040 epx701103808.h1

Method

BLASTX

NCBI GI BLAST score g3800951

E value

153

Match length

6.0e-10 57

% identity

NCBI Description

(AF100657) No definition line found [Caenorhabditis

elegans]

Seq. No.

28199

Contig ID

170831 1.R1040  $gsv701\overline{0}56216.h1$ 

5'-most EST

Seq. No.

28200

Contig ID 5'-most EST 170838 1.R1040 uC-gmronoir004b07b1

Seq. No.

28201



Contig ID 170844 1.R1040 5'-most EST kll701206615.h1

Method BLASTX
NCBI GI g457517
BLAST score 261
E value 1.0e-22
Match length 126
% identity 41

NCBI Description (L12579) alternatively spliced [Homo sapiens]

>gi\_4503169\_ref\_NP\_001904.1\_pCUTL1\_ cut (Drosophila)-like 1

(CCAAT displacement protein)

Seq. No. 28202

Contig ID 170862\_1.R1040 5'-most EST pxt700944333.h1

Seq. No. 28203

Contig ID 170870\_1.R1040 5'-most EST zzp700834111.h1

Method BLASTN
NCBI GI g4235150
BLAST score 46
E value 7.0e-17
Match length 130
% identity 84

NCBI Description Arabidopsis thaliana chromosome I BAC T25B24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 28204

Contig ID 170873\_1.R1040 5'-most EST eep700866455.h1

Seq. No. 28205

Contig ID 170876\_1.R1040 5'-most EST jC-gmst02400049b04a1

Method BLASTX
NCBI GI g1707642
BLAST score 703
E value 6.0e-74
Match length 249
% identity 58

NCBI Description (Y07748) TMK [Oryza sativa]

Seq. No. 28206

Contig ID 170919 1.R1040 5'-most EST hrw701057932.h1

Seq. No. 28207

Contig ID 170928 1.R1040

5'-most EST uC-gmrominsoy258c09b1

Seq. No. 28208

Contig ID 170935\_1.R1040 5'-most EST eep700864995.h1

Seq. No. 28209

Contig ID 170952\_1.R1040



zzp700830712.h1 5'-most EST 28210 Seq. No. 170953 1.R1040 Contig ID 5'-most EST eep700865030.h1 Seq. No. 28211 170954 1.R1040 Contig ID 5'-most EST fC-gmro700865034a4 Method BLASTX NCBI GI g4262226 BLAST score 246 3.0e-20 E value 166 Match length 39 % identity (AC006200) putative protein kinase [Arabidopsis thaliana] NCBI Description 28212 Seq. No. 171008 1.R1040 Contig ID 5'-most EST eep700870119.hl Method BLASTX NCBI GI g1777443 BLAST score 297 5.0e-27 E value 71 Match length 75 % identity (U28422) CCA1 [Arabidopsis thaliana] >gi 3510263 (AC005310) NCBI Description DNA-binding protein CCA1 [Arabidopsis thaliana] >gi 4090569 (U79156) CCA1 [Arabidopsis thaliana] 28213 Seq. No. Contig ID 171025\_1.R1040 fC-gmro700865758a3 5'-most EST Method BLASTX NCBI GI g1930081 556 BLAST score 1.0e-56 E value 247 Match length % identity (U92878) acyl-ACP thioesterase [Garcinia mangostana] NCBI Description Seq. No. 28214 171074 1.R1040 Contig ID 5'-most EST eep700865319.h1 28215 Seq. No. Contig ID 171078 1.R1040 zhf700957058.hl 5'-most EST 28216 Seq. No. 171101 1.R1040 Contig ID

Contig ID 171101\_1.R1040 5'-most EST eep700865363.h1 Method BLASTX

NCBI GI g3646450
BLAST score 230
E value 2.0e-19
Match length 90



% identity 49

NCBI Description (AL031603) conserved hypothetical protein.

[Schizosaccharomyces pombe]

Seq. No. 28217

Contig ID 171107\_1.R1040 5'-most EST rca700995907.h1

Method BLASTX
NCBI GI g3953463
BLAST score 360
E value 1.0e-34
Match length 95
% identity 72

NCBI Description (AC002328) F20N2.8 [Arabidopsis thaliana]

Seq. No. 28218

Contig ID 171111\_1.R1040 5'-most EST eep700865381.h1

Seq. No. 28219

Contig ID 171125\_1.R1040

5'-most EST uC-gmflminsoy077d10b1

Method BLASTX
NCBI GI g4263770
BLAST score 242
E value 2.0e-20
Match length 96
% identity 56

NCBI Description (AC006218) unknown protein [Arabidopsis thaliana]

Seq. No. 28220

Contig ID 171128\_1.R1040 5'-most EST gsv701051170.h1

Method BLASTX
NCBI GI g3193293
BLAST score 322
E value 7.0e-30
Match length 122
% identity 54

NCBI Description (AF069298) contains a short region of similarity to another

Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)

[Arabidopsis thaliana]

Seq. No. 28221

Contig ID 171136 1.R1040

5'-most EST jC-gmf102220053a06d1

Seq. No. 28222

Contig ID 171147\_1.R1040 5'-most EST uC-gmropic041f02b1

Seq. No. 28223

Contig ID 171162\_1.R1040 5'-most EST fC-qmro700865482a3

Method BLASTX NCBI GI g136753 BLAST score 935

4372



E value 1.0e-113 Match length 345 60 % identity

NCBI Description GLYCOGEN (STARCH) SYNTHASE, ISOFORM 1 >gi 101338 pir A38326 UDPglucose--starch

glucosyltransferase (EC 2.4.1.11) 1 - yeast (Saccharomyces

cerevisiae) >gi\_172870 (M60919) glycogen synthase [Saccharomyces cerevisiae] >gi 836770 dbj BAA09254 (D50617) glycogen synthase isoform 1 [Saccharomyces cerevisiae] >gi 1122228 dbj BAA08032 (D44599) Glycogen

synthase GSY1 [Saccharomyces cerevisiae]

28224 Seq. No.

Contig ID 171254 1.R1040 5'-most EST eep700865645.h1

Seq. No. 28225

171298 1.R1040 Contig ID

5'-most EST g5057577

Seq. No. 28226

171319 1.R1040 Contig ID eep700865761.h1 5'-most EST

28227 Seq. No.

Contig ID 171328 1.R1040 5'-most EST eep700865773.h1

28228 Seq. No.

Contig ID 171346 1.R1040 5'-most EST  $eep700\overline{8}65813.h1$ 

Method BLASTX NCBI GI q4539327 BLAST score 172 8.0e-13 E value Match length 47

% identity 72

NCBI Description (AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No. 28229

Contig ID 171379 1.R1040 5'-most EST eep700865879.h1

Method BLASTX NCBI GI q3077640 BLAST score 846 6.0e-91 E value Match length 279 60 % identity

NCBI Description (AJ223151) O-methyltransferase [Prunus dulcis]

Seq. No. 28230

Contig ID 171388 1.R1040 5'-most EST pxt700945512.h1

Method BLASTX NCBI GI g3608261 BLAST score 275 E value 4.0e-24



Match length % identity

NCBI Description (AB017564) dof zinc finger protein [Arabidopsis thaliana]

Seq. No. 28231

171401 1.R1040 Contig ID 5'-most EST zsg701127091.h1

Method BLASTX NCBI GI g729273 BLAST score 432 E value 7.0e-43 Match length 111 % identity 77

CYPRO4 PROTEIN >gi\_322804\_pir\_\_S28592 cypro4 protein -cardoon >gi\_17959\_emb\_CAA49354\_ (X69672) cypro4 [Cynara NCBI Description

cardunculus]

Seq. No. 28232

171422 1.R1040 Contig ID 5'-most EST asn701136905.h1

Method BLASTX NCBI GI q2829887 BLAST score 164 E value 2.0e-11 Match length 105 % identity 37

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 28233

Contig ID 171429 1.R1040 5'-most EST eep700865982.h1

Method BLASTX NCBI GI q4314358 BLAST score 400 E value 4.0e-39 Match length 110 % identity

(AC006340) putative kinesin heavy chain protein NCBI Description

[Arabidopsis thaliana]

Seq. No. 28234

Contig ID 171468 1.R1040 5'-most EST awf700837144.h1

Seq. No. 28235

Contig ID 171486 1.R1040 5'-most EST fde700873229.h1

Seq. No. 28236

Contig ID 171494 1.R1040 5'-most EST eep700866113.h1

Method BLASTX NCBI GI g3236253 BLAST score 231 E value 6.0e-19 Match length 121 % identity 47



NCBI Description (AC004684) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 28237

Contig ID 171514\_1.R1040

5'-most EST jC-gmf102220115f12d1

Method BLASTN
NCBI GI 94336139
BLAST score 41
E value 1.0e-13

E value 1.0e-13
Match length 89
% identity 87

NCBI Description Arabidopsis thaliana serine/threonine protein phosphatase

2A 65 kDa A regulatory subunit alpha isoform gene, promoter

region

Seq. No. 28238

Contig ID 171520\_1.R1040

5'-most EST jC-gmle01810068e09a1

Method BLASTX
NCBI GI g2827160
BLAST score 149
E value 1.0e-09
Match length 103
% identity 28

NCBI Description (AF032667) rexo70 [Rattus norvegicus]

Seq. No. 28239

Contig ID 171524 1.R1040 5'-most EST eep700866164.h1

Seq. No. 28240

Contig ID 171534 1.R1040 5'-most EST zhf700965012.h1

Seq. No. 28241

Contig ID 171578\_1.R1040 5'-most EST zsg701120879.h1

Method BLASTX
NCBI GI g3810676
BLAST score 234
E value 1.0e-19
Match length 71
% identity 59

NCBI Description (AJ223357) SKOR [Arabidopsis thaliana]

Seq. No. 28242

Contig ID 171580\_1.R1040 5'-most EST eep700866259.h1

Seq. No. 28243

Contig ID 171584\_1.R1040 5'-most EST gsv701051394.h1

Method BLASTX
NCBI GI g4539291
BLAST score 340
E value 5.0e-32



Match length 129 % identity 53

NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

Seq. No. 28244

Contig ID 171592\_1.R1040 5'-most EST fde700875827.h1

Seq. No. 28245

Contig ID 171598\_1.R1040 5'-most EST epx701108483.h1

Method BLASTX
NCBI GI g2979543
BLAST score 254
E value 7.0e-22
Match length 102
% identity 53

NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28246

Contig ID 171603 1.R1040 5'-most EST jC-gmfl02220054c12a1

Seq. No. 28247

Contig ID 171605\_1.R1040 5'-most EST zsg701122004.h1

Method BLASTX
NCBI GI g3402690
BLAST score 166
E value 3.0e-19
Match length 107
% identity 52

NCBI Description (AC004697) hypothetical protein, 3' partial [Arabidopsis

thaliana]

Seq. No. 28248

Contig ID 171609\_1.R1040 5'-most EST eep700866305.h1

Seq. No. 28249

Contig ID 171627 1.R1040

5'-most EST g5058235

Seq. No. 28250

Contig ID 171631\_1.R1040 5'-most EST eep700866336.h1

Method BLASTX
NCBI GI g2131161
BLAST score 115
E value 8.0e-12
Match length 64
% identity 61

NCBI Description 4-nitrophenylphosphatase (EC 3.1.3.41) - yeast

(Saccharomyces cerevisiae) >gi\_1431400\_emb\_CAA98816\_

(Z74284) ORF YDL236w [Saccharomyces cerevisiae]

Seq. No. 28251



Contig ID 171634 1.R1040 5'-most EST jC-gmst02400065e10a2 Seq. No. 28252 Contig ID

171640 1.R1040

5'-most EST eep700866353.hl Seq. No. 28253

Contig ID 171693 1.R1040 5'-most EST eep700866907.hl

Seq. No. 28254 Contig ID 171693 2.R1040 5'-most EST uC-gmrominsoy215e09b1 Method BLASTX

NCBI GI q3395440 BLAST score 219 E value 2.0e-18 Match length 71 % identity 59

NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28255

Contig ID 171732 1.R1040 eep700866533.h1 5'-most EST

Seq. No. 28256

171734 1.R1040 Contig ID 5'-most EST rca700998788.hl

Seq. No. 28257

Contig ID 171742 1.R1040

5'-most EST jC-gmle01810087e03d1

Seq. No. 28258

Contig ID 171746 1.R1040 5'-most EST eep700866563.hl

Method BLASTX NCBI GI g3047085 BLAST score 277 E value 2.0e-24 Match length 121 % identity 76

NCBI Description (AF058914) No definition line found [Arabidopsis thaliana]

Seq. No. 28259

Contig ID 171746 2.R1040 5'-most EST jsh701069885.h1

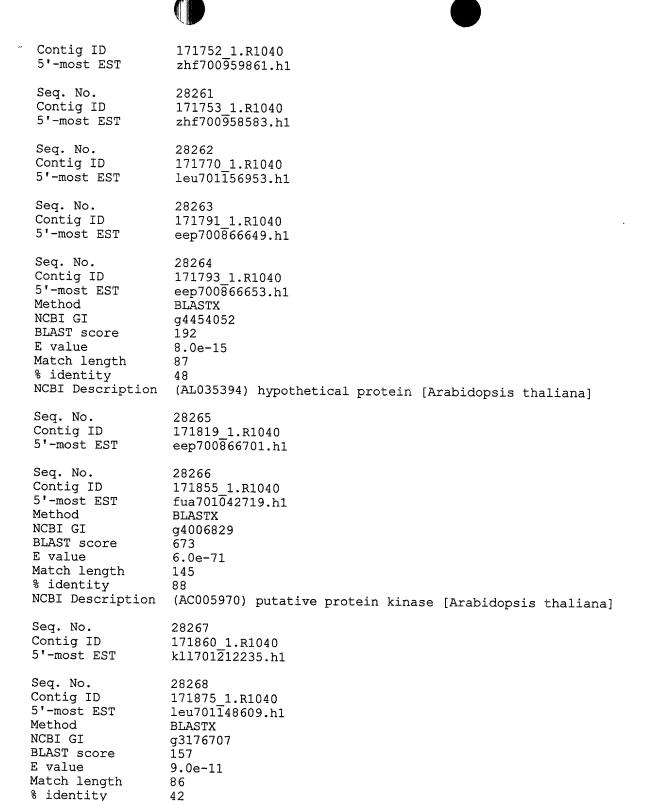
Method BLASTX NCBI GI g3047085 BLAST score 152 E value 3.0e-10Match length 40 % identity 65

NCBI Description (AF058914) No definition line found [Arabidopsis thaliana]

Seq. No. 28260

NCBI Description

thaliana]



(AC002392) putative proline-rich protein APG [Arabidopsis



```
Seq. No.
                   28269
Contig ID
                   171887 1.R1040
5'-most EST
                   eep700866850.h1
Method
                   BLASTX
NCBI GI
                   q4508079
BLAST score
                   417
E value
                   3.0e-41
Match length
                   98
                   77
% identity
NCBI Description
                  (AC005882) 66284 [Arabidopsis thaliana]
Seq. No.
                   28270
Contig ID
                   171889 1.R1040
5'-most EST
                   cks700764749.h1
Method
                   BLASTX
NCBI GI
                   g2252863
BLAST score
                   573
E value
                   3.0e-59
Match length
                   132
% identity
                   83
                   (AF013294) similar to nucleolin protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   28271
Contig ID
                   171890 1.R1040
5'-most EST
                   eep700866853.h1
Method
                   BLASTX
NCBI GI
                   q1841475
BLAST score
                   281
E value
                   2.0e-25
Match length
                   71
% identity
                   68
NCBI Description
                   (Y11105) Myb26 [Pisum sativum]
Seq. No.
                   28272
Contig ID
                   171894 1.R1040
5'-most EST
                   jC-gmst02400029g09a1
Method
                   BLASTX
NCBI GI
                  g3334162
BLAST score
                   200
E value
                  2.0e-15
Match length
                  117
% identity
                   35
                  DOWN SYNDROME CRITICAL REGION PROTEIN A
NCBI Description
                  >gi_2588993_dbj_BAA23270_ (AB001990) Dcra [Mus musculus]
Seq. No.
                  28273
Contig ID
                  171894 2.R1040
                  leu701149436.h1
                  BLASTX
                  g3334162
```

5'-most EST

Method NCBI GI BLAST score 221 E value 4.0e-18 Match length 87 % identity 44

NCBI Description DOWN SYNDROME CRITICAL REGION PROTEIN A

>gi 2588993 dbj\_BAA23270\_ (AB001990) Dcra [Mus musculus]

```
Seq. No.
                   28274
Contig ID
                   171907 1.R1040
5'-most EST
                   jC-gmst02400073f11a1
Seq. No.
                   28275
Contig ID
                   171908 1.R1040
5'-most EST
                   leu701146451.h1
Method
                   BLASTN
NCBI GI
                   q2143322
BLAST score
                   42
E value
                   2.0e-14
Match length
                   82
% identity
                   88
NCBI Description
                   P.deltoides chloroplast DNA for psbB operon
Seq. No.
                   28276
Contig ID
                   171916 1.R1040
5'-most EST
                   sat701002934.h1
Method
                   BLASTX
NCBI GI
                   q2760830
BLAST score
                   597
E value
                   3.0e-62
Match length
                   123
% identity
                   (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   28277
Contig ID
                   171917 1.R1040
5'-most EST
                   pmv700891158.h1
Seq. No.
                   28278
Contig ID
                   171929 1.R1040
5'-most EST
                   eep700867235.h1
Method
                   BLASTX
NCBI GI
                   g2346978
BLAST score
                   147
E value
                   1.0e-09
Match length
                   74
% identity
                   47
NCBI Description
                   (AB006601) ZPT2-14 [Petunia x hybrida]
Seq. No.
                  28279
Contig ID
                  171930 1.R1040
5'-most EST
                  eep700867282.h1
Method
                  BLASTX
NCBI GI
                  g4038055
BLAST score
                  261
E value
                  5.0e-23
```

Match length 88 % identity 58

(AC005897) putative cytochrome P450 [Arabidopsis thaliana] NCBI Description >gi\_4557077\_gb\_AAD22516.1\_AC007045 16 (AC007045) putative

cytochrome  $\overline{p}45\overline{0}$  [Arabidopsis thaliana]

Seq. No. 28280

E value

Match length

2.0e-41

174

```
Contig ID
                     171976 1.R1040
  5'-most EST
                     asn701140943.h1
  Seq. No.
                     28281
  Contig ID
                     171977 1.R1040
  5'-most EST
                     leu701156653.h1
  Method
                     BLASTX
 NCBI GI
                     g4454567
 BLAST score
                     124
 E value
                     3.0e-10
 Match length
                     118
 % identity
                     44
 NCBI Description (AF128407) lipase homolog [Arabidopsis thaliana]
 Seq. No.
                    28282
 Contig ID
                    171980 1.R1040
 5'-most EST
                    leu701\overline{1}46017.h1
 Seq. No.
                    28283
 Contig ID
                    172016 1.R1040
 5'-most EST
                    pmv700894106.h1
 Seq. No.
                    28284
 Contig ID
                    172026 1.R1040
 5'-most EST
                    eep700867125.hl
 Seq. No.
                    28285
 Contig ID
                    172036 1.R1040
 5'-most EST
                    uC-gmrominsoy170d05b1
Seq. No.
                    28286
Contig ID
                    172037 1.R1040
5'-most EST
                    eep700\overline{8}67149.h1
Method
                    BLASTX
NCBI GI
                    g1769903
BLAST score
                    164
E value
                    1.0e-11
Match length
                    82
% identity
                    41
NCBI Description
                   (X95738) proline transporter 2 [Arabidopsis thaliana]
Seq. No.
                   28287
Contig ID
                   172073 1.R1040
5'-most EST
                   jC-gmr002910026d02a1
Seq. No.
                   28288
Contig ID
                   172081_1.R1040
5'-most EST
                   eep700867239.h1
Seq. No.
                   28289
Contig ID
                   172086 1.R1040
5'-most EST
                   bth700848572.h1
Method
                   BLASTX
NCBI GI
                   q3402697
BLAST score
                   423
```



% identity 24

NCBI Description (AC004261) putative phosphatidylinositol-4-phosphate

5-kinase [Arabidopsis thaliana]

Seq. No. 28290

Contig ID 172145\_1.R1040 5'-most EST dpv701097666.h1

Seq. No. 28291

Contig ID 172159\_1.R1040 5'-most EST eep700867465.h1

Method BLASTX
NCBI GI g4099833
BLAST score 162
E value 2.0e-11
Match length 77
% identity 42

NCBI Description (U90265) bifunctional nuclease [Zinnia elegans]

Seq. No. 28292

Contig ID 172168\_1.R1040 5'-most EST eep700867487.h1

Seq. No. 28293

Contig ID 172173 1.R1040

5'-most EST  $jC-gmf\overline{1}02220148c08a1$ 

Method BLASTX
NCBI GI g4165861
BLAST score 536
E value 9.0e-55
Match length 164
% identity 29

NCBI Description (AF006603) histone deacetylase mHDA2 [Mus musculus]

Seq. No. 28294

Contig ID 172181 1.R1040

5'-most EST jC-gmro02910054a03d1

Seq. No. 28295

Contig ID 172192\_1.R1040 5'-most EST eep700867563.h1

Seq. No. 28296

Contig ID 172212 1.R1040 5'-most EST asn701131028.h1

Method BLASTX
NCBI GI g3775999
BLAST score 291
E value 2.0e-26
Match length 66
% identity 82

NCBI Description (AJ010463) RNA helicase [Arabidopsis thaliana]

Seq. No. 28297

Contig ID 172218\_1.R1040 5'-most EST eep700867656.h1



Seq. No. 28298

Contig ID 172224\_1.R1040 5'-most EST asn701137416.h1

Method BLASTX
NCBI GI g3511285
BLAST score 555
E value 3.0e-57
Match length 121
% identity 85

NCBI Description (AF081534) cellulose synthase [Populus alba x Populus

tremula]

Seq. No. 28299

Contig ID 172227\_1.R1040 5'-most EST eep700869572.h1

Seq. No. 28300

Contig ID 172245\_1.R1040 5'-most EST rlr700899532.h1

Method BLASTN
NCBI GI g1142620
BLAST score 150
E value 8.0e-79
Match length 358
% identity 89

NCBI Description Phaseolus vulgaris phaseolin G-box binding protein PG2

(PG2) mRNA, partial cds

Seq. No. 28301

Contig ID 172264\_1.R1040 5'-most EST eep700870273.h1

Seq. No. 28302

Contig ID 172267\_1.R1040 5'-most EST zsg701123293.h1

Seq. No. 28303

Contig ID 172278\_1.R1040 5'-most EST fua701040559.h1

Method BLASTX
NCBI GI g2507198
BLAST score 343
E value 3.0e-32
Match length 121
% identity 57

NCBI Description PROTEIN KINASE CEK1 >gi 1853976 dbj BAA06551 (D31773)

protein kinase [Schizosaccharomyces pombe]

Seq. No. 28304

Contig ID 172301\_1.R1040
5!-most FST iC-cmst02400043

5'-most EST jC-gmst02400043f07d1
Method BLASTX

NCBI GI g3341687 BLAST score 150 E value 1.0e-09 Match length 45 % identity 69



NCBI Description (AC003672) putative ras protein [Arabidopsis thaliana]

Seq. No. 28305

Contig ID 172304 1.R1040 5'-most EST crh700855002.h1

Seq. No. 28306

Contig ID 172305\_1.R1040 5'-most EST eep700867833.h1

Method BLASTX
NCBI GI g4454550
BLAST score 201
E value 1.0e-15
Match length 104
% identity 23

NCBI Description (AF113002) silencing mediator of retinoic acid and thyroid

hormone receptor beta [Mus musculus]

Seq. No. 28307

Contig ID 172318 1.R1040 5'-most EST leu701153303.h1

Seq. No. 28308

Contig ID 172335\_1.R1040 5'-most EST eep700867882.h1

Seq. No. 28309

Contig ID 172354\_1.R1040 5'-most EST eep700867926.h1

Method BLASTX
NCBI GI g4204283
BLAST score 271
E value 4.0e-24
Match length 71
% identity 72

NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 28310

Contig ID 172361\_1.R1040 5'-most EST pxt700941884.h1

Method BLASTX
NCBI GI g285741
BLAST score 228
E value 4.0e-19
Match length 87
% identity 56

NCBI Description (D14550) EDGP precursor [Daucus carota]

Seq. No. 28311

Contig ID 172373\_1.R1040 5'-most EST fua701038295.h1

Method BLASTX
NCBI GI g399427
BLAST score 519
E value 5.0e-53
Match length 121
% identity 78

4384



NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi\_99392\_pir\_\_S24996 phosphopyruvate hydratase (EC 4.2.1.11) - Chlamydomonas reinhardtii >gi\_18143\_emb\_CAA47043\_ (X66412) enolase

[Chlamydomonas reinhardtii]

Seq. No. 28312

Contig ID 172383 1.R1040 5'-most EST  $k11701\overline{2}13623.h1$ 

Seq. No. 28313

Contig ID 172388 1.R1040 5'-most EST eep700868002.h1

Method BLASTX NCBI GI g3063448 BLAST score 344 E value 1.0e-32 Match length 101 % identity

NCBI Description (AC003981) F22013.10 [Arabidopsis thaliana]

Seq. No. 28314

172398 1.R1040 Contig ID 5'-most EST rlr700902336.h1

Method BLASTX NCBI GI q1943751 BLAST score 726 E value 4.0e-77 Match length 149 % identity 95

NCBI Description (U93845) Arabidopsis thaliana ER-type calcium pump

protein, complete sequence >gi\_2078292 (U96455) ER-type

Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No. 28315

Contig ID 172412 1.R1040 5'-most EST zsg701117349.h1

Seq. No. 28316

Contig ID 172445 1.R1040 5'-most EST eep700868125.h1

Seq. No. 28317

Contig ID 172453 1.R1040 5'-most EST xpa700797315.h1

Method BLASTX NCBI GI g4102600 BLAST score 213 E value 2.0e-17 Match length 46 % identity

NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]

Seq. No. 28318

Contig ID 172480 1.R1040 5'-most EST eep700868196.h1

% identity

70

```
Seq. No.
                     28319
  Contig ID
                    172510 1.R1040
  5'-most EST
                    eep700868455.h1
  Seq. No.
                    28320
  Contig ID
                    172511 1.R1040
  5'-most EST
                    zhf700965043.h1
  Method
                    BLASTX
  NCBI GI
                    q3329368
: BLAST score
                    326
 E value
                    2.0e-30
 Match length
                    103
  % identity
                    64
 NCBI Description
                    (AF031244) nodulin-like protein [Arabidopsis thaliana]
 Seq. No.
                    28321
 Contig ID
                    172541 1.R1040
 5'-most EST
                    zhf700961577.hl
 Method
                    BLASTX
 NCBI GI
                    q2583118
 BLAST score
                    227
 E value
                    4.0e-28
 Match length
                    105
 % identity
                    66
 NCBI Description
                    (AC002387) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    28322
 Contig ID
                    172593 1.R1040
 5'-most EST
                    sat701007218.h2
 Seq. No.
                    28323
 Contig ID
                    172603 1.R1040
 5'-most EST
                    eep700868417.h1
 Method
                    BLASTX
 NCBI GI
                    g3287695
 BLAST score
                    454
 E value
                    5.0e-84
 Match length
                    316
 % identity
                    56
 NCBI Description
                    (AC003979) Similar to hypothetical protein C34B7.2
                    gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis
                    thaliana]
 Seq. No.
                    28324
 Contig ID
                    172630 1.R1040
 5'-most EST
                    dpv701097185.h1
 Seq. No.
                    28325
 Contig ID
                    172645 1.R1040
 5'-most EST
                    epx701104373.h1
 Method
                   BLASTX
 NCBI GI
                    g1710587
 BLAST score
                   194
 E value
                   3.0e-15
Match length
                   53
```

NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN PO >gi\_1196897 (L46848) acidic



## ribosomal protein PO [Glycine max]

```
Seq. No.
                  28326
                  172654 1.R1040
Contig ID
5'-most EST
                  jex700907645.h1
Method
                  BLASTX
NCBI GI
                  g4567197
BLAST score
                  172
E value
                  2.0e-12
Match length
                  37
% identity
NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]
                  28327
Seq. No.
Contig ID
                  172670 1.R1040
5'-most EST
                  jC-gmro02910007b10a1
Seq. No.
                  28328
                  172672 1.R1040
Contig ID
5'-most EST
                  gsv701048066.hl
Method
                  BLASTN
NCBI GI
                  g2624382
BLAST score
                  74
                  1.0e-33
E value
                  217
Match length
% identity
                  83
NCBI Description P.vulgaris mRNA for cinnamate 4-hydroxylase
Seq. No.
                  28329
                  172676 1.R1040
Contig ID
5'-most EST
                  eep700868519.hl
Method
                  BLASTX
NCBI GI
                  g2832304
BLAST score
                  181
E value
                  2.0e-13
Match length
                  93
% identity
                  38
NCBI Description (AF044489) receptor-like protein kinase [Oryza sativa]
Seq. No.
                  28330
Contig ID
                  172694 1.R1040
5'-most EST
                  eep700868542.h1
Seq. No.
                  28331
Contig ID
                  172703 1.R1040
5'-most EST
                  q4396761
Seq. No.
                  28332
Contig ID
                  172707 1.R1040
                  zhf700953295.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3928090
BLAST score
                  320
E value
                  9.0e-30
Match length
                  100
                  58
% identity
NCBI Description (AC005770) putative MTN3 protein [Arabidopsis thaliana]
```



Seq. No. 28333

Contig ID 172716 1.R1040 5'-most EST eep700868582.h1

Seq. No. 28334

Contig ID 172720 1.R1040

5'-most EST uC-gmrominsoy040f09b1

Method BLASTX NCBI GI a3287696 BLAST score 517 E value 1.0e-52 Match length 158 % identity 44

NCBI Description

(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb\_D86180 from Pisum sativum. This ORF may be

part of a larger gene that lies in the overlapping region.

[Arabidopsis thaliana]

Seq. No. 28335

172725 1.R1040 Contig ID 5'-most EST jex700905667.h1

Method BLASTX NCBI GI q2443886 BLAST score 156 4.0e-10 E value Match length 117 % identity 35

NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No. 28336

Contig ID 172738 1.R1040 5'-most EST eep700868615.h1

Seq. No. 28337

Contig ID 172748 1.R1040 5'-most EST pmv700890005.h1

Seq. No. 28338

Contig ID 172761 1.R1040 5'-most EST eep700868657.h1

Seq. No. 28339

Contig ID 172770 1.R1040

5'-most EST uC-gmrominsoy202h02b1

Seq. No. 28340

Contig ID 172773 1.R1040 5'-most EST eep700868688.h1

Seq. No. 28341

Contig ID 172798 1.R1040 5'-most EST eep700868740.hl

Method BLASTX NCBI GI g2191136 BLAST score 185 E value 4.0e-14



Match length 88 % identity 41

NCBI Description (AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A.

thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidopsis thaliana]

Seq. No. 28342

Contig ID 172811\_1.R1040 5'-most EST eep700868770.h1

Method BLASTX
NCBI GI g4580472
BLAST score 423
E value 5.0e-42
Match length 92

Match length 92 % identity 86

NCBI Description (AC006081) DNA binding protein; similar to CDC27 and nuclear

scaffold proteins [Arabidopsis thaliana]

Seq. No. 28343

Contig ID 172849 1.R1040

5'-most EST uC-gmflminsoy081h07b1

Seq. No. 28344

Contig ID 172907 1.R1040

5'-most EST jC-gmf102220063d07a1

Seq. No. 28345

Contig ID 172914\_1.R1040 5'-most EST eep700870123.h1

Seq. No. 28346

Contig ID 172932\_1.R1040 5'-most EST fC-gmro700846765d3 Method BLASTN

Method BLASTN
NCBI GI g1416513
BLAST score 56
E value 2.0e-22
Match length 112
% identity 88

NCBI Description Brassica napus mRNA for CTP:phosphocholine

cytidylyltransferase, complete cds

Seq. No. 28347

Contig ID 172955\_1.R1040 5'-most EST eep700869078.h1

Seq. No. 28348

Contig ID 172971\_1.R1040 5'-most EST eep700869104.h1

Seq. No. 28349

Contig ID 172982 1.R1040 5'-most EST eep700869123.h1

Seq. No. 28350

Contig ID 172995\_1.R1040



5'-most EST eep700869140.h1

Method BLASTX
NCBI GI g3482917
BLAST score 456
E value 9.0e-71
Match length 214
% identity 69

NCBI Description (AC003970) Similar to Glucose-6-phosphate dehydrogenases,

gi\_2276344, gi\_2829880, gi\_2352919 and others. [Arabidopsis

thaliana]

Seq. No. 28351

Contig ID 173013 1.R1040

5'-most EST g5678068
Method BLASTX
NCBI GI g3367568
BLAST score 272
E value 3.0e-36
Match length 117
% identity 62

NCBI Description (AL031135) protein kinase - like protein [Arabidopsis

thaliana]

Seq. No. 28352

Contig ID 173020 1.R1040 5'-most EST eep700869182.h1

Seq. No. 28353

Contig ID 173034\_1.R1040 5'-most EST leu701155874.h1

Method BLASTX
NCBI GI g2827631
BLAST score 420
E value 2.0e-41
Match length 95
% identity 85

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 28354

Contig ID 173048\_1.R1040

5'-most EST uC-gmrominsoy093d04b1

Method BLASTX
NCBI GI g3193306
BLAST score 403
E value 2.0e-39
Match length 116
% identity 70

NCBI Description (AF069300) contains similarity to Arabidopsis

membrane-associated salt-inducible-like protein

(GB:AL021637) [Arabidopsis thaliana]

Seq. No. 28355

Contig ID 173065\_1.R1040 5'-most EST eep700869336.h1

Seq. No. 28356

Contig ID 173085 1.R1040

```
5'-most EST
                   eep700869339.h1
Seq. No.
                   28357
Contig ID
                   173092 1.R1040
5'-most EST
                   uC-gmrominsoy264g09b1
Method
                   BLASTX
NCBI GI
                   g2191136
BLAST score
                   151
E value
                   8.0e-10
Match length
                   76
% identity
                   43
                   (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                   coded for by A. thaliana cDNA T46230; coded for by A.
                   thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
                   28358
Seq. No.
                   173102 1.R1040
Contig ID
5'-most EST
                   eep700869377.h1
Seq. No.
                   28359
Contig ID
                   173108 1.R1040
5'-most EST
                   g4300365
Seq. No.
                   28360
Contig ID
                   173127 1.R1040
5'-most EST
                   jC-gmro02910014a04d1
Seq. No.
                   28361
                   173149 1.R1040
Contig ID
5'-most EST
                   jC-gmf\(\bar{1}\)02220126g11a1
Seq. No.
                   28362
Contig ID
                   173150 1.R1040
5'-most EST
                  pmv700894867.h1
Method
                   BLASTX
NCBI GI
                   q1685005
BLAST score
                   390
E value
                   8.0e-38
Match length
                   132
% identity
NCBI Description
                  (U32644) immediate-early salicylate-induced
                  glucosyltransferase [Nicotiana tabacum]
Seq. No.
                  28363
Contig ID
                  173162 1.R1040
5'-most EST
                  jC-qmro02910009e07a1
Method
                  BLASTX
NCBI GI
                  g4249419
BLAST score
                  412
```

E value 4.0e-40 Match length 240 % identity 45

NCBI Description (AC006072) hypothetical protein, 3' partial [Arabidopsis

thaliana]

Seq. No. 28364



111

```
Contig ID
                   173176 1.R1040
5'-most EST
                   eep700869562.h1
Seq. No.
                   28365
                   173210 1.R1040
Contig ID
5'-most EST
                   g4313501
Method
                   BLASTX
NCBI GI
                   q1706189
BLAST score
                   186
E value
                   2.0e-13
```

% identity 35 NCBI Description

Match length

LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2) (TEA PROTEIN) (T-CELL EARLY ACTIVATION PROTEIN) (20.5) >gi\_627850\_pir\_ A54011 CAT1/ecoR protein - mouse >gi\_293315 (L11600) cationic amino acid transporter-2 [Mus

musculus] >gi 517493 (L29006) membrane protein [Mus

musculus!

Seq. No. 28366

Contig ID 173216 1.R1040

5'-most EST jC-gmro02910052h01a1

Seq. No. 28367

Contig ID 173220 1.R1040

5'-most EST jC-gmst02400056h01d1

Method BLASTX NCBI GI q3281867 BLAST score 183 E value 2.0e-13 Match length 42 % identity 79

(AL031004) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 28368

Contig ID 173220 2.R1040 5'-most EST eep700869660.h1

Method BLASTX NCBI GI g3281867 BLAST score 291 E value 1.0e-26 Match length 85 % identity

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 28369

Contig ID 173243 1.R1040 5'-most EST eep700869954.h1

Method BLASTX NCBI GI g1084334 BLAST score 367 E value 2.0e-35 Match length 92 % identity 78

NCBI Description calcium-dependent protein kinase (EC 2.7.1.-) 1 -

Arabidopsis thaliana >gi\_604880\_dbj\_BAA04829\_ (D21805) calcium-dependent protein kinase [Arabidopsis thaliana]

```
Seq. No.
                   28370
Contig ID
                   173253 1.R1040
5'-most EST
                   eep700869735.h1
Method
                   BLASTX
NCBI GI
                   g4038043
BLAST score
                   174
E value
                   2.0e-12
Match length
                   100
% identity
                   37
                   (AC005936) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   28371
Contig ID
                   173289 1.R1040
5'-most EST
                   eep700869833.h1
Seq. No.
                   28372
Contig ID
                   173305 1.R1040
5'-most EST
                   jC-gmle01810049a03d1
Method
                   BLASTX
NCBI GI
                   q3176715
BLAST score
                   240
E value
                   4.0e-20
Match length
                   69
% identity
                   65
NCBI Description
                   (AC002392) putative receptor-like protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   28373
Contig ID
                   173308 1.R1040
5'-most EST
                   zsq701124666.h1
Method
                   BLASTX
NCBI GI
                   q3687223
BLAST score
                   365
E value
                   7.0e-35
Match length
                   89
% identity
                   87
NCBI Description
                  (AC005169) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   28374
Contig ID
                   173326 1.R1040
5'-most EST
                   xzm700763704.h1
Method
                   BLASTX
NCBI GI
                   g4467124
BLAST score
                   505
E value
                   2.0e-51
Match length
                   116
% identity
                   73
NCBI Description
                   (AL035538) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   28375
Contig ID
                   173342 1.R1040
5'-most EST
                  uC-gmropic101b04b1
Method
                  BLASTX
NCBI GI
```

q2388577

303

BLAST score



E value 6.0e-28 Match length 92 % identity 62

(AC000098) Similar to Arabidopsis putative ion-channel NCBI Description PID:g2262157 (gb\_AC002329). [Arabidopsis thaliana]

Seq. No. 28376 Contig ID

173380 1.R1040 5'-most EST jex700908292.h1

Seq. No. 28377

Contig ID 173381 1.R1040 5'-most EST eep700869975.hl

Method BLASTX NCBI GI g3004552 BLAST score 358 E value 5.0e-34 Match length 127 % identity 57

(AC003673) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

28378 Contig ID 173430 1.R1040 5'-most EST hrw701058040.h1

Seq. No. 28379

Contig ID 173436 1.R1040

5'-most EST jC-gmst02400055d05a1 Method

BLASTX NCBI GI g1850546 BLAST score 206 E value 2.0e-16 Match length 83 % identity 57

NCBI Description (U88045) syntaxin related protein AtVam3p [Arabidopsis

thaliana]

Seq. No. 28380

Contig ID 173438 1.R1040 5'-most EST uC-gmropic101b08b1

Seq. No. 28381

Contig ID 173458 1.R1040 5'-most EST eep700870137.hl

28382 Seq. No.

Contig ID 173466 1.R1040 5'-most EST fua701036904.hl

Method BLASTX NCBI GI g3128187 BLAST score 166 E value 8.0e-12 Match length 53 % identity 58

NCBI Description (AC004521) putative beta-glucosidase [Arabidopsis thaliana]



Contig ID 173499 1.R1040 5'-most EST eep700870218.h1

Seq. No. 28384

Contig ID 173500\_1.R1040 5'-most EST uC-gmropic016e02b1

Seq. No. 28385

Contig ID 173526\_1.R1040 5'-most EST eep700870276.h1

Method BLASTX
NCBI GI g4490316
BLAST score 243
E value 4.0e-21
Match length 65
% identity 71

NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No. 28386

Contig ID 173527 1.R1040 5'-most EST zhf700958181.h1

Seq. No. 28387

Contig ID 173533\_1.R1040 5'-most EST jC-gmro02910027h12a1

Method BLASTX
NCBI GI g3885334
BLAST score 430
E value 1.0e-42
Match length 110
% identity 69

NCBI Description (AC005623) putative argonaute protein [Arabidopsis

thaliana]

Seq. No. 28388

Contig ID 173536\_1.R1040 5'-most EST eep700870290.h1

Method BLASTX
NCBI GI g2244814
BLAST score 378
E value 2.0e-36
Match length 115
% identity 62

NCBI Description (Z97336) protein kinase [Arabidopsis thaliana]

Seq. No. 28389

Contig ID 173555\_1.R1040 5'-most EST jC-gmle01810034b08a2

Method BLASTX
NCBI GI g2143290
BLAST score 202
E value 2.0e-15
Match length 162
% identity 33

NCBI Description (Z95972) hypothetical protein Rv0669c [Mycobacterium

tuberculosis]



Contig ID 173557\_1.R1040

5'-most EST  $g42602\overline{5}0$ 

Seq. No. 28391

Contig ID 173593 1.R1040 5'-most EST eep700870382.h1

Seq. No. 28392

Contig ID 173615\_1.R1040 5'-most EST eep700870429.h1

Seq. No. 28393

Contig ID 173622\_1.R1040 5'-most EST eep700870441.h1

Method BLASTX
NCBI GI g112947
BLAST score 258
E value 2.0e-22
Match length 102
% identity 43

NCBI Description AAC-RICH MRNA CLONE AAC3 PROTEIN >gi\_84121\_pir\_\_S05357

hypothetical protein (clone AAC3) - slime mold

(Dictyostelium discoideum) (fragment)

 $>gi_7176_emb_CAA34531_ (X16524)$  coding region (AA 1 - 437)

[Dictyostelium discoideum]

Seq. No. 28394

Contig ID 173632 1.R1040 5'-most EST gsv701050008.h1

Method BLASTX
NCBI GI g2262177
BLAST score 530
E value 3.0e-54
Match length 138
% identity 70

NCBI Description (AC002329) hypothetical protein similar to T18A10.3

[Arabidopsis thaliana]

Seq. No. 28395

Contig ID 173661\_1.R1040 5'-most EST zlv700807517.h1

Seq. No. 28396

Contig ID 173705\_1.R1040 5'-most EST uC-gmropic042a04b1

Seq. No. 28397

Contig ID 173728\_1.R1040 5'-most EST zlv700807612.h1

Method BLASTX
NCBI GI g3402758
BLAST score 428
E value 2.0e-45
Match length 152
% identity 62

NCBI Description (AL031187) serine/threonine kinase - like protein



## [Arabidopsis thaliana]

Seq. No. 28398

Contig ID 173787 1.R1040 5'-most EST gsf700698326.h1

Method BLASTX
NCBI GI g3785989
BLAST score 195
E value 3.0e-15
Match length 107
% identity 48

NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]

Seq. No. 28399

Contig ID 173806\_1.R1040 5'-most EST gsf700698355.h1

Seq. No. 28400

Contig ID 173821 1.R1040 5'-most EST xpa700795033.h1

Seq. No. 28401

Contig ID 173822\_1.R1040

5'-most EST jC-gmro02910016g07d1

Method BLASTX
NCBI GI g2262100
BLAST score 314
E value 8.0e-29
Match length 71
% identity 75

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 28402

Contig ID 173829\_1.R1040 5'-most EST dpv701102034.h1

Method BLASTX
NCBI GI g2129635
BLAST score 411
E value 5.0e-40
Match length 188
% identity 50

NCBI Description light repressible receptor protein kinase - Arabidopsis

thaliana >gi\_1321686\_emb\_CAA66376\_ (X97774) light

repressible receptor protein kinase [Arabidopsis thaliana]

Seq. No. 28403

Contig ID 173864\_1.R1040 5'-most EST fC-gmro700698445a1

Method BLASTX
NCBI GI g2224911
BLAST score 225
E value 3.0e-18
Match length 145
% identity 39

NCBI Description (U93048) somatic embryogenesis receptor-like kinase [Daucus

carota]



Contig ID 173878\_1.R1040 5'-most EST gsf700698471.h1

Seq. No. 28405

Contig ID 173897\_1.R1040 5'-most EST leu701150681.h1

Method BLASTX
NCBI GI g3947733
BLAST score 168
E value 3.0e-14
Match length 93
% identity 47

NCBI Description (AJ009719) NL25 [Solanum tuberosum]

Seq. No. 28406

Contig ID 173905\_1.R1040 5'-most EST zsg701124722.h1

Seq. No. 28407

Contig ID 173912 1.R1040

5'-most EST uC-gmflminsoy061a05b1

Method BLASTN NCBI GI g4159706 BLAST score 37

E value 4.0e-11 Match length 192 % identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGL6, complete sequence [Arabidopsis thaliana]

Seq. No. 28408

Contig ID 174024\_1.R1040 5'-most EST zhf700952960.h1

Seq. No. 28409

Contig ID 174026 1.R1040

5'-most EST uC-gmrominsoy198f01b1

Method BLASTN
NCBI GI g1370171
BLAST score 131
E value 2.0e-67
Match length 259
% identity 88

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB1X

Seq. No. 28410

Contig ID 174088\_1.R1040 5'-most EST xpa700792630.h1

Seq. No. 28411

Contig ID 174089\_1.R1040 5'-most EST bth700844710.h1

Method BLASTX
NCBI GI g3164222
BLAST score 288
E value 9.0e-26

```
Match length
                   90
% identity
                   61
NCBI Description
                   (AB008518) RMA1 [Arabidopsis thaliana] >qi 4206205
                   (AF071527) RMA1 RING zinc finger protein [Arabidopsis
                   thaliana]
Seq. No.
                   28412
Contig ID
                   174089 3.R1040
5'-most EST
                   xpa700792631.h1
Seq. No.
                   28413
Contig ID
                   174096 1.R1040
5'-most EST
                   uC-gmflminsoy097f12b1
Method
                   BLASTX
NCBI GI
                   g2909781
BLAST score
                   234
E value
                   1.0e-38
Match length
                   118
% identity
                   71
                   (AF020288) MgATP-energized glutathione S-conjugate pump
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   28414
Contig ID
                   174107 1.R1040
5'-most EST
                   g5606668
Method
                   BLASTX
NCBI GI
                   g2505877
BLAST score
                   323
E value
                   8.0e-30
Match length
                   195
% identity
                   42
NCBI Description
                   (Y12776) dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   28415
Contig ID
                   174146 1.R1040
5'-most EST
                   xpa700797244.h1
Seq. No.
                   28416
Contig ID
                   174147 1.R1040
5'-most EST
                  xpa700792742.h1
Seq. No.
                  28417
Contig ID
                  174192 1.R1040
5'-most EST
                  jC-gmro02910049a02a1
Seq. No.
                  28418
Contig ID
                  174194 1.R1040
5'-most EST
                  jC-gmle01810094g03a1
Method
                  BLASTX
```

NCBI GI g4092774
BLAST score 268
E value 2.0e-23
Match length 134
% identity 43

NCBI Description (AF105140) disease resistance gene homolog 9N [Brassica

napus]



Contig ID 174205\_1.R1040 5'-most EST xpa700792836.h1

Method BLASTX
NCBI GI g3461831
BLAST score 244
E value 9.0e-21
Match length 61
% identity 75

NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]

Seq. No. 28420

Contig ID 174217\_1.R1040 5'-most EST bth700846982.h1

Method BLASTX
NCBI GI g2894603
BLAST score 339
E value 9.0e-32
Match length 103
% identity 41

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 28421

Contig ID 174223\_1.R1040 5'-most EST xpa700792871.h1

Seq. No. 28422

Contig ID 174225\_1.R1040 5'-most EST uC-gmronoir012d05b1

Seq. No. 28423

Contig ID 174232\_1.R1040 5'-most EST dpv701101304.h1

Seq. No. 28424

Contig ID 174241\_1.R1040 5'-most EST xpa700792912.h1

Method BLASTN
NCBI GI g516102
BLAST score 361
E value 0.0e+00
Match length 492
% identity 96

NCBI Description Soybean phytochrome B (phyB) gene exons 1-5, complete cds

Seq. No. 28425

Contig ID 174243\_1.R1040 5'-most EST pxt700945748.h1

Method BLASTN
NCBI GI g3510247
BLAST score 39
E value 1.0e-12
Match length 71
% identity 89

NCBI Description Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence, complete sequence [Arabidopsis thaliana]



28426 Seq. No. Contig ID 174246 1.R1040 5'-most EST xpa700792922.h1 Seq. No. 28427 174252 1.R1040 Contig ID 5'-most EST xpa700792933.h1 28428 Seq. No. 174266 1.R1040 Contig ID sat701005932.h1 5'-most EST Seq. No. 28429 174295 1.R1040 Contig ID 5'-most EST uC-gmflminsoy020c09b1 28430 Seq. No. 174299 1.R1040 Contig ID 5'-most EST sat701013788.h1 Method BLASTX g3646451 NCBI GI BLAST score 154 E value 4.0e-10 130 Match length 36 % identity NCBI Description (AL031603) mRNA cap methyltransferase [Schizosaccharomyces pombe] 28431 Seq. No. Contig ID 174302 1.R1040 5'-most EST xpa700793016.h1 Seq. No. 28432 174337 1.R1040 Contig ID 5'-most EST sat701009233.h1 Method BLASTX g3822036 NCBI GI BLAST score 354 E value 4.0e-33 191 Match length % identity 42 NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays] 28433 Seq. No. 174356 1.R1040 Contig ID 5'-most EST xpa700793402.h1 Method BLASTN NCBI GI g3063438 BLAST score 71 E value 6.0e-32 Match length 183 % identity 85 NCBI Description Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No. 28434

Contig ID 174384\_1.R1040

NCBI Description

ananassa]



```
kl1701212438.hl
5'-most EST
Method
                  BLASTX
                  q3075397
NCBI GI
                  169
BLAST score
                  1.0e-11
E value
Match length
                  133
% identity
                  34
NCBI Description (AC004484) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  28435
                  174390 1.R1040
Contig ID
5'-most EST
                  hrw701063062.hl
Seq. No.
                  28436
                  174403 1.R1040
Contig ID
5'-most EST
                  xpa700793202.hl
Seq. No.
                  28437
                  174423 1.R1040
Config ID
5'-most EST
                  xpa700793236.hl
Method
                  BLASTX
NCBI GI
                  g2511715
BLAST score
                   682
                   6.0e-72
E value
                  175
Match length
                  74
% identity
NCBI Description (AF019380) putative phosphatidylinositol-4-phosphate
                  5-kinase [Arabidopsis thaliana]
Seq. No.
                  28438
Contig ID
                  174436 1.R1040
5'-most EST
                  xpa700793265.hl
                  28439
Seq. No.
Contig ID
                  174452 1.R1040
5'-most EST
                  xpa700793295.h1
Method
                  BLASTX
NCBI GI
                  g4097522
BLAST score
                  317
                  5.0e-29
E value
Match length
                  131
% identity
                  51
NCBI Description
                  (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
                  ananassa]
Seq. No.
                  28440
Contig ID
                   174452 2.R1040
5'-most EST
                   jC-gmf102220091a11a1
Method
                  BLASTX
NCBI GI
                   g4097522
BLAST score
                  204
E value
                   5.0e-16
Match length
                  68
% identity
                   62
```

(U63534) cinnamyl alcohol dehydrogenase [Fragaria x



Contig ID 174467\_1.R1040

5'-most EST jC-gmst02400011f04a1

Seq. No. 28442

Contig ID 174470\_1.R1040

5'-most EST jC-gmle01810086a06a1

Method BLASTX
NCBI GI g2598573
BLAST score 161
E value 8.0e-11
Match length 89

% identity 43

NCBI Description (Y15292) MtN26 [Medicago truncatula]

Seq. No. 28443

Contig ID 174474\_1.R1040 5'-most EST leu701148768.h1

Seq. No. 28444

Contig ID 174490\_1.R1040 5'-most EST xpa700794557.h1

Seq. No. 28445

Contig ID 174499\_1.R1040 5'-most EST uC-gmropic019g08b1

Seq. No. 28446

Contig ID 174501 1.R1040

5'-most EST jC-gmle01810087a06a1

Method BLASTX
NCBI GI g2208988
BLAST score 392
E value 6.0e-38
Match length 91
% identity 75

NCBI Description (Y10117) signal recognition particle subunit 9 [Zea mays]

Seq. No. 28447

Contig ID 174582\_1.R1040 5'-most EST xpa700793537.h1

Seq. No. 28448

Contig ID 174593\_1.R1040 5'-most EST xpa700793551.h1

Seq. No. 28449

Contig ID 174641\_1.R1040 5'-most EST xpa700793647.h1

Seq. No. 28450

Contig ID 174654\_1.R1040 5'-most EST pmv700892326.h1

Seq. No. 28451

Contig ID 174654\_2.R1040

5'-most EST uC-gmflminsoy062e06b1

Contig ID

28460

174913 1.R1040



```
Seq. No.
                  28452
                  174688 1.R1040
Contig ID
5'-most EST
                  xpa700793734.hl
                  BLASTX
Method
NCBI GI
                  q3869278
BLAST score
                  226
E value
                  2.0e-18
Match length
                  89
% identity
                  52
NCBI Description (AF058285) nicotinamidase/pyrazinamidase [Mycobacterium
                  smegmatis]
Seq. No.
                  28453
                  174723 1.R1040
Contig ID
5'-most EST
                  kl1701205451.hl
                   28454
Seq. No.
                  174758_1.R1040
Contig ID
5'-most EST
                  g4313318
Method
                  BLASTX
NCBI GI
                  g2443329
                  580
BLAST score
E value
                  8.0e-60
                  221
Match length
% identity
                  55
NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]
                   28455
Seq. No.
Contig ID
                  174771 1.R1040
5'-most EST
                  asn701136955.hl
                  28456
Seq. No.
                  174786 1.R1040
Contig ID
5'-most EST
                  xpa700793966.hl
Method
                  BLASTX
NCBI GI
                  g1724100
BLAST score
                  175
E value
                   6.0e-13
Match length
                  76
                  43
% identity
NCBI Description (U79765) porin [Mesembryanthemum crystallinum]
                   28457
Seq. No.
Contig ID
                   174845 1.R1040
5'-most EST
                  dpv701097293.hl
Seq. No.
                   28458
                   174873 1.R1040
Contig ID
5'-most EST
                  xpa700794112.hl
Seq. No.
                   28459
                  174896 1.R1040
Contig ID
5'-most EST
                  xpa700794163.hl
```



```
xpa700794190.h1
5'-most EST
                  BLASTX
Method
                  g3288817
NCBI GI
                  142
BLAST score
                  9.0e-09
E value
                  82
Match length
                  35
% identity
                   (AF058922) GLE1 [Homo sapiens]
NCBI Description
                  >gi_4557627_ref_NP_001490.1_pGLE1L_ GLE1-like, RNA export
                  mediator
                  28461
Seq. No.
                  174932 1.R1040
Contig ID
                  xpa700794222.hl
5'-most EST
                  BLASTX
Method
                   g4454468
NCBI GI
                   279
BLAST score
                   4.0e-25
E value
                   84
Match length
                   58
% identity
                   (AC006234) putative NADH dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   28462
Seq. No.
                   174937 1.R1040
Contig ID
                   xpa700794227.h1
5'-most EST
                   BLASTX
Method
                   g3885339
NCBI GI
                   157
BLAST score
                   1.0e-10
E value
                   44
Match length
                   75
% identity
                  (AC005623) putative bzip protein [Arabidopsis thaliana]
NCBI Description
                   28463
Seq. No.
                   174964 1.R1040
Contig ID
                   jC-gmle01810085e08a1
5'-most EST
                   BLASTX
Method
                   g4432867
NCBI GI
                   166
BLAST score
                   2.0e-11
E value
                   41
Match length
                   66
% identity
                   (AC006300) putative dnaJ-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   28464
Seq. No.
                   174981 1.R1040
Contig ID
```

zhf700962440.h1 5'-most EST

28465 Seq. No.

174993 1.R1040 Contig ID crh700850729.h1 5'-most EST

Seq. No. 28466

174998 1.R1040 Contig ID 5'-most EST xpa700794641.hl



28467 Seq. No. 175057 1.R1040 Contig ID xpa700794496.hl 5'-most EST 28468 Seq. No. 175077 1.R1040 Contig ID dpv701099318.hl 5'-most EST BLASTX Method g2130024 NCBI GI 332 BLAST score 5.0e-31 E value 111 Match length 58 % identity DNA-binding protein ABF2 - wild oat NCBI Description >gi\_1159879\_emb\_CAA88331\_ (Z48431) DNA-binding protein [Avena fatua] 28469 Seq. No. 175084 1.R1040 Contig ID bth700847836.h1 5'-most EST 28470 Seq. No. 175086 1.R1040 Contig ID xpa700794548.h15'-most EST Seq. No. 28471 175093 1.R1040 Contig ID crh700854472.h1 5'-most EST 28472 Seq. No. 175100 1.R1040 Contig ID dpv701103314.hl 5'-most EST 28473 Seq. No. 175108 1.R1040 Contig ID hrw701059917.hl 5'-most EST BLASTX Method g2134385 NCBI GI 638 BLAST score 1.0e-66 E value 170 Match length 69 % identity NCBI Description protein kinase - chicken >gi\_571460 (U16656) protein kinase [Gallus gallus] 28474 Seq. No. 175127 1.R1040 Contig ID xpa700794634.hl 5'-most EST

Method BLASTX
NCBI GI g2570342
BLAST score 355
E value 4.0e-34
Match length 91
% identity 69

NCBI Description (U90929) glyoxalase II cytoplasmic isozyme [Arabidopsis

thaliana]

Contig ID

5'-most EST



```
28475
Seq. No.
Contig ID
                  175129 1.R1040
5'-most EST
                  uC-gmropic098a10b1
                  28476
Seq. No.
Contig ID
                  175140_1.R1040
                  fde700873132.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3068717
BLAST score
                  424
E value
                  5.0e-42
Match length
                  98
                  79
% identity
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                  28477
                  175147_1.R1040
Contig ID
5'-most EST
                  jC-gmst02400030h07a1
                  BLASTX
Method
NCBI GI
                  g1669591
                  520
BLAST score
                  1.0e-52
E value
                  155
Match length
                  63
% identity
NCBI Description (D88742) O-methyltransferase [Glycyrrhiza echinata]
                  28478
Seq. No.
                  175151 1.R1040
Contig ID
5'-most EST
                  zzp700831230.hl
Seq. No.
                  28479
Contig ID
                  175199 1.R1040
5'-most EST
                  xpa700794766.hl
Method
                  BLASTX
                  g1388078
NCBI GI
BLAST score
                  191
E value
                  9.0e-15
Match length
                  62
                  52
% identity
NCBI Description (U35826) thioredoxin h [Arabidopsis thaliana]
Seq. No.
                  28480
Contig ID
                  175230 1.R1040
5'-most EST
                  xpa700794824.h1
Method
                  BLASTX
NCBI GI
                  g2961348
BLAST score
                  271
                  3.0e-24
E value
                  83
Match length
% identity
NCBI Description (AL022140) putative protein [Arabidopsis thaliana]
Seq. No.
                  28481
```

175270 1.R1040

xpa700795083.hl

 $\mathcal{J}_{I}^{\pm}[-$ 



Seq. No. 175271 1.R1040 Contig ID 5'-most EST xpa700794883.h1 28483 Seq. No. 175334 1.R1040 Contig ID uC-gmrominsoy110a04b1 5'-most EST 28484 Seq. No. 175389 1.R1040 Contig ID jC-gmle01810087e06d1 5'-most EST 28485 Seq. No. 175390 1.R1040 Contig ID xpa700795801.h1 5'-most EST BLASTX Method g3047116 NCBI GI 453 BLAST score 2.0e-45E value 93 Match length 92 % identity (AF058919) No definition line found [Arabidopsis thaliana] NCBI Description 28486 Seq. No. 175444 1.R1040 Contig ID bth700845016.hl 5'-most EST 28487 Seq. No. 175465 1.R1040 Contig ID 5'-most EST jC-gmf102220127d05d1 Seq. No. 28488 175465 2.R1040 Contig ID xpa700795266.h1 5'-most EST 28489 Seq. No. 175483 1.R1040 Contig ID uC-gmflminsoy049d09b1 5'-most EST BLASTX Method q2443880 NCBI GI BLAST score 159 1.0e-10 E value 44 Match length 68 % identity NCBI Description (AC002294) Hypothetical protein [Arabidopsis thaliana] 28490 Seq. No.

175509 1.R1040 Contig ID rlr700898432.h1 5'-most EST

BLASTX Method q4432839 NCBI GI BLAST score 357 5.0e-34 E value 130 Match length % identity

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]



```
28491
Seq. No.
                  175586 1.R1040
Contig ID
                  uC-gmropic099e01b1
5'-most EST
                  BLASTN
Method
                  g347452
NCBI GI
                  60
BLAST score
                  6.0e-25
E value
                  300
Match length
                  20
% identity
                  Soybean hydroxyproline-rich glycoprotein (sbHRGP3) mRNA,
NCBI Description
                  partial cds
                  28492
Seq. No.
                  175687 1.R1040
Contia ID
                  xpa700795752.h1
5'-most EST
```

175690\_1.R1040 Contig ID 5'-most EST zsg701120031.hl

28494 Seq. No. Contig ID

175711 1.R1040 5'-most EST jC-qmf102220104g12d1

Method BLASTX q393707 NCBI GI 205 BLAST score 3.0e-16 E value Match length 42 % identity 93

(X67696) acetyl-CoA acyltransferase [Cucumis sativus] NCBI Description

28495 Seq. No.

175757 1.R1040 Contig ID xpa700795893.hl 5'-most EST

28496 Seq. No.

175763 1.R1040 Contig ID xpa700795943.hl 5'-most EST

BLASTX Method q3688173 NCBI GI 409 BLAST score 4.0e-40 E value 123 Match length 64 % identity

(AL031804) putative protein [Arabidopsis thaliana] NCBI Description

28497 Seq. No.

175764 1.R1040 Contig ID kl1701205492.hl 5'-most EST

28498 Seq. No.

175779 1.R1040 Contig ID jC-gmst02400028d08a1 5'-most EST

28499 Seq. No.

175805 1.R1040 Contig ID uC-gmronoir073g02b1 5'-most EST

Bullion 1975 .



Seq. No. 28500 Contig ID 175813\_1.

Contig ID 175813\_1.R1040 5'-most EST xpa700796037.h1

Method BLASTX
NCBI GI g3850584
BLAST score 278
E value 7.0e-25
Match length 79

% identity 71 NCBI Description (AC005278) ESTs gb\_H37641 and gb\_AA651422 come from this

gene. [Arabidopsis thaliana]

Seq. No. 28501

Contig ID 175818 1.R1040 5'-most EST bth700843582.h1

Seq. No. 28502

Contig ID 175830\_1.R1040

5'-most EST uC-gmrominsoy145g03b1

Seq. No. 28503

Contig ID 175881\_1.R1040 5'-most EST rca701002319.h1

Method BLASTX
NCBI GI 94249384
BLAST score 330
E value 1.0e-30
Match length 124
% identity 54

NCBI Description (AC005966) Similar to gi\_4056506 F3G5.25 nodulin-like

protein from Arabidopsis thaliana BAC gb\_AC005896.

[Arabidopsis thaliana]

Seq. No. 28504

Contig ID 175896 1.R1040 5'-most EST xpa700796213.h1

Seq. No. 28505

Contig ID 175903\_1.R1040 5'-most EST epx701104094.h1

Method BLASTN
NCBI GI g1628472
BLAST score 190
E value 1.0e-103
Match length 258
% identity 93

NCBI Description Soybean mosiac virus mRNA for NIb and coat protein

Seq. No. 28506

Contig ID 175907\_1.R1040 5'-most EST uC-gmropic021c01b1

Seq. No. 28507

Contig ID 175907\_2.R1040 5'-most EST bth700847615.h1



Seq. No. 175924 1.R1040 Contig ID 5'-most EST uC-gmropic031f10b1 28509 Seq. No. 175942 1.R1040 Contig ID xpa700796325.h1 5'-most EST BLASTX Method NCBI GI g4467148 237 BLAST score 5.0e-20 E value 112 Match length 53 % identity NCBI Description (AL035540) putative protein [Arabidopsis thaliana] 28510 Seq. No. 175947 1.R1040 Contig ID uC-gmflminsoy059f11b1 5'-most EST BLASTX Method q3319682 NCBI GI 625 BLAST score E value 2.0e-65 Match length 147 23 % identity NCBI Description (Y17720) SPINDLY protein [Petunia x hybrida] 28511 Seq. No. 175951 1.R1040 Contig ID sat701008991.h1 5'-most EST BLASTN Method NCBI GI g2246441 BLAST score 97 2.0e-47 E value 221 Match length 86 % identity NCBI Description Pisum sativum farnesyltransferase alpha subunit mRNA, complete cds 28512 Seq. No. 175974 1.R1040 Contig ID 5'-most EST xpa700796432.h1 Method BLASTX

NCBI GI g3063445 308 BLAST score E value 5.0e-28 174 Match length

NCBI Description (AC003981) F22013.7 [Arabidopsis thaliana]

28513 Seq. No.

% identity

175980 1.R1040 Contig ID

5'-most EST uC-gmflminsoy031g08b1

28514 Seq. No.

Contig ID 175983 1.R1040 5'-most EST xpa700796455.hl



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28515
Seq. No.
                  175989 1.R1040
Contig ID
                  xpa700796471.hl
5'-most EST
                  BLASTX
Method
                  g2288887
NCBI GI
BLAST score
                  257
                  1.0e-22
E value
                  74
Match length
                  66
% identity
                  (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis
NCBI Description
                  thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate
                  diphosphate decarboxylase [Arabidopsis thaliana]
                  >qi 3786002 (AC005499) mevalonate diphosphate decarboxylase
                   [Arabidopsis thaliana]
                  28516
Seq. No.
                  176000 1.R1040
Contig ID
                  xpa700796504.hl
5'-most EST
                  28517
Seq. No.
                  176040 1.R1040
Contig ID
                  xpa700796593.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1928886
                   233
BLAST score
                   1.0e-19
E value
                   76
Match length
                   58
% identity
                  (U92010) lin-10 protein homolog [Rattus norvegicus]
NCBI Description
                   28518
Seq. No.
                   176060 1.R1040
Contig ID
5'-most EST
                   xpa700796633.h1
                   28519
Seq. No.
                   176085 1.R1040
Contiq ID
                   jC-gmle01810018a06a2
5'-most EST
                   28520
Seq. No.
                   176100 1.R1040
Contig ID
                   uC-gmronoir006d12b1
5'-most EST
                   BLASTX
Method
                   g1498731
NCBI GI
                   527
BLAST score
                   2.0e-53
E value
                   155
Match length
% identity
                  (U64806) pathogenesis-related protein PR1 [Brassica napus]
NCBI Description
```

Contig ID 176115\_1.R1040 5'-most EST gsv701047079.h1

Seq. No. 28522

Contig ID 176127\_1.R1040

5'-most EST g5677573 Method BLASTX



NCBI GI g3242708 BLAST score 404 E value 3.0e-39 Match length 196 % identity 45

NCBI Description (AC003040) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 28523

Contig ID 176133\_1.R1040 5'-most EST xpa700797096.h1

Method BLASTX
NCBI GI g3822223
BLAST score 543
E value 1.0e-55
Match length 141
% identity 69

NCBI Description (AF077955) branched-chain alpha keto-acid dehydrogenase E1

alpha subunit [Arabidopsis thaliana]

Seq. No. 28524

Contig ID 176158 1.R1040 5'-most EST xpa700796894.h1

Seq. No. 28525

Contig ID 176166 1.R1040

5'-most EST g4306800
Method BLASTX
NCBI GI g3258575
BLAST score 672
E value 2.0e-70
Match length 279
% identity 54

NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 28526

Contig ID 176215 1.R1040

5'-most EST uC-gmrominsoy165g09b1

Seq. No. 28527

Contig ID 176231\_1.R1040 5'-most EST xpa700797085.h1

Method BLASTX
NCBI GI g4006896
BLAST score 178
E value 8.0e-13
Match length 131
% identity 37

NCBI Description (Z99708) SCARECROW-like protein [Arabidopsis thaliana]

Seq. No. 28528

Contig ID 176287\_1.R1040 5'-most EST zsg701117806.h2

Method BLASTX
NCBI GI g434759
BLAST score 1130
E value 1.0e-124



Match length 266 % identity 78

NCBI Description (D21163) similar to human elongation factor 2 mRNA (HSEF2).

[Homo sapiens]

Seq. No. 28529

Contig ID 176298\_1.R1040 5'-most EST xpa700797257.h1

Method BLASTX
NCBI GI g2104536
BLAST score 464
E value 1.0e-46
Match length 124
% identity 65

NCBI Description (AF001308) predicted glycosyl transferase [Arabidopsis

thaliana]

Seq. No. 28530

Contig ID 176299\_1.R1040 5'-most EST zzp700834854.h1

Method BLASTX
NCBI GI g2789660
BLAST score 337
E value 6.0e-40
Match length 107
% identity 79

NCBI Description (AF040102) p105 [Arabidopsis thaliana]

Seq. No. 28531

Contig ID 176380\_1.R1040

5'-most EST uC-gmflminsoy002a07b1

Seq. No. 28532

Contig ID 176408\_1.R1040 5'-most EST fua701037928.h1

Method BLASTX
NCBI GI g4158219
BLAST score 687
E value 3.0e-98
Match length 271
% identity 65

NCBI Description (Y18623) amylogenin [Oryza sativa]

Seq. No. 28533

Contig ID 176427\_1.R1040 5'-most EST sat701014313.h1

Seq. No. 28534

Contig ID 176432 1.R1040 5'-most EST gsv701050659.h1

Seq. No. 28535

Contig ID 176512\_1.R1040

5'-most EST uC-gmrominsoy027a11b1

Method BLASTX NCBI GI g2346966 BLAST score 158



E value 2.0e-10 Match length 47 % identity 68

NCBI Description (AB004871) CPC [Arabidopsis thaliana]

>gi\_4559383\_gb\_AAD23043.1\_AC006526\_8 (AC006526) putative

DNA binding protein CPC [Arabidopsis thaliana]

Seq. No. 28536

Contig ID 176528\_1.R1040

5'-most EST jC-gmst02400004c12d1

Seq. No. 28537

Contig ID 176570\_1.R1040 5'-most EST xpa700797851.h1

Method BLASTX
NCBI GI g3033391
BLAST score 284
E value 7.0e-26
Match length 78
% identity 72

NCBI Description (AC004238) putative amino acid transporter [Arabidopsis

thaliana]

Seq. No. 28538

Contig ID 176584\_1.R1040 5'-most EST dpv701097015.h1

Method BLASTX
NCBI GI g3941524
BLAST score 299
E value 2.0e-27
Match length 68
% identity 76

NCBI Description (AF062916) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 28539

Contig ID 176611\_1.R1040 5'-most EST xpa700797933.h1

Seq. No. 28540

Contig ID 176614 1.R1040 5'-most EST xpa700797938.h1

Method BLASTX
NCBI GI g2894600
BLAST score 162
E value 3.0e-11
Match length 81
% identity 36

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 28541

Contig ID 176739\_1.R1040 5'-most EST uC-gmronoir062h08b1

Seq. No. 28542

Contig ID 176784 1.R1040 5'-most EST xpa700798275.h1



 Seq. No.
 28543

 Contig ID
 176809\_1.R1040

 5'-most EST
 uC-gmflminsoy109g06b1

 Seq. No.
 28544

Contig ID 176813\_1.R1040
5'-most EST rca700995923.h1
Method BLASTX
NCBI GI 93549665

NCBI GI g3549665 BLAST score 522 E value 2.0e-53 Match length 122 % identity 75

NCBI Description (AL031394) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28545

Contig ID 176834\_1.R1040 5'-most EST rca700995956.h1

Seq. No. 28546

Contig ID 176835\_1.R1040 5'-most EST zhf700960168.h1

Method BLASTX
NCBI GI g2088650
BLAST score 238
E value 5.0e-20
Match length 78
% identity 60

NCBI Description (AF002109) peroxisomal ATP/ADP carrier protein isolog

[Arabidopsis thaliana]

Seq. No. 28547

Contig ID 176845\_1.R1040 5'-most EST rca700995973.h1

Seq. No. 28548

Contig ID 176861 1.R1040 5'-most EST rca700998463.h1

Method BLASTX
NCBI GI g4206195
BLAST score 539
E value 2.0e-55
Match length 118
% identity 83

NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]

>gi\_4262169\_gb\_AAD14469\_ (AC005275) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 28549

Contig ID 176867\_1.R1040 5'-most EST rca700996004.h1

Method BLASTX
NCBI GI g3402705
BLAST score 362
E value 2.0e-34
Match length 118



% identity 61
NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28550

Contig ID 176869\_1.R1040 5'-most EST gsv701045327.h1

Method BLASTX
NCBI GI g3582340
BLAST score 240
E value 3.0e-20
Match length 81
% identity 60

NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 28551

Contig ID 176879\_1.R1040 5'-most EST rca700996463.h1

Method BLASTX
NCBI GI g4530327
BLAST score 418
E value 2.0e-41
Match length 95
% identity 84

NCBI Description (AF110494) mitochondrial precursor protein import receptor

tom70 [Neurospora crassa]

Seq. No. 28552

Contig ID 176892\_1.R1040

5'-most EST uC-gmrominsoy043g04b1

Method BLASTX
NCBI GI g4335735
BLAST score 435
E value 7.0e-60
Match length 228
% identity 58

NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28553

Contig ID 176913\_1.R1040 5'-most EST rca700996067.h1

Method BLASTX
NCBI GI g2760832
BLAST score 322
E value 8.0e-30
Match length 118
% identity 59

NCBI Description (AC003105) similar to barley ids-4 gene product

[Arabidopsis thaliana]

Seq. No. 28554

Contig ID 176953\_1.R1040 5'-most EST kl1701204366.h2

Seq. No. 28555

Contig ID 176960\_1.R1040 5'-most EST zzp700830482.h1



Seg. No. 28556

Contig ID 176974\_1.R1040 5'-most EST rca700996145.h1

Method BLASTX
NCBI GI g2226378
BLAST score 168
E value 4.0e-12
Match length 58
% identity 48

NCBI Description (AF006493) ACBP/ECHM [Cyprinus carpio]

Seq. No. 28557

Contig ID 176977\_1.R1040 5'-most EST rca700996150.h1

Method BLASTX
NCBI GI g2827649
BLAST score 217
E value 1.0e-17
Match length 74
% identity 58

NCBI Description (AL021637) putative protein [Arabidopsis thaliana]

Seq. No. 28558

Contig ID 176988 1.R1040 5'-most EST jex700906126.h1

Seq. No. 28559

Contig ID 177021 1.R1040 5'-most EST rca700996209.h1

Seq. No. 28560

Contig ID 177071\_1.R1040 5'-most EST zsg701129370.h1

Method BLASTX
NCBI GI g543063
BLAST score 197
E value 2.0e-15
Match length 88
% identity 44

NCBI Description zinc-finger protein, BR140 - human

Seq. No. 28561

Contig ID 177074\_1.R1040 5'-most EST rca700996279.h1

Method BLASTX
NCBI GI g1208497
BLAST score 150
E value 1.0e-09
Match length 132
% identity 36

NCBI Description (D38125) EREBP-4 [Nicotiana tabacum]

Seq. No. 28562

Contig ID 177093\_1.R1040 5'-most EST rca700996307.h1



Contig ID 177100\_1.R1040 5'-most EST rca700996315.h1

Seq. No. 28564

Contig ID 177114\_1.R1040 5'-most EST rca700996332.h1

Method BLASTX
NCBI GI g4580521
BLAST score 309
E value 6.0e-28
Match length 100
% identity 65

NCBI Description (AF036304) scarecrow-like 7 [Arabidopsis thaliana]

Seq. No. 28565

Contig ID 177120\_1.R1040 5'-most EST rca700996340.h1

Method BLASTX
NCBI GI g2244865
BLAST score 562
E value 3.0e-59
Match length 199
% identity 63

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28566

Contig ID 177128 1.R1040 5'-most EST rca700996355.h1

Method BLASTX
NCBI GI g4510421
BLAST score 569
E value 2.0e-58
Match length 314
% identity 46

NCBI Description (AC006929) unknown protein [Arabidopsis thaliana]

Seq. No. 28567

Contig ID 177146\_1.R1040 5'-most EST leu701156337.h1

Seq. No. 28568

Contig ID 177150\_1.R1040 5'-most EST rca700996388.h1

Seq. No. 28569

Contig ID 177170\_1.R1040

5'-most EST uC-gmrominsoy061d12b1

Method BLASTX
NCBI GI g4557060
BLAST score 471
E value 3.0e-47
Match length 182
% identity 53

NCBI Description (AC007154) putative chromosome-associated polypeptide, 5'

partial [Arabidopsis thaliana]



Contig ID 177201\_1.R1040 5'-most EST uC-gmronoir048b12b1

Method BLASTX
NCBI GI g2829888
BLAST score 418
E value 5.0e-41
Match length 162
% identity 56

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 28571

Contig ID 177221 1.R1040 5'-most EST rca700996515.h1

Method BLASTX
NCBI GI g1363051
BLAST score 210
E value 5.0e-17
Match length 85
% identity 47

NCBI Description P58 protein - bovine >gi 468012 (U04631) PKR inhibitor P58

[Bos taurus]

Seq. No. 28572

Contig ID 177227 1.R1040 5'-most EST fua701042066.h1

Method BLASTX
NCBI GI g3334665
BLAST score 355
E value 5.0e-38
Match length 143
% identity 58

NCBI Description (Y10492) putative cytochrome P450 [Glycine max]

Seq. No. 28573

Contig ID 177295\_1.R1040 5'-most EST uC-gmropic062f09b1

Method BLASTX
NCBI GI g3831457
BLAST score 548
E value 6.0e-56
Match length 201
% identity 52

NCBI Description (AC005700) putative ion channel protein [Arabidopsis

thaliana]

Seq. No. 28574

Contig ID 177309\_1.R1040 5'-most EST jC-gmro02910074f01a1

Method BLASTX
NCBI GI g3341680
BLAST score 231
E value 6.0e-19
Match length 144
% identity 39

NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Match length

% identity

79

47



```
177315 1.R1040
Contig ID
5'-most EST
                  g4396419
                  BLASTX
Method
                  q2352084
NCBI GI
                  300
BLAST score
                  4.0e-27
E value
                  72
Match length
% identity
                  82
NCBI Description (U96613) serine/threonine kinase [Arabidopsis thaliana]
                  28576
Seq. No.
                  177323 1.R1040
Contig ID
5'-most EST
                  crh700850145.hl
Method
                  BLASTX
                  g3402684
NCBI GI
                   241
BLAST score
                   9.0e-21
E value
                   65
Match length
                   69
% identity
                  (AC004697) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   28577
Seq. No.
                   177327 1.R1040
Contig ID
5'-most EST
                   leu701149343.hl
                   28578
Seq. No.
                   177328 1.R1040
Contig ID
                   jC-gmro02910056d05a1
5'-most EST
                   28579
Seq. No.
                   177339 1.R1040
Contig ID
                   rca701002590.h1
5'-most EST
                   28580
Seq. No.
                   177341 1.R1040
Contig ID
                   943974\overline{9}1
5'-most EST
                   BLASTX
Method
                   g2245100
NCBI GI
                   189
BLAST score
E value
                   5.0e-14
                   152
Match length
% identity
NCBI Description (Z97343) DNA-binding protein homolog [Arabidopsis thaliana]
Seq. No.
                   28581
                   177354 1.R1040
Contig ID
5'-most EST
                   zhf700960441.h1
Seq. No.
                   28582
                   177381 1.R1040
Contig ID
5'-most EST
                   q5509673
Method
                   BLASTX
                   q2829865
NCBI GI
BLAST score
                   158
E value
                   2.0e-10
```



NCBI Description (AC002396) N-terminal region similar to DNA-J proteins [Arabidopsis thaliana]

Seq. No. 28583

Contig ID 177399\_1.R1040 5'-most EST rca700996938.h1

Seq. No. 28584

Contig ID 177434\_1.R1040 5'-most EST rca700996985.h1

Seq. No. 28585

Contig ID 177482\_2.R1040 5'-most EST pxt700944584.h1

Method BLASTX
NCBI GI g3176715
BLAST score 319
E value 7.0e-30
Match length 81
% identity 77

NCBI Description (AC002392) putative receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 28586

Contig ID 177500\_1.R1040 5'-most EST rca701002187.h1

Seq. No. 28587

Contig ID 177509\_1.R1040 5'-most EST kl1701211222.h1

Method BLASTX
NCBI GI g4006868
BLAST score 135
E value 6.0e-11
Match length 104
% identity 39

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 28588

Contig ID 177510\_1.R1040 5'-most EST zhf700958041.h1

Method BLASTN
NCBI GI g1853969
BLAST score 303
E value 1.0e-169
Match length 774
% identity 86

NCBI Description Vigna unguiculata mRNA for CPRD46 protein, complete cds

Seq. No. 28589

Contig ID 177557\_1.R1040 5'-most EST leu701155389.h1

Seq. No. 28590

Contig ID 177565\_1.R1040 5'-most EST rca700998043.h1



Contig ID 177566\_1.R1040 5'-most EST rca700997214.h1

Seq. No. 28592

Contig ID 177570\_1.R1040

5'-most EST g5606878

Method BLASTX

NCBI GI g4468817

BLAST score 241

E value 2.0e-20

Match length 115

% identity 45

NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 28593

Contig ID 177592\_1.R1040 5'-most EST jC-gmle01810093c05a1

Seq. No. 28594

Contig ID 177598\_1.R1040 5'-most EST rca700997269.h1

Method BLASTX
NCBI GI g1929056
BLAST score 219
E value 3.0e-18
Match length 75
% identity 59

NCBI Description (Y12090) putative 3,4-dihydroxy-2-butanone kinase

[Lycopersicon esculentum]

Seq. No. 28595

Contig ID 177607 1.R1040

5'-most EST  $g56778\overline{6}5$ 

Seq. No. 28596

Contig ID 177623\_1.R1040

5'-most EST jC-gmro02910038a03a1

Method BLASTX
NCBI GI g4314363
BLAST score 376
E value 5.0e-36
Match length 179
% identity 42

NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28597

Contig ID 177631\_1.R1040 5'-most EST uC-gmropic091e09b1

Seq. No. 28598

Contig ID 177673\_1.R1040 5'-most EST jex700906354.h1

Seq. No. 28599

Contig ID 177684\_1.R1040 5'-most EST rca700997413.h1



 Seq. No.
 28600

 Contig ID
 177693\_1.R1040

 5'-most EST
 rca700997422.h1

 Method
 BLASTX

 NCBI GI
 g1669341

 BLAST score
 533

BLAST score 533 E value 3.0e-54 Match length 193 % identity 53

NCBI Description (D45066) AOBP (ascorbate oxidase promoter-binding protein)

[Cucurbita maxima]

Seq. No. 28601

Contig ID 177709\_1.R1040 5'-most EST rca700997439.h1

Seq. No. 28602

Contig ID 177728\_1.R1040 5'-most EST rca700997479.h1

Seq. No. 28603

Contig ID 177751\_1.R1040 5'-most EST rca701001310.h1

Method BLASTX
NCBI GI g4056502
BLAST score 323
E value 3.0e-30
Match length 97
% identity 68

NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No. 28604

Contig ID 177757\_1.R1040 5'-most EST rca700997518.h1

Seq. No. 28605

Contig ID 177761\_1.R1040 5'-most EST rca700997522.h1

Method BLASTX
NCBI GI g3201627
BLAST score 166
E value 1.0e-13
Match length 80
% identity 64

NCBI Description (AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No. 28606

Contig ID 177778 1.R1040 5'-most EST rca701002305.h1

Method BLASTX
NCBI GI g3138972
BLAST score 351
E value 1.0e-33
Match length 90
% identity 73

NCBI Description (AF038505) dihydrolipoylacyltransferase subunit of the



branched-chain alpha-keto acid dehydrogenase complex [Arabidopsis thaliana]

Seq. No. 28607

Contig ID 177787\_1.R1040 5'-most EST rca700997717.h1

Seq. No. 28608

Contig ID 177809\_1.R1040 5'-most EST rca700997580.h1

Method BLASTX
NCBI GI g3600039
BLAST score 619
E value 1.0e-64
Match length 160
% identity 69

NCBI Description (AF080119) similar to Schizosaccharomyces pombe isp4

protein (GB:D14061) [Arabidopsis thaliana]

Seq. No. 28609

Contig ID 177824\_1.R1040 5'-most EST gsv701044388.h1

Seq. No. 28610

Contig ID 177883\_1.R1040 5'-most EST zhf700964771.h1

Method BLASTX
NCBI GI g3136056
BLAST score 253
E value 2.0e-21
Match length 238
% identity 28

NCBI Description (AL023592) RanBP7/importin-beta/Cselp superfamily protein

[Schizosaccharomyces pombe]

Seq. No. 28611

Contig ID 177884\_1.R1040

5'-most EST g4286329

Seq. No. 28612

Contig ID 177928\_1.R1040 5'-most EST dpv701099792.h1

Seq. No. 28613

Contig ID 177938\_1.R1040 5'-most EST leu701146354.h1

Seq. No. 28614

Contig ID 177941 1.R1040 5'-most EST fde700876196.h1

Seq. No. 28615

Contig ID 177960\_1.R1040

5'-most EST jC-gmfl02220125e08a1

Seq. No. 28616

Contig ID 177986 1.R1040

4425

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jC-qmle01810088b05a1
5'-most EST
                   28617
Seq. No.
Contig ID
                   177995 1.R1040
5'-most EST
                   rca700997975.hl
                   28618
Seq. No.
Contig ID
                   178058 1.R1040
5'-most EST
                   rca700997969.hl
Seq. No.
                   28619
                   178064 1.R1040
Contig ID
                   epx701\overline{1}08039.h1
5'-most EST
                   BLASTX
Method
                   g3059095
NCBI GI
BLAST score
                   270
E value
                   9.0e-24
Match length
                   69
% identity
                   (AJ001091) magnesium chelatase subunit [Glycine max]
NCBI Description
                   28620
Seq. No.
                   178083 1.R1040
Contig ID
                   gsv701052083.hl
5'-most EST
                   28621
Seq. No.
Contig ID
                   178087 1.R1040
                   rca700998035.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2935529
```

Method BLASTX
NCBI GI g2935529
BLAST score 139
E value 5.0e-09
Match length 31
% identity 77

NCBI Description (AF049069) No definition line found [Pinus radiata]

Seq. No. 28622

Contig ID 178113 1.R1040 5'-most EST rca701002365.h1

Seq. No. 28623

Contig ID 178121\_1.R1040 5'-most EST rca700998192.h1

Method BLASTX
NCBI GI g1351643
BLAST score 157
E value 8.0e-11
Match length 78
% identity 40

NCBI Description HYPOTHETICAL 43.0 KD PROTEIN C8A4.09C IN CHROMOSOME I

>gi 2130450 pir S62525 hypothetical protein SPAC8A4.09c -

fission yeast (Schizosaccharomyces pombe) >gi\_1052540\_emb\_CAA91519\_ (Z66569) unknown

[Schizosaccharomyces pombe] >gi\_4456834\_emb\_CAB37424.1\_ (AL032824) hypothetical protein [Schizosaccharomyces pombe]



Contig ID 178122 1.R1040 5'-most EST rca700998093.h1

Seq. No. 28625

Contig ID 178122\_2.R1040 5'-most EST fde700871420.h1

Seq. No. 28626

Contig ID 178150\_1.R1040 5'-most EST fde700874357.h1

Method BLASTX
NCBI GI g2500139
BLAST score 597
E value 4.0e-62
Match length 154
% identity 71

NCBI Description PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1)

>gi\_1653916\_dbj\_BAA18826\_ (D90917) peptide chain release

factor [Synechocystis sp.]

Seq. No. 28627

Contig ID 178158\_1.R1040 5'-most EST rca700998149.h1

Method BLASTX
NCBI GI g4455359
BLAST score 171
E value 2.0e-12
Match length 96
% identity 36

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 28628

Contig ID 178196\_1.R1040 5'-most EST uC-gmronoir047c08b1

Seq. No. 28629

Contig ID 178216 1.R1040

5'-most EST g4283398
Method BLASTX
NCBI GI g4006878
BLAST score 255
E value 7.0e-22
Match length 123
% identity 48

NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No. 28630

Contig ID 178242\_1.R1040

5'-most EST jC-gmro02910072f04a1

Seq. No. 28631

Contig ID 178248\_1.R1040 5'-most EST rca700998277.h1

Seq. No. 28632

Contig ID 178342 1.R1040 5'-most EST fua701037580.h1



Method BLASTX
NCBI GI g2827552
BLAST score 202
E value 2.0e-28
Match length 76
% identity 75

NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

Seq. No. 28633

Contig ID 178365\_1.R1040 5'-most EST fC-gmse700655491d4

Seq. No. 28634

Contig ID 178381\_1.R1040 5'-most EST rca700998483.h1

Seq. No. 28635

Contig ID 178425\_1.R1040

5'-most EST uC-gmrominsoy139c02b1

Seq. No. 28636

Contig ID 178428\_1.R1040 5'-most EST asn701133668.h2

Method BLASTX
NCBI GI g3850588
BLAST score 147
E value 4.0e-09
Match length 315
% identity 27

NCBI Description (AC005278) Contains similarity to gb\_AB011110 KIAA0538

protein from Homo sapiens brain and to phospholipid-binding domain C2 PF\_00168. ESTs gb\_AA585988 and gb\_T04384 come

from this gene. [Arabidopsis thaliana]

Seq. No. 28637

Contig ID 178465 1.R1040 5'-most EST zhf700964765.h1

Seq. No. 28638

Contig ID 178470 1.R1040

5'-most EST g5677023

Seq. No. 28639

Contig ID 178500 1.R1040

5'-most EST uC-gmflminsoy022b11b1

Seq. No. 28640

Contig ID 178504 1.R1040

5'-most EST jC-gmle01810067g05a1

Seq. No. 28641

Contig ID 178525\_1.R1040 5'-most EST zhf700961951.h1

Seq. No. 28642

Contig ID 178532\_1.R1040 5'-most EST rca700998705.h1



```
BLASTX
Method
                  g4106683
NCBI GI
                  171
BLAST score
                  5.0e-12
E value
                  111
Match length
% identity
                   32
NCBI Description (AL035065) hypothetical protein [Schizosaccharomyces pombe]
                   28643
Seq. No.
                   178540 1.R1040
Contig ID
                   jC-qmf\overline{1}02220100b01a1
5'-most EST
                   28644
Seq. No.
                   178552 1.R1040
Contig ID
                   jC-gmro02910037h10a1
5'-most EST
                   28645
Seq. No.
                   178579 1.R1040
Contig ID
                   zsg701117701.h2
5'-most EST
                   BLASTX
Method
                   q1255448
NCBI GI
                   441
BLAST score
                   1.0e-43
E value
                   124
Match length
                   69
% identity
                   (D50468) mitogen-activated protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   28646
Seq. No.
                   178579 2.R1040
Contig ID
                   uC-gmrominsoy117g11b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1255448
                   158
BLAST score
                   1.0e-14
E value
                   83
Match length
% identity
                   (D50468) mitogen-activated protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   28647
Seq. No.
                   178592 1.R1040
Contig ID
 5'-most EST
                   zhf700963061.h1
Method
                   BLASTX
                   q3759184
NCBI GI
BLAST score
                   188
E value
                   2.0e-14
Match length
                   66
 % identity
                   55
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                   28648
 Seq. No.
```

Contig ID 178613 1.R1040 rca700998818.hl 5'-most EST

28649 Seq. No.

178646 1.R1040 Contig ID



5'-most EST rca700998922.h1

Seq. No. 28650

Contig ID 178648 1.R1040 5'-most EST kl1701210150.h1

Seq. No. 28651

Contig ID 178688 1.R1040 5'-most EST rca700998964.h1

Seq. No. 28652

Contig ID 178742 1.R1040

5'-most EST uC-gmrominsoy250f08b1

Method BLASTN
NCBI GI g2055227
BLAST score 46
E value 1.0e-16
Match length 66
% identity 92

NCBI Description Glycine max mRNA for SRC1, complete cds

Seq. No. 28653

Contig ID 178799 1.R1040 5'-most EST rca700999148.h1

Seq. No. 28654

Contig ID 178831\_1.R1040 5'-most EST fC-gmse700660737g3

Seq. No. 28655

Contig ID 178843\_1.R1040 5'-most EST rca700999269.h1

Seq. No. 28656

Contig ID 178862 1.R1040 5'-most EST rca700999302.h1

Seq. No. 28657

Contig ID 178874 1.R1040 5'-most EST zhf700952248.h1

Seq. No. 28658

Contig ID 178932 1.R1040 5'-most EST rca700999506.h1

Seq. No. 28659

Contig ID 178950\_1.R1040 5'-most EST jC-gmfl02220077g11d1

Seq. No. 28660

Contig ID 178969\_1.R1040 5'-most EST zhf700962302.h1

Seq. No. 28661

Contig ID 179028\_1.R1040 5'-most EST zsg701124449.h1

Method BLASTX



NCBI GI g3402684
BLAST score 535
E value 1.0e-54
Match length 138
% identity 74

NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28662

Contig ID 179074\_1.R1040 5'-most EST zsg701122609.h1

Seq. No. 28663

Contig ID 179083\_1.R1040 5'-most EST jC-gmle01810085d07d1

Method BLASTX
NCBI GI g3080421
BLAST score 177
E value 1.0e-12
Match length 83
% identity 41

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 28664

Contig ID 179117\_1.R1040 5'-most EST fde700876425.h1

Seq. No. 28665

Contig ID 179118\_1.R1040 5'-most EST rca700999823.h1

Seq. No. 28666

Contig ID 179141\_1.R1040 5'-most EST leu701157279.h1

Method BLASTX
NCBI GI g4056507
BLAST score 229
E value 9.0e-19
Match length 91
% identity 51

NCBI Description (AC005896) putative RNA binding protein [Arabidopsis

thaliana]

Seq. No. 28667

Contig ID 179143 1.R1040

5'-most EST jC-gmro02910062a03d1

Method BLASTX
NCBI GI g2673918
BLAST score 212
E value 7.0e-17
Match length 57
% identity 70

NCBI Description (AC002561) unknwon protein [Arabidopsis thaliana]

Seq. No. 28668

Contig ID 179198 1.R1040

5'-most EST uC-gmrominsoy219b02b1



 Seq. No.
 28669

 Contig ID
 17921

 5'-most EST
 zhf70

179216\_1.R1040 zhf700954425.h1

Seq. No.

28670

Contig ID 179239\_1.R1040 5'-most EST rca701000716.h1

Seq. No.

28671

Contig ID 179265\_1.R1040 5'-most EST zsg701126938.h1

Method BLASTX
NCBI GI g1276977
BLAST score 660
E value 3.0e-69
Match length 152
% identity 84

NCBI Description (U47143) nonsymbiotic hemoglobin [Glycine max]

Seq. No.

28672

Contig ID 5'-most EST

179274\_1.R1040 zhf700958082.h1

Seq. No. 28673

Contig ID 179300\_1.R1040 5'-most EST all700863273.h1

Method BLASTN
NCBI GI g2253091
BLAST score 44
E value 1.0e-15
Match length 104
% identity 86

NCBI Description Spinacia oleracea ORF, clone SAM2B4.1T7

Seq. No.

28674

Contig ID 179301\_1.R1040

5'-most EST g5126612
Method BLASTX
NCBI GI g3096949
BLAST score 239
E value 2.0e-20
Match length 98
% identity 47

NCBI Description (Y16328) putative cyclic nucleotide-regulated ion channel

[Arabidopsis thaliana] >gi\_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]

Seq. No. 28675

Contig ID 179349\_1.R1040 5'-most EST rca701000362.h1

Seq. No. 28676

Contig ID 179357\_1.R1040 5'-most EST rca701000382.h1

Method BLASTX
NCBI GI g3550661
BLAST score 416



E value 1.0e-40
Match length 101
% identity 44

NCBI Description (AJ001310) 39 kDa EF-Hand containing protein [Solanum

tuberosum]

Seq. No. 28677

Contig ID 179361\_1.R1040

5'-most EST jC-gmle01810094h09d1

Method BLASTX
NCBI GI g4006861
BLAST score 362
E value 2.0e-34
Match length 115
% identity 57

NCBI Description (Z99707) tubulin-like protein [Arabidopsis thaliana]

Seq. No. 28678

Contig ID 179419\_1.R1040 5'-most EST rca701000472.h1

Seq. No. 28679

Contig ID 179420\_1.R1040

5'-most EST g5509254

Seq. No. 28680

Contig ID 179438\_1.R1040 5'-most EST rca701000509.h1

Seq. No. 28681

Contig ID 179447 1.R1040 5'-most EST fde700873138.h1

Seq. No. 28682

Contig ID 179515\_1.R1040 5'-most EST rca701000646.h1

Method BLASTX
NCBI GI g1352269
BLAST score 179
E value 4.0e-13
Match length 135
% identity 29

NCBI Description DIAPHANOUS PROTEIN >gi\_575927 (U11288) diaphanous protein

[Drosophila melanogaster]

Seq. No. 28683

Contig ID 179516 1.R1040 5'-most EST rca701000648.h1

Seq. No. 28684

Contig ID 179534\_1.R1040 5'-most EST rca701002356.h1

Seq. No. 28685

Contig ID 179563\_1.R1040 5'-most EST uC-gmropic110d12b1

Method BLASTX



NCBI GI q2832717 BLAST score 672 7.0e-71 E value Match length 139 89 % identity

(AJ003114) alkaline/neutral invertase [Lolium temulentum] NCBI Description

28686 Seq. No.

179589 1.R1040 Contig ID  $rca701\overline{0}00848.h1$ 5'-most EST

28687 Seq. No.

179595 1.R1040 Contig ID 5'-most EST uC-gmropic037b06b1

28688 Seq. No.

179606 1.R1040 Contig ID  $rca701\overline{0}01387.h1$ 5'-most EST

BLASTX Method q4102839 NCBI GI 749 BLAST score 9.0e-80 E value Match length 172 76 % identity

NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

28689 Seq. No.

179609 1.R1040 Contig ID  $rca701\overline{0}00785.h1$ 5'-most EST

Seq. No. 28690

179610 1.R1040 Contig ID

5'-most EST g5605841

Seq. No. 28691

Contig ID 179612 1.R1040 5'-most EST hrw701062674.h1

Seq. No.

28692 Contig ID 179613 1.R1040 5'-most EST sat701003330.h1

Seq. No.

179626 1.R1040 Contig ID 5'-most EST  $jex700\overline{9}04934.h1$ 

28693

28694 Seq. No.

Contig ID 179632 1.R1040 5'-most EST rca701000817.hl

Seq. No. 28695

179642 1.R1040 Contig ID 5'-most EST rca701000831.hl

Seq. No. 28696

179666 1.R1040 Contig ID 5'-most EST rca701000858.hl



Seq. No. 28697

Contig ID 179728\_1.R1040 5'-most EST rca701000962.h1

Seq. No. 28698

Contig ID 179734\_1.R1040 5'-most EST rca701000972.h1

Method BLASTX
NCBI GI g3582333
BLAST score 274
E value 4.0e-24
Match length 146
% identity 40

NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28699

Contig ID 179738\_1.R1040 5'-most EST uC-gmropic092f12b1

Method BLASTX
NCBI GI g1657621
BLAST score 362
E value 1.0e-34
Match length 97
% identity 66

NCBI Description (U72505) G6p [Arabidopsis thaliana] >gi\_3068711 (AF049236)

putative acyl-coA dehydrogenase [Arabidopsis thaliana]

Seq. No. 28700

Contig ID 179742\_1.R1040 5'-most EST rca701000981.h1

Method BLASTX
NCBI GI g3005576
BLAST score 298
E value 6.0e-27
Match length 103
% identity 55

NCBI Description (AF047718) putative high affinity nitrate transporter;

GmNRT2 [Glycine max]

Seq. No. 28701

Contig ID 179757\_1.R1040 5'-most EST rca701001007.h1

Method BLASTX
NCBI GI g3218550
BLAST score 147
E value 2.0e-09
Match length 74
% identity 41

NCBI Description (AB009399) Cdk-activating kinase 1At [Arabidopsis thaliana]

Seq. No. 28702

Contig ID 179769 1.R1040 5'-most EST rca701001068.h1

Seq. No. 28703

Contig ID 179791\_1.R1040



```
jC-gmst02400055g12a1
5'-most EST
                    BLASTX
Method
                    g132127
NCBI GI
BLAST score
                     155
                     4.0e-10
E value
                     140
Match length
% identity
                     31
                    RIBOKINASE >gi_66667_pir__KIECRB ribokinase (EC 2.7.1.15) - Escherichia coli >gi_2981974_pdb_1RKD__ E. Coli Ribokinase
NCBI Description
                     Complexed With Ribose And Adp >gi 147516 (M13169) ribokinase [Escherichia coli] >gi 290602 (L10328)
                     ribokinase [Escherichia coli] >gi_1790193 (AE000452)
                     ribokinase [Escherichia coli]
                     28704
Seq. No.
Contig ID
                     179805 1.R1040
                     uC-gmronoir060e06b1
5'-most EST
Method
                     BLASTX
                     g2791896
NCBI GI
BLAST score
                     914
E value
                     4.0e-99
Match length
                     186
% identity
                     96
                     (Y08997) 146kDa nuclear protein [Xenopus laevis]
NCBI Description
                     28705
Seq. No.
                     179824 1.R1040
Contig ID
                     rca701001087.hl
5'-most EST
Seq. No.
                     28706
                     179858 1.R1040
Contig ID
                     rca701\overline{0}01127.h1
5'-most EST
                     28707
Seq. No.
                     179858 2.R1040
Contig ID
                     jC-gmle01810022a08d1
5'-most EST
                     28708
Seq. No.
                     179876 1.R1040
Contig ID
                     rca701001211.hl
5'-most EST
                     28709
Seq. No.
                     179884 1.R1040
Contig ID
                     rca701001160.hl
 5'-most EST
                     BLASTX
Method
                      q416730
NCBI GI
                      876
BLAST score
                      2.0e-94
 E value
                      213
Match length
                      73
 % identity
```

NCBI Description BETA-UREIDOPROPIONASE (BETA-ALANINE SYNTHASE) (N-CARBAMOYL-BETA-ALANINE AMIDOHYDROLASE)

>gi\_285064\_pir\_\_S27881 beta-alanine synthase - rat >gi\_203106 (M97662) beta-alanine synthase [Rattus

norvegicus]

28710 Seq. No.



Contig ID 179889 1.R1040 5'-most EST rca701001167.h1

Seq. No. 28711

Contig ID 179912\_1.R1040 5'-most EST rca701001195.h1

Method BLASTX
NCBI GI g228403
BLAST score 277
E value 6.0e-25
Match length 83
% identity 65

NCBI Description glycolate oxidase [Lens culinaris]

Seq. No. 28712

Contig ID 179913\_1.R1040 5'-most EST rca701001675.h1

Method BLASTN
NCBI GI g12137
BLAST score 90
E value 5.0e-43
Match length 196
% identity 89

NCBI Description Pea chloroplast DNA (4.7 kb) 5' to ATP-synthase a subunit

gene

Seq. No. 28713

Contig ID 179957\_1.R1040 5'-most EST rca701001268.h1

Method BLASTX
NCBI GI g4098582
BLAST score 162
E value 4.0e-11
Match length 116
% identity 39

NCBI Description (U79567) RBM1 [Sminthopsis macroura]

Seq. No. 28714

Contig ID 179983\_1.R1040 5'-most EST rca701001303.h1

Seq. No. 28715

Contig ID 179999\_1.R1040 5'-most EST rca701001322.h1

Seq. No. 28716

Contig ID 180001\_1.R1040 5'-most EST rca701001395.h1

Seq. No. 28717

Contig ID 180010\_1.R1040

5'-most EST uC-gmrominsoy043b11b1

Seq. No. 28718

Contig ID 180025\_1.R1040 5'-most EST rca701001353.h1

Method BLASTX



NCBI GI g2224695 BLAST score 171 E value 4.0e-12 Match length 65 % identity 51

NCBI Description (AB002375) KIAA0377 [Homo sapiens]

Seq. No. 28719

Contig ID 180032 1.R1040

5'-most EST g4396732

Seq. No. 28720

Contig ID 180037\_1.R1040 5'-most EST rca701001368.h1

Seq. No. 28721

Contig ID 180047\_1.R1040 5'-most EST rca701001380.h1

Method BLASTX
NCBI GI g2499570
BLAST score 268
E value 2.0e-23
Match length 74
% identity 69

NCBI Description PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE

(PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN

L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN

CARBOXYL METHYLTRANSFERASE) >gi\_414332 (L07941) L-isoaspartyl methyltransferase [Triticum aestivum]

Seq. No. 28722

Contig ID 180076\_1.R1040 5'-most EST rca701001423.h1

Seq. No. 28723

Contig ID 180082\_1.R1040

5'-most EST jC-gmro02910010g02d1

Method BLASTX
NCBI GI g4455366
BLAST score 204
E value 1.0e-15
Match length 52
% identity 75

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 28724

Contig ID 180111 1.R1040 5'-most EST zhf700958630.h1

Seq. No. 28725

Contig ID 180162\_1.R1040 5'-most EST rca701001548.h1

Method BLASTX
NCBI GI g2582351
BLAST score 374
E value 9.0e-36
Match length 173



% identity (AF018639) unknown [Dictyostelium discoideum] NCBI Description 28726 Seq. No. Contig ID 180165 1.R1040 uC-gmflminsoy012h02b1 5'-most EST BLASTX Method q4415920 NCBI GI BLAST score 325 9.0e-30 E value Match length 277 33 % identity (AC006282) putative glucosyl transferase [Arabidopsis NCBI Description thaliana] 28727 Seq. No. 180180 1.R1040 Contig ID jC-gmf102220108e05a1 5'-most EST BLASTX Method a3819099 NCBI GI BLAST score 257 E value 4.0e-22 142 Match length % identity 37 (AJ009825) copper amine oxidase [Cicer arietinum] NCBI Description Seq. No. 28728 180190 1.R1040 Contig ID jC-qmf102220057a10d1 5'-most EST Method BLASTX q1871187 NCBI GI BLAST score 253 E value 1.0e-42 Match length 130 % identity 71 (U90439) unknown protein [Arabidopsis thaliana] NCBI Description 28729 Seq. No. 180202 1.R1040 Contig ID rca701001603.hl 5'-most EST Method BLASTX q2244835 NCBI GI 837 BLAST score 5.0e-90 E value 188 Match length 79 % identity (Z97337) protein kinase homolog [Arabidopsis thaliana] NCBI Description 28730

Seq. No. 28730 Contiq ID 180216 1.R1040

Contig ID 180216\_1.R1040 5'-most EST rca701001618.h1 Method BLASTX

 NCBI GI
 g1407705

 BLAST score
 533

 E value
 2.0e-54

 Match length
 140

 % identity
 66



NCBI Description (U60202) lipoxygenase [Solanum tuberosum]

Seq. No. 28731

Contig ID 180229\_1.R1040 5'-most EST zhf700954791.h1

Method BLASTX
NCBI GI g2760832
BLAST score 138
E value 2.0e-15
Match length 76
% identity 55

NCBI Description (AC003105) similar to barley ids-4 gene product

[Arabidopsis thaliana]

Seq. No. 28732

Contig ID 180248\_1.R1040 5'-most EST jC-gmle01810024g07a1

Method BLASTX
NCBI GI 9730751
BLAST score 200
E value 2.0e-15
Match length 149
% identity 36

NCBI Description DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1)

>gi\_401776 (L14754) DNA-binding protein [Homo sapiens]
>gi\_4504623\_ref\_NP\_002171.1\_pIGHMBP2\_ immunoglobulin mu

binding protein

Seq. No. 28733

Contig ID 180284\_1.R1040 5'-most EST jC-gmle01810024b08a1

Seq. No. 28734

Contig ID 180293\_1.R1040

5'-most EST jC-gmle01810048c05a1

Method BLASTX
NCBI GI g2281088
BLAST score 416
E value 1.0e-40
Match length 205
% identity 43

NCBI Description (AC002333) indole-3-acetate beta-glucosyltransferase isolog

[Arabidopsis thaliana]

Seq. No. 28735

Contig ID 180315 1.R1040

5'-most EST uC-gmrominsoy033a05b1

Method BLASTX
NCBI GI g4220480
BLAST score 501
E value 2.0e-50
Match length 246
% identity 45

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 28736

Contig ID 180343 1.R1040

4440



5'-most EST jC-gmle01810014e10d1

Seq. No. 28737

Contig ID 180419\_1.R1040 5'-most EST asn701134847.h2

Seq. No. 28738

Contig ID 180443\_1.R1040 5'-most EST rlr700901202.h1

Seq. No. 28739

Contig ID 180462\_1.R1040 5'-most EST jC-gmro02910022g06a1

Method BLASTX
NCBI GI g1483230
BLAST score 440
E value 2.0e-43
Match length 143
% identity 64

NCBI Description (X99654) MADS4 protein [Betula pendula]

Seq. No. 28740

Contig ID 180471 1.R1040

5'-most EST g4396628
Method BLASTX
NCBI GI g4204288
BLAST score 470
E value 8.0e-47
Match length 153
% identity 58

NCBI Description (AC003027) lcl\_prt\_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 28741

Contig ID 180480\_1.R1040 5'-most EST zhf700964493.h1

Seq. No. 28742

Contig ID 180504\_1.R1040 5'-most EST uC-gmropic047a12b1

Seq. No. 28743

Contig ID 180511 1.R1040 5'-most EST rca701002449.h1

Seq. No. 28744

Contig ID 180520\_1.R1040 5'-most EST dpv701098607.h1

Seq. No. 28745

Contig ID 180523\_1.R1040

5'-most EST g5126709

Seq. No. 28746

Contig ID 180523\_2.R1040 5'-most EST rca701002214.h1

Method BLASTX

4441



NCBI GI g4164473 BLAST score 185 E value 1.0e-13 Match length 65 % identity 65

NCBI Description (AF061157) negatively light-regulated protein [Vernicia

fordii]

Seq. No. 28747

Contig ID 180553\_1.R1040 5'-most EST rca701002275.h1

Seq. No. 28748

Contig ID 180576\_1.R1040 5'-most EST fde700875914.h1

Seq. No. 28749

Contig ID 180581\_1.R1040

5'-most EST jC-gmfl02220052d02a1

Seq. No. 28750

Contig ID 180584\_1.R1040 5'-most EST rca701002324.h1

Method BLASTX
NCBI GI g2262111
BLAST score 358
E value 6.0e-34
Match length 136
% identity 54

NCBI Description (AC002343) ribitol dehydrogenase isolog [Arabidopsis

thaliana]

Seq. No. 28751

Contig ID 180631\_1.R1040 5'-most EST fua701040090.h1

Seq. No. 28752

Contig ID 180649\_1.R1040 5'-most EST uC-gmropic067g02b1

Method BLASTX
NCBI GI g3395432
BLAST score 812
E value 7.0e-87
Match length 220
% identity 66

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 28753

Contig ID 180662\_1.R1040 5'-most EST rca701002520.h1

Seq. No. 28754

Contig ID 180690 1.R1040 5'-most EST rca701002466.h1

Method BLASTX
NCBI GI g1076685
BLAST score 210



4.0e-17 E value Match length 79 62 % identity SPF1 protein - sweet potato >gi\_484261\_dbj\_BAA06278\_ NCBI Description (D30038) SPF1 protein [Ipomoea batatas] 28755 Seq. No. 180691 1.R1040 Contig ID 5'-most EST jC-qmle01810052g02a1 BLASTX Method NCBI GI g4206197 BLAST score 176 2.0e-12 E value 227 Match length % identity (AF071527) putative pre-mRNA splicing factor [Arabidopsis NCBI Description thaliana] 28756 Seq. No. 180714 1.R1040 Contig ID q4405586 5'-most EST Method BLASTX q3395432 NCBI GI 509 BLAST score 8.0e-52 E value 126 Match length % identity (AC004683) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 28757 180733 1.R1040 Contig ID 5'-most EST leu701146108.h1 28758 Seq. No. 180733 2.R1040 Contig ID  $k11701\overline{2}14442.h1$ 5'-most EST 28759 Seq. No. 180738 1.R1040 Contig ID rca701002651.h1 5'-most EST Seq. No. 28760 180745 1.R1040 Contig ID jC-qmle01810086g01d1 5'-most EST BLASTX Method g1220453 NCBI GI 246 BLAST score 8.0e-21 E value 66 Match length 68 % identity (M79328) alpha-amylase [Solanum tuberosum] NCBI Description 28761 Seq. No.

Contig ID 180760\_1.R1040

5'-most EST jC-gmro02910075h08a1

Method BLASTX NCBI GI g4539525



BLAST score 5.0e-19 E value 165 Match length 33 % identity

(AJ012370) NAALADase II protein [Homo sapiens] NCBI Description

Seq. No.

28762

180775 1.R1040 Contig ID uC-qmropic107h03b1 5'-most EST

Seq. No.

28763

Contig ID 5'-most EST 180780 1.R1040  $rca701\overline{0}02592.h1$ 

Method BLASTX NCBI GI q4415942 BLAST score 341 E value 3.0e-32 Match length 106 % identity 65

(AC006418) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

28764

Contig ID 5'-most EST 180784 1.R1040 uC-gmropic027g02b1

BLASTX Method NCBI GI g2190544 BLAST score 299 1.0e-48 E value 119 Match length % identity 87

(ACO01229) Similar to Saccharomyces hypothetical protein NCBI Description

P9642.2 (gb U40828). [Arabidopsis thaliana]

Seq. No.

28765

Contig ID 5'-most EST 180815 1.R1040  $rca701\overline{0}02662.h1$ 

Seq. No.

28766

Contig ID

180821 1.R1040

5'-most EST

jC-gmst02400015b12d1

Method BLASTX NCBI GI g2833380 BLAST score 343 2.0e-32 E value Match length 98 % identity 68

NCBI Description

RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 2 (PHOSPHORIBOSYL

PYROPHOSPHATE SYNTHETASE 2) (PRS II)

>gi 2146772\_pir\_\_S71262 ribose-phosphate pyrophosphokinase

(EC 2.7.6.1) II - Arabidopsis thaliana (fragment) >gi\_1064885\_emb\_CAA63552\_ (X92974) phosphoribosyl pyrophosphate synthetase II [Arabidopsis thaliana]

Seq. No.

28767

Contig ID 5'-most EST Method

180834 1.R1040  $jex700\overline{9}04870.h1$ 

BLASTX



g2252840 NCBI GI 157 BLAST score E value 8.0e-11 Match length 83 % identity 39

(AF013293) contains regions of similarity to Haemophilus NCBI Description influenzae permease (SP:P38767) [Arabidopsis thaliana]

28768 Seq. No.

Contig ID 180844 1.R1040 fde700870511.hl 5'-most EST

28769 Seq. No.

Contig ID 180850 1.R1040 fC-qmst700889683f3 5'-most EST

Method BLASTX NCBI GI q128195 BLAST score 187 1.0e-13 E value 110 Match length % identity

NITRATE REDUCTASE (NR) >gi\_66203\_pir\_\_RDTONH nitrate NCBI Description

reductase (NADH) (EC 1.6.6.1) - tomato

>gi\_19283\_emb\_CAA32218\_ (X14060) nitrate reductase

[Lycopersicon esculentum]

Seq. No. 28770

Contig ID 180866 1.R1040 5'-most EST fde700870539.h1

Seq. No.

28771 180872 1.R1040 Contig ID fde700872774.h1 5'-most EST

Seq. No.

28772 180886 1.R1040 Contig ID  $fde700\overline{8}70562.h1$ 5'-most EST

Seq. No.

28773 180912 1.R1040 Contig ID fde700870606.hl 5'-most EST

Seq. No.

28774 180917 1.R1040 Contig ID fde700870769.hl 5'-most EST

28775 Seq. No.

180978 1.R1040 Contig ID fde700870695.h1 5'-most EST

BLASTX Method g1800147 NCBI GI BLAST score 277 2.0e-24 E value Match length 71 76 % identity

(U83655) membrane associated protein [Arabidopsis thaliana] NCBI Description



28776 Seq. No.

180982 1.R1040 Contig ID 5'-most EST fC-qmst700889363h1

BLASTX Method NCBI GI q1345955 BLAST score 723 3.0e-76E value 391 Match length 41

% identity GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH) NCBI Description

(FALDH) >gi\_496118 (L33464) alcohol dehydrogenase 3

[Methylobacter marinus]

28777 Seq. No.

180990 1.R1040 Contig ID 5'-most EST fde700870714.h1

Method BLASTN NCBI GI q416037 BLAST score 120 4.0e-61 E value 165 Match length % identity 16

NCBI Description O.sativa rub1 mRNA for polyubiquitin

Seq. No.

180994 1.R1040 Contig ID  $dpv701\overline{1}01807.h1$ 5'-most EST

Seq. No.

28779 180996 1.R1040 Contig ID fde700873111.hl 5'-most EST

28778

Seq. No.

28780

181007 1.R1040 Contig ID

jC-gmf102220141d11a1 5'-most EST

Seq. No.

28781

181044 1.R1040 Contig ID fde700876004.h1 5'-most EST

Seq. No.

28782

181056 1.R1040 Contig ID fde700870809.hl 5'-most EST

Seq. No.

28783

181075 1.R1040 Contig ID fC-gmst700889690a3 5'-most EST

BLASTX Method q2388985 NCBI GI BLAST score 272 5.0e-24 E value Match length 90 % identity 57

(Z98980) transcription factor [Schizosaccharomyces pombe] NCBI Description

Seq. No.

28784

Contig ID

181087\_1.R1040



fde700870845.hl 5'-most EST

Seq. No. 28785

181094 1.R1040 Contig ID fde700875879.h1 5'-most EST

28786 Seq. No.

181110 1.R1040 Contig ID fde700870873.hl 5'-most EST

28787 Seq. No.

181117 1.R1040 Contig ID  $k11701\overline{2}05580.h1$ 5'-most EST

28788 Seq. No.

Contig ID 181117 2.R1040 5'-most EST uC-gmronoir038a08b1

28789 Seq. No.

181121 1.R1040 Contig ID 5'-most EST fjg700968353.hl

28790 Seq. No.

181127 1.R1040 Contig ID fde700871025.h1 5'-most EST

Seq. No. 28791

Contig ID 181144 1.R1040 hrw701061362.hl 5'-most EST

Method BLASTX g2792155 NCBI GI BLAST score 562 E value 1.0e-57 Match length 179 % identity

(AJ223291) chalcone reductase [Sesbania rostrata] NCBI Description

28792 Seq. No.

181148 1.R1040 Contig ID fde700870931.hl 5'-most EST

Method BLASTX NCBI GI q4375833 BLAST score 969 1.0e-105 E value 318 Match length 60 % identity

(AL021713) receptor serine/threonine kinase-like protein NCBI Description

[Arabidopsis thaliana]

28793 Seq. No.

181150 1.R1040 Contig ID dpv701097108.hl 5'-most EST

Method BLASTX g3142301 NCBI GI 606 BLAST score 7.0e-63 E value 217 Match length



% identity NCBI Description

(AC002411) Contains similarity to neural cell adhesion molecule 2, large isoform precursor gb\_M76710 from Xenopus laevis, and beta transducin from S. cerevisiae gb\_Q05946. ESTs gb\_N65081 gb\_Z30910, gb\_Z34190, gb\_Z34611, gb\_R30101, gb\_H3630

Seq. No. 28794

Contig ID 181156\_1.R1040 5'-most EST fde700870946.h1

Method BLASTX
NCBI GI g2642448
BLAST score 282
E value 1.0e-25
Match length 79
% identity 38

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana] >gi 3169187 (AC004401) hypothetical protein [Arabidopsis

+balianal

thaliana]

Seq. No. 28795

Contig ID 181158\_1.R1040

5'-most EST uC-gmrominsoy080e12b1

Method BLASTN
NCBI GI g2264321
BLAST score 46
E value 1.0e-16
Match length 94
% identity 42

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXM12, complete sequence [Arabidopsis thaliana]

Seq. No. 28796

Contig ID 181204\_1.R1040 5'-most EST fde700871020.h1

Method BLASTX
NCBI GI g3550554
BLAST score 373
E value 3.0e-36
Match length 84
% identity 82

NCBI Description (Y17469) sarco/endoplasmic reticulum Ca2+ -ATPase

[Paramecium tetraurelia]

Seq. No. 28797

Contig ID 181232\_1.R1040 5'-most EST uC-gmropic026c02b1

Method BLASTX
NCBI GI g2262105
BLAST score 323
E value 7.0e-30
Match length 96
% identity 64

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 28798

Contig ID 181273\_1.R1040



5'-most EST fde700871115.hl

Seq. No. 28799

Contig ID 181302\_1.R1040 5'-most EST fde700871158.h1

Method BLASTX
NCBI GI g2832629
BLAST score 176
E value 1.0e-12
Match length 115
% identity 37

NCBI Description (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis

thaliana]

Seq. No. 28800

Contig ID 181320\_1.R1040

5'-most EST g5677137

Method BLASTN

NCBI GI g3046710

BLAST score 320

E value 1.0e-180

Match length 468

% identity 92

NCBI Description Cicer arietinum mRNA for replication factor C/activator 1

subunit, partial

Seq. No. 28801

Contig ID 181375\_1.R1040 5'-most EST fde700871370.h1

Seq. No. 28802

Contig ID 181378\_1.R1040 5'-most EST fde700871384.h1

Seq. No. 28803

Contig ID 181380\_1.R1040 5'-most EST fde700871475.h1

Seq. No. 28804

Contig ID 181406\_1.R1040 5'-most EST fde700875863.h1

Method BLASTX
NCBI GI g421842
BLAST score 263
E value 6.0e-31
Match length 86
% identity 81

NCBI Description potassium channel protein - Arabidopsis thaliana >gi\_166774

(M86990) potassium channel protein [Arabidopsis thaliana] >gi 1065906 (U25088) potassium channel protein [Arabidopsis

thaliana]

Seq. No. 28805

Contig ID 181414\_1.R1040 5'-most EST fde700872880.h1

Seq. No. 28806



181441 1.R1040 Contig ID fde700871614.hl 5'-most EST

28807 Seq. No.

Contig ID 181446 1.R1040 fde700873667.hl 5'-most EST

28808 Seq. No.

181448 1.R1040 Contig ID jex700909437.hl 5'-most EST

28809 Seq. No.

181457 1.R1040 Contig ID zzp700831121.h1 5'-most EST BLASTX Method

NCBI GI q1706884 BLAST score 365 2.0e-34 E value 276 Match length

34 % identity

FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR NCBI Description

(FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS)

28810 Seq. No.

181461 1.R1040 Contig ID 5'-most EST fde700875886.hl

Seq. No. 28811

181486 1.R1040 Contig ID 5'-most EST fde700875642.hl

Method BLASTX q4567263 NCBI GI BLAST score 366 2.0e-35 E value 84 Match length % identity

(AC006841) putative cell division inhibitor [Arabidopsis NCBI Description

thaliana]

28812 Seq. No.

181510 1.R1040 Contig ID bth700845762.h1 5'-most EST

28813 Seq. No.

181514 1.R1040 Contig ID hrw701063367.hl 5'-most EST

Seq. No. 28814

181541 1.R1040 Contig ID  $asn701\overline{1}36708.h1$ 5'-most EST

BLASTX Method q4490317 NCBI GI BLAST score 380 2.0e-36 E value 188 Match length 43 % identity

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]



```
28815
Seq. No.
                  181610 1.R1040
Contig ID
                  fde700871835.hl
5'-most EST
                  28816
Seq. No.
                  181620 1.R1040
Contig ID
                  jC-gmf102220055g03a1
5'-most EST
                  BLASTX
Method
                  g2565297
NCBI GI
                  332
BLAST score
                  6.0e-31
E value
                  158
Match length
                  50
% identity
                  (AF024590) RNA polymerase sigma subunit 1 [Arabidopsis
NCBI Description
                  thaliana]
                   28817
Seq. No.
                   181635 1.R1040
Contig ID
                   fde700871879.hl
5'-most EST
                   28818
Seq. No.
                   181645 1.R1040
Contig ID
                  pxt700942623.hl
5'-most EST
                   28819
Seq. No.
                   181649 1.R1040
Contig ID
                   fde700874147.hl
5'-most EST
                   28820
Seq. No.
                   181672 1.R1040
Contig ID
                   pmv700888202.h1
5'-most EST
                   BLASTN
Method
                   g4263753
NCBI GI
BLAST score
                   32
                   1.0e-08
E value
                   76
Match length
                   86
% identity
                   Arabidopsis thaliana chromosome V map near 60.5 cM,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   28821
Seq. No.
                   181688 1.R1040
Contig ID
                   q4296088
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3065814
BLAST score
                   213
                   7.0e-17
E value
                   169
Match length
```

% identity

(AF058714) sodium-dicarboxylate cotransporter SDCT1 [Rattus NCBI Description

norvegicus] >gi\_3168585\_dbj\_BAA28609\_ (AB001321) sodium-dependent dicarboxylate transporter [Rattus

norvegicus]

28822 Seq. No.

181706 1.R1040 Contig ID



```
fde700872031.hl
5'-most EST
Seq. No.
                  28823
Contig ID
                  181714 1.R1040
                  uC-gmrominsoy111g01b1
5'-most EST
Method
                  BLASTX
                  q3236247
NCBI GI
BLAST score
                  386
                  7.0e-49
E value
                   155
Match length
% identity
NCBI Description (AC004684) SCARECROW-like protein [Arabidopsis thaliana]
Seq. No.
                   181721 1.R1040
Contig ID
5'-most EST
                   fde700872030.h1
Seq. No.
                   28825
                   181743 1.R1040
Contig ID
                   fde700872078.h1
5'-most EST
Seq. No.
                   28826
                   181778 1.R1040
Contig ID
                   zhf700\overline{9}58516.h1
5'-most EST
                   BLASTX
Method
                   g3402717
NCBI GI
BLAST score
                   162
                   9.0e-15
E value
                   63
Match length
% identity
                   (AC004261) putative heat shock protein [Arabidopsis
NCBI Description
                   thaliana]
                   28827
Seq. No.
                   181790 1.R1040
Contig ID
                   fde700876485.hl
5'-most EST
                   28828
Seq. No.
                   181798 1.R1040
Contig ID
                   jC-qmro02910060f04a1
5'-most EST
                   BLASTX
Method
                   q4467148
NCBI GI
                   588
BLAST score
                   7.0e-61
E value
                   178
Match length
% identity
                   72
                   (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                   28829
Seq. No.
                   181807 1.R1040
Contig ID
                   jC-qmle01810019b10a2
5'-most EST
                   BLASTX
Method
                   g3914136
NCBI GI
                   282
BLAST score
                   8.0e-25
E value
```

87

63

Match length

% identity



NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)

>gi\_2632171\_emb\_CAA05771\_ (AJ002958) lipid transfer protein

[Cicer arietinum]

Seq. No. 28830

Contig ID 181815\_1.R1040 5'-most EST zsg701130235.h1

Method BLASTX
NCBI GI g1723832
BLAST score 154
E value 5.0e-10
Match length 71
% identity 44

NCBI Description HYPOTHETICAL 15.9 KD PROTEIN IN OLE1-DUP1 INTERGENIC REGION

>gi\_2132531\_pir\_\_S64058 probable membrane protein YGL054c yeast (Saccharomyces cerevisiae) >gi\_1322550\_emb\_CAA96756\_

(Z72576) ORF YGL054c [Saccharomyces cerevisiae]

Seq. No. 28831

Contig ID 181817\_1.R1040 5'-most EST fde700876653.h1

Seq. No. 28832

Contig ID 181846\_1.R1040 5'-most EST fde700872278.h1

Method BLASTX
NCBI GI g3176726
BLAST score 474
E value 2.0e-47
Match length 181
% identity 51

NCBI Description (AC002392) putative serine proteinase [Arabidopsis

thaliana]

Seq. No. 28833

Contig ID 181858\_1.R1040 5'-most EST fde700872310.h1

Seq. No. 28834

Contig ID 181861 2.R1040 5'-most EST fde700872465.h1

Seq. No. 28835

Contig ID 181865\_1.R1040 5'-most EST fde700873959.h1

Method BLASTX
NCBI GI g2605714
BLAST score 140
E value 8.0e-09
Match length 59
% identity 46

NCBI Description (AF026275) beta-tonoplast intrinsic protein [Arabidopsis

thaliana]

Seq. No. 28836

Contig ID 181887\_1.R1040 5'-most EST fde700872369.h1

```
28837
Seq. No.
                  181896 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy048d07b1
                  28838
Seq. No.
                  181915 1.R1040
Contig ID
                  fde700876846.h1
5'-most EST
                  BLASTX
Method
                  g1652649
NCBI GI
                   478
BLAST score
                   7.0e-48
E value
Match length
                  161
                   55
% identity
                  (D90907) hypothetical protein [Synechocystis sp.]
NCBI Description
                   28839
Seq. No.
                   181927 1.R1040
Contig ID
                   jC-qmle01810011e07a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g728905
                   159
BLAST score
                   2.0e-10
E value
                   155
Match length
                   27
% identity
                   PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC
NCBI Description
                   RETICULUM CA2+-ATPASE) >gi_1078206_pir__S51995 probable
                   ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae)
                   >gi_171114 (L01795) ATPase [Saccharomyces cerevisiae]
                   >gi_595560 (U12980) Drs2p: Membrane spanning
                   Ca-ATPase (P-type), member of the cation transport (E1-E2)
                   ATPase [Saccharomyces cerevisiae]
                   28840
Seq. No.
                   181953 1.R1040
Contig ID
                   k11701\overline{2}09449.h1
5'-most EST
                   BLASTX
Method
                   g4559396
NCBI GI
                   259
BLAST score
                   8.0e-23
E value
                   66
Match length
                   71
% identity
NCBI Description (AC006526) unknown protein [Arabidopsis thaliana]
                   28841
Seq. No.
                   181971 1.R1040
Contig ID
                   crh700850692.h1
5'-most EST
                   BLASTX
Method
                   q4490304
NCBI GI
BLAST score
                   521
E value
                   3.0e-53
Match length
                   121
                   82
% identity
                   (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
```

28842

181984\_1.R1040

Seq. No. Contig ID



5'-most EST fde700872574.h1

Seq. No. 28843

Contig ID 182038\_1.R1040 5'-most EST dpv701102023.h1

Method BLASTN
NCBI GI g289124
BLAST score 202
E value 1.0e-110
Match length 270
% identity 94

NCBI Description Medicago sativa MAP kinase MsERK1 mRNA, complete cds

Seq. No. 28844

Contig ID 182050\_1.R1040 5'-most EST fde700872717.h1

Method BLASTN
NCBI GI g1134881
BLAST score 118
E value 7.0e-60
Match length 262
% identity 86

NCBI Description P.sativum mRNA for cysteine protease

Seq. No. 28845

Contig ID 182065\_1.R1040 5'-most EST sat701015446.h1

Method BLASTX
NCBI GI g2129820
BLAST score 190
E value 9.0e-15
Match length 82
% identity 49

NCBI Description chitinase (EC 3.2.1.14) class II - peanut

>gi\_1237025\_emb\_CAA57773\_ (X82329) chitinase (class II)

[Arachis hypogaea]

Seq. No. 28846

Contig ID 182066\_1.R1040 5'-most EST fde700872743.h1

Seq. No. 28847

Contig ID 182067\_1.R1040 5'-most EST fde700875456.h1

Seq. No. 28848

Contig ID 182077\_1.R1040 5'-most EST fde700872757.h1

Seq. No. 28849

Contig ID 182078\_1.R1040

5'-most EST jC-gmro02910008g10a1

Method BLASTX
NCBI GI g3877656
BLAST score 324
E value 8.0e-30
Match length 203

4455



% identity (272511) similar to nucleotide translocator [Caenorhabditis NCBI Description elegans] Seq. No. 28850 182078 2.R1040 Contig ID fde700872758.hl 5'-most EST BLASTN Method q3510339 NCBI GI BLAST score 36 6.0e-11 E value 96 Match length % identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K3K7, complete sequence [Arabidopsis thaliana] Seq. No. 28851 Contig ID 182078 3.R1040 leu701156558.hl 5'-most EST BLASTN q3510339 BLAST score 32

Method NCBI GI 1.0e-08 E value 96 Match length % identity 83

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K3K7, complete sequence [Arabidopsis thaliana]

28852 Seq. No. 182079 1.R1040 Contig ID fde700875724.hl 5'-most EST

BLASTX Method g4063746 NCBI GI BLAST score 221 4.0e-18 E value 85 Match length % identity 57

(AC005851) nodulin-like protein [Arabidopsis thaliana] NCBI Description

Seq. No. 28853

182131 1.R1040 Contig ID

5'-most EST uC-gmrominsoy195e05b1

BLASTX Method g2765817 NCBI GI 493 BLAST score 1.0e-49 E value 214 Match length 47 % identity

(Z95352) AtMlo-h1 [Arabidopsis thaliana] NCBI Description

>gi 3892049\_gb\_AAC78258.1\_AAC78258 (AC002330) AtMlo-h1

[Arabidopsis thaliana]

28854 Seq. No.

182141 1.R1040 Contig ID

g50580<del>5</del>7 5'-most EST

28855 Seq. No.



```
Contig ID
                  182209 1.R1040
5'-most EST
                  fde700873982.hl
                  BLASTX
Method
                  g4558556
NCBI GI
BLAST score
                  230
E value
                  5.0e-19
Match length
                  107
                  44
% identity
                  (AC007138) predicted protein of unknown function
NCBI Description
                  [Arabidopsis thaliana]
```

Seq. No. 28856

Contig ID 182214\_1.R1040 5'-most EST uC-gmropic032b02b1

Seq. No. 28857

Contig ID 182217\_1.R1040 5'-most EST pmv700892710.h1

Seq. No. 28858

Contig ID 182218\_1.R1040 5'-most EST kl1701206235.h1

Seq. No. 28859

Contig ID 182228 1.R1040 5'-most EST bth700848581.h1

Method BLASTX
NCBI GI g4049399
BLAST score 167
E value 5.0e-12
Match length 66
% identity 39

NCBI Description (Y09581) FRO2 [Arabidopsis thaliana]

Seq. No.

Contig ID 182240\_1.R1040 5'-most EST fde700873913.h1

Seq. No.

Contig ID 182249\_1.R1040 5'-most EST fde700873010.h1

28860

28861

Method BLASTX
NCBI GI g2979546
BLAST score 142
E value 4.0e-09
Match length 44
% identity 61

NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]

Seq. No. 28862

Contig ID 182257\_1.R1040 5'-most EST fC-gmle700873022a1

Method BLASTX
NCBI GI g113626
BLAST score 590
E value 4.0e-61
Match length 162



% identity NCBI Description

FRUCTOSE-BISPHOSPHATE ALDOLASE >gi 68202 pir ADBY2 fructose-bisphosphate aldolase (EC 4.1.2.13) II - yeast (Saccharomyces cerevisiae) >gi 3696 emb CAA33111 (X15003) fructose-bisphosphate aldolase [Saccharomyces cerevisiae]

>gi 433637 emb CAA53412\_ (X75781) yeast

fructose-bisphate-aldolase [Saccharomyces cerevisiae]

>gi\_486081\_emb\_CAA81897\_ (Z28060) ORF YKL060c

[Saccharomyces cerevisiae] >gi\_1587557\_prf\_\_2206495F fructosebisphosphate aldolase [Saccharomyces cerevisiae]

Seq. No. 28863

Contig ID 182281\_1.R1040 5'-most EST jex700909558.h1

Method BLASTX
NCBI GI g473874
BLAST score 379
E value 8.0e-37
Match length 93
% identity 41

NCBI Description (U08285) a membrane-associated salt-inducible protein

[Nicotiana tabacum]

Seq. No. 28864

Contig ID 182283\_1.R1040 5'-most EST fde700873065.h1

Method BLASTX
NCBI GI 94406820
BLAST score 285
E value 4.0e-34
Match length 108
% identity 76

NCBI Description (AC006201) putative ras superfamily member [Arabidopsis

thaliana]

Seq. No. 28865

Contig ID 182308\_1.R1040 5'-most EST fde700874276.h1

Method BLASTX
NCBI GI g4106690
BLAST score 151
E value 4.0e-10
Match length 46
% identity 61

NCBI Description (AL035065) putative urea active transporter

[Schizosaccharomyces pombe]

Seq. No. 28866

Contig ID 182340\_1.R1040 5'-most EST leu701155963.h1

Seq. No. 28867

Contig ID 182350\_1.R1040 5'-most EST fde700873155.h1

Seq. No. 28868

Contig ID 182365\_1.R1040



5'-most EST all700863165.hl

Method BLASTX
NCBI GI g3183377
BLAST score 238
E value 9.0e-20
Match length 148
% identity 22

NCBI Description HYPOTHETICAL 79.3 KD PROTEIN C24C9.05C IN CHROMOSOME I

>gi 2330788\_emb\_CAB11262\_ (Z98601) hypothetical protein.

[Schizosaccharomyces pombe]

Seq. No. 28869

Contig ID 182390\_1.R1040

5'-most EST uC-gmflminsoy063a03b1

Seq. No. 28870

Contig ID 182441 1.R1040

5'-most EST uC-gmflminsoy084d03b1

Method BLASTX
NCBI GI g3292826
BLAST score 182
E value 1.0e-13
Match length 88
% identity 42

NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28871

Contig ID 182455\_1.R1040 5'-most EST fde700873293.h1

Seq. No. 28872

Contig ID 182458\_1.R1040

5'-most EST g5510075
Method BLASTX
NCBI GI g1171577
BLAST score 273
E value 9.0e-34
Match length 149
% identity 58

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 28873

Contig ID 182465 1.R1040

5'-most EST uC-gmrominsoy273g01b1

Method BLASTX
NCBI GI 94544383
BLAST score 414
E value 1.0e-40
Match length 110
% identity 74

NCBI Description (AC007047) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28874

Contig ID 182482\_1.R1040 5'-most EST fde700873332.h1

Seq. No. 28875

E value

Match length

% identity

414

95



```
182489 1.R1040
Contig ID
                  fde700873647.hl
5'-most EST
                  28876
Seq. No.
                  182497 1.R1040
Contig ID
5'-most EST
                  sat701009071.h1
                  BLASTN
Method
                  q1354856
NCBI GI
                  396
BLAST score
                  0.0e+00
E value
Match length
                  707
                   89
% identity
                  Phaseolus vulgaris bZIP transcriptional repressor ROM1
NCBI Description
                  mRNA, complete cds
                   28877
Seq. No.
                   182516 1.R1040
Contig ID
                   zhf700965290.h1
5'-most EST
                   BLASTX
Method
                   g2245065
NCBI GI
                   175
BLAST score
                   5.0e-13
E value
                   43
Match length
                   13
% identity
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
                   28878
Seq. No.
                   182525 1.R1040
Contig ID
                   fC-qmle700873411a1
5'-most EST
                   BLASTX
Method
                   q4512667
NCBI GI
                   248
BLAST score
                   3.0e-37
E value
                   118
Match length
% identity
                   (AC006931) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   28879
                   182528 1.R1040
Contig ID
                   bth700845409.h1
5'-most EST
                   BLASTX
Method
                   q2792155
NCBI GI
BLAST score
                   504
                   5.0e-51
E value
                   183
Match length
 % identity
                   56
                   (AJ223291) chalcone reductase [Sesbania rostrata]
NCBI Description
                   28880
 Seq. No.
                   182536 1.R1040
 Contig ID
                   crh700851111.h1
 5'-most EST
                   BLASTN
 Method
 NCBI GI
                   g516102
                   268
 BLAST score
                   1.0e-149
```



```
NCBI Description Soybean phytochrome B (phyB) gene exons 1-5, complete cds

Seq. No. 28881
Contig ID 182540_1.R1040
5'-most EST fC-gmle700873428r1
Method BLASTX
NCBI GI g1168409
```

BLAST score 147
E value 2.0e-09
Match length 95
% identity 43

NCBI Description PROBABLE FRUCTOSE-BISPHOSPHATE ALDOLASE 2

>gi\_709990\_dbj\_BAA03299\_ (D14399) hypothetical protein
[Bacillus subtilis] >gi\_2636513\_emb\_CAB16003\_ (Z99124)
fructose-1,6-bisphosphate aldolase [Bacillus subtilis]

Seq. No. 28882
Contig ID 182542\_1.R1040
5'-most EST fde700873430.h1
Method BLASTN
ACT CL. 28882
182542\_1.R1040
BLASTN
ACT CL. 28882

Method BLASTN
NCBI GI g10789
BLAST score 136
E value 1.0e-70
Match length 247
% identity 21

NCBI Description T.pyriformis TU20 gene for ubiquitin

Seq. No. 28883

Contig ID 182556\_1.R1040 5'-most EST jC-gmst02400047g05d1

Method BLASTX
NCBI GI g4115382
BLAST score 407
E value 9.0e-40
Match length 101
% identity 75

NCBI Description (AC005967) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28884

Contig ID 182562\_1.R1040 5'-most EST fde700873462.h1

Method BLASTX
NCBI GI g3164140
BLAST score 283
E value 1.0e-25
Match length 78
% identity 64

NCBI Description (D78605) cytochrome P450 monooxygenase [Arabidopsis

thaliana]

Seq. No. 28885

Contig ID 182597\_1.R1040 5'-most EST fde700874048.h1

Seq. No. 28886

Contig ID 182612\_1.R1040 5'-most EST fde700873542.h1



BLASTX Method q2735017 NCBI GI 394 BLAST score 2.0e-38 E value 96 Match length % identity 79 NCBI Description (U82481) KI domain interacting kinase 1 [Zea mays]

28887 Seq. No.

182617 1.R1040 Contig ID 5'-most EST fde700874501.h1

28888 Seq. No.

182630 1.R1040 Contig ID fde700873984.hl 5'-most EST

28889 Seq. No.

182636 1.R1040 Contig ID

uC-gmflminsoy071a12b2 5'-most EST

28890 Seq. No.

182649 1.R1040 Contig ID sat701015457.h1 5'-most EST

BLASTN Method g857396 NCBI GI 134 BLAST score 2.0e-69 E value 250 Match length 89 % identity

Glycine max mRNA for mitotic cyclin a2-type, complete cds NCBI Description

28891 Seq. No.

Contig ID 182665 1.R1040 pxt700941060.hl 5'-most EST

BLASTX Method q3355478 NCBI GI BLAST score 141 E value 5.0e-09 74 Match length % identity 43

(ACO04218) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 28892

182687 1.R1040 Contig ID fde700873651.h1 5'-most EST

BLASTX Method q4006851 NCBI GI BLAST score 204 2.0e-31 E value Match length 116 % identity

(Z99707) cytochrome P450-like protein [Arabidopsis NCBI Description

thaliana]

28893 Seq. No.

182688 1.R1040 Contig ID fde700873652.h1 5'-most EST



```
28894
Seq. No.
                   182738 1.R1040
Contig ID
                   fde700874019.hl
5'-most EST
                   BLASTN
Method
                   q20880
NCBI GI
                   32
BLAST score
                   1.0e-08
E value
                   36
Match length
                   97
% identity
NCBI Description Pea mRNA for plastid ribosomal protein CL9
Seq. No.
                   28895
                   182746 1.R1040
Contig ID
                   fde700873732.hl
5'-most EST
                   28896
Seq. No.
                   182752 1.R1040
Contig ID
                   iC-gmst02400008h09a1
5'-most EST
                   BLASTX
Method
                   q3152592
NCBI GI
BLAST score
                   330
                   1.0e-30
E value
                   110
Match length
% identity
                   (AC002986) Contains similarity to 8A-2V protein gb Y10496
NCBI Description
                   from Mus musculus. [Arabidopsis thaliana]
                   28897
Seq. No.
                   182753 1.R1040
Contig ID
                   fde700873744.hl
5'-most EST
                   28898
Seq. No.
                   182764 1.R1040
Contig ID
                   pmv700892512.h1
 5'-most EST
                   BLASTX
Method
NCBI GI
                   q2129698
BLAST score
                   454
                   3.0e-45
E value
                   132
Match length
                   67
 % identity
                   protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana
 NCBI Description
                   >qi 1054633 emb CAA63387_ (X92728) protein kinase
                    [Arabidopsis thaliana]
                   28899
 Seq. No.
                   182797 1.R1040
 Contig ID
                   zhf700960172.h1
 5'-most EST
                   28900
 Seq. No.
```

Contig ID 182808\_1.R1040 5'-most EST jex700905406.h1

Seq. No. 28901

Contig ID 182840\_1.R1040 5'-most EST jC-gmle01810073f03a1

Method BLASTX

4463



```
q3292824
NCBI GI
                  237
BLAST score
                  9.0e-20
E value
                   65
Match length
% identity
                  (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
                  28902
Seq. No.
                  182840 2.R1040
Contig ID
                   jC-gmle01810016e06a1
5'-most EST
                  BLASTX
Method
                   g3292824
NCBI GI
                   182
BLAST score
                   2.0e-13
E value
Match length
                   57
% identity
                   61
                  (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
                   28903
Seq. No.
                   182851 1.R1040
Contig ID
                   fde700873885.hl
5'-most EST
                   28904
Seq. No.
                   182860 1.R1040
Contig ID
                   jC-gmf102220138b08d1
5'-most EST
                   28905
Seq. No.
                   182882 1.R1040
Contig ID
                   fde700873968.hl
5'-most EST
                   28906
Seq. No.
                   182894 1.R1040
Contig ID
                   fde700873956.hl
5'-most EST
                   BLASTN
Method
                   g4521152
NCBI GI
                   100
BLAST score
                   4.0e-49
E value
                   272
Match length
% identity
                   84
                  Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
NCBI Description
                   complete sequence
                   28907
Seq. No.
                   182919 1.R1040
Contig ID
5'-most EST
                   fde700873986.hl
                   BLASTX
Method
                   g3953463
NCBI GI
                   204
BLAST score
E value
                   6.0e-16
                   47
Match length
 % identity
                   79
                   (AC002328) F20N2.8 [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 28908

Contig ID 182920\_1.R1040 5'-most EST jC-gmle01810051d08a1

Method BLASTX

4464



```
g4490317
NCBI GI
                   228
BLAST score
E value
                   1.0e-18
                   100
Match length
% identity
                   (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   28909
Seq. No.
                   182945 1.R1040
Contig ID
                   fde700874024.hl
5'-most EST
                   28910
Seq. No.
                   182948 1.R1040
Contig ID
                   dpv701\overline{0}99247.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2342717
BLAST score
                   52
                   2.0e-20
E value
Match length
                   80
                   91
% identity
                   Arabidopsis thaliana chromosome II BAC T14G11 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

Contig ID 183009\_1.R1040 5'-most EST jC-gmle01810025e05a1

Seq. No. 28912

Contig ID 183014\_1.R1040 5'-most EST jsh701069970.h2

Method BLASTX
NCBI GI g1279640
BLAST score 449
E value 1.0e-44
Match length 126
% identity 66

NCBI Description (X92204) NAM [Petunia x hybrida]

Seq. No. 28913

Contig ID 183027\_1.R1040 5'-most EST fde700874161.h1

Seq. No. 28914

Contig ID 183032\_1.R1040 5'-most EST epx701107729.h1

Seq. No. 28915

Contig ID 183069\_1.R1040 5'-most EST zsg701118022.h2

Seq. No. 28916

Contig ID 183074\_1.R1040 5'-most EST fua701037884.h1

Method BLASTX
NCBI GI g2827637
BLAST score 141
E value 1.0e-08



77 Match length 40 % identity

(AL021636) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

28917 183097 1.R1040 Contig ID k11701205752.h1 5'-most EST

Seq. No.

183132 1.R1040 Contig ID kl1701202418.h1 5'-most EST

28918

28919 Seq. No.

183161 1.R1040 Contig ID 5'-most EST fde700874663.h1

Seq. No. 28920

183169 1.R1040 Contig ID fde700874373.h1 5'-most EST

28921 Seq. No.

183202 1.R1040 Contig ID fde700874417.hl 5'-most EST

28922 Seq. No.

183216 1.R1040 Contig ID fde700874745.hl 5'-most EST

Seq. No. 28923

183247 1.R1040 Contig ID jC-gmro02910057c12a1 5'-most EST

Method BLASTX q3377803 NCBI GI 477 BLAST score 5.0e-48 E value 133 Match length 71

% identity (AF075597) Similar to (p)ppGpp synthetase; T2H3.9 NCBI Description

[Arabidopsis thaliana]

28924 Seq. No.

183256 1.R1040 Contig ID

jC-gmle01810012g08d1 5'-most EST

BLASTX Method g3367522 NCBI GI BLAST score 412 3.0e-40 E value 106 Match length % identity

(AC004392) EST gb\_T04691 comes from this gene. [Arabidopsis NCBI Description

thaliana]

28925 Seq. No.

183282 1.R1040 Contig ID

uC-gmrominsoy241f03b1 5'-most EST

BLASTX Method g4454469 NCBI GI



BLAST score 451 E value 8.0e-45 Match length 161 % identity 54

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 28926

Contig ID 183311\_1.R1040 5'-most EST zhf700963066.h1

Method BLASTX
NCBI GI g4140326
BLAST score 212
E value 5.0e-27
Match length 126
% identity 50

NCBI Description (AL031282) dJ283E3.6.1 (PUTATIVE novel protein similar to

many (archae) bacterial, worm and yeast hypothetical

proteins) [Homo sapiens]

Seq. No. 28927

Contig ID 183325\_1.R1040 5'-most EST zhf700960204.h1

Method BLASTX
NCBI GI g282881
BLAST score 202
E value 1.0e-15
Match length 134
% identity 39

NCBI Description receptor-like protein kinase precursor - Arabidopsis

thaliana >gi\_166846 (M84658) receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 28928

Contig ID 183331\_1.R1040 5'-most EST pxt700941705.h1

Seq. No. 28929

Contig ID 183334 1.R1040 5'-most EST jC-gmle01810075c07a1

Method BLASTX
NCBI GI g4455367
BLAST score 169
E value 8.0e-12
Match length 144
% identity 35

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 28930

Contig ID 183350\_1.R1040 5'-most EST fde700874675.h1

Seq. No. 28931

Contig ID 183356\_1.R1040

5'-most EST uC-gmrominsoy245b09b1

Method BLASTX
NCBI GI g4371292
BLAST score 318



E value 5.0e-29
Match length 138
% identity 46

NCBI Description (AC006260) unknown protein [Arabidopsis thaliana]

Seq. No. 28932

Contig ID 183358\_1.R1040 5'-most EST hrw701059607.h1

Method BLASTX
NCBI GI g4102839
BLAST score 138
E value 1.0e-08
Match length 50
% identity 54

NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No. 28933

Contig ID 183359\_1.R1040 5'-most EST fde700875018.h1

Seq. No. 28934

Contig ID 183363\_1.R1040 5'-most EST fde700874836.h1

Seq. No. 28935

Contig ID 183377\_1.R1040 5'-most EST fde700874667.h1

Method BLASTX
NCBI GI g2465923
BLAST score 596
E value 1.0e-61
Match length 186
% identity 61

NCBI Description (AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. 28936

Contig ID 183386\_1.R1040

5'-most EST uC-gmrominsoy067f06b1

Method BLASTX
NCBI GI g1438875
BLAST score 183
E value 1.0e-13
Match length 40
% identity 80

NCBI Description (U31462) violaxanthin de-epoxidase precursor [Lactuca

sativa]

Seq. No. 28937

Contig ID 183394 1.R1040

5'-most EST jC-gmle01810042b03d1

Seq. No. 28938

Contig ID 183440\_1.R1040 5'-most EST fde700874742.h1

Seq. No. 28939



Contig ID 183479\_1.R1040 5'-most EST uC-gmronoir060d04b1

Seq. No. 28940

Contig ID 183489\_1.R1040 5'-most EST fde700874808.h1

Seq. No. 28941

Contig ID 183510\_1.R1040 5'-most EST fde700874837.h1

Seq. No. 28942

Contig ID 183513\_1.R1040 5'-most EST ary700764453.h1

Method BLASTX
NCBI GI g629669
BLAST score 182
E value 2.0e-13
Match length 62
% identity 50

NCBI Description hypothetical protein - tomato

Seq. No. 28943

Contig ID 183520\_1.R1040 5'-most EST fde700874852.h1

Seq. No. 28944

Contig ID 183535\_1.R1040 5'-most EST fde700874875.h1

Seq. No. 28945

Contig ID 183542\_1.R1040 5'-most EST jC-gmro02910051e10a1

Method BLASTX
NCBI GI g2444174
BLAST score 852
E value 9.0e-92
Match length 195
% identity 82

NCBI Description (U94781) unconventional myosin [Helianthus annuus]

Seq. No. 28946

Contig ID 183596\_1.R1040 5'-most EST awf700836895.h1

Method BLASTX
NCBI GI g2129656
BLAST score 292
E value 2.0e-39
Match length 140
% identity 61

NCBI Description OBP33pep protein - Arabidopsis thaliana (fragment) >qi 1022801 (U37699) OBP33pep [Arabidopsis thaliana]

Seq. No. 28947

Contig ID 183598\_1.R1040 5'-most EST fde700874962.h1



183615 1.R1040 Contig ID leu701155293.hl 5'-most EST

Seq. No. 28949

183624 1.R1040 Contig ID fua701037786.h1 5'-most EST

28950 Seq. No.

183631 1.R1040 Contig ID

jC-gmle01810094e07a1 5'-most EST

BLASTN Method g868002 NCBI GI BLAST score 122 4.0e-62 E value Match length 338 % identity

NCBI Description Pumpkin mRNA for aconitase, complete cds

Seq. No. 28951

183638 1.R1040 Contig ID fde700875021.hl 5'-most EST

28952 Seq. No.

183646 1.R1040 Contig ID fde700875129.hl 5'-most EST

BLASTN Method g1235600 NCBI GI BLAST score 154 2.0e-81 E value 234 Match length % identity 92

NCBI Description S.macrospora EF1-alpha gene

28953 Seq. No.

183651 1.R1040 Contig ID fde700875216.hl 5'-most EST

28954 Seq. No.

183665 1.R1040 Contig ID 5'-most EST sat701011418.hl

28955 Seq. No.

183677 1.R1040 Contig ID zhf700958916.h1 5'-most EST

BLASTX Method q1076365 NCBI GI 170 BLAST score 8.0e-12 E value 184 Match length 29 % identity

pectinesterase (EC 3.1.1.11) PME1 precursor - Arabidopsis NCBI Description

thaliana >gi\_2129666\_pir\_\_JC4778 pectinesterase (EC 3.1.1.11) 1 - Arabidopsis thaliana >gi\_550306\_emb\_CAA57275\_ (X81585) ATPME1 [Arabidopsis thaliana] >gi\_903895 (U25649)

ATPME1 precursor [Arabidopsis thaliana]



Contig ID 183684\_1.R1040

5'-most EST jC-gmle01810062d09a1

Seq. No. 28957

Contig ID 183714\_1.R1040

5'-most EST jC-gmf $\overline{1}$ 022220070d06a1

Seq. No. 28958

Contig ID 183842 1.R1040 5'-most EST fde700875315.h1

Seq. No. 28959

Contig ID 183845\_1.R1040 5'-most EST fde700875318.h1

Method BLASTX
NCBI GI g2947063
BLAST score 231
E value 4.0e-19
Match length 144
% identity 38

NCBI Description (AC002521) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 28960

Contig ID 183856\_1.R1040 5'-most EST fde700875338.h1

Seq. No. 28961

Contig ID 183890\_1.R1040 5'-most EST fde700875379.h1

Seq. No. 28962

Contig ID 183919\_1.R1040 5'-most EST kl1701205968.h1

Seq. No. 28963

Contig ID 183975\_1.R1040 5'-most EST fde700875494.h1

Method BLASTX
NCBI GI g1653767
BLAST score 330
E value 7.0e-31
Match length 121
% identity 53

NCBI Description (D90916) oligopeptidase A [Synechocystis sp.]

Seq. No. 28964

Contig ID 183992 1.R1040

5'-most EST g5677624

Seq. No. 28965

Contig ID 184065\_1.R1040 5'-most EST fde700875620.h1

Seq. No. 28966

Contig ID 184078\_1.R1040



```
fde700875640.h1
5'-most EST
Seq. No.
                  28967
Contig ID
                  184084 1.R1040
                  leu701149946.hl
5'-most EST
                  28968
Seq. No.
                  184089 1.R1040
Contig ID
                  jC-gmro02910012g06d1
5'-most EST
                  28969
Seq. No.
                  184089 2.R1040
Contig ID
                  asn701142114.h1
5'-most EST
                  BLASTX
Method
                  g2244936
NCBI GI
BLAST score
                  142
                  5.0e-09
E value
Match length
                  42
                  67
% identity
                  (Z97339) similarity to chloroplast outer envelope protein
NCBI Description
                  OEP8 [Arabidopsis thaliana]
                  28970
Seq. No.
                  184119 1.R1040
Contig ID
                  jC-gmle01810014e03d1
5'-most EST
                   28971
Seq. No.
                  184136 1.R1040
Contig ID
                   fde700875730.hl
5'-most EST
                  BLASTX
Method
                   g2160173
NCBI GI
BLAST score
                   263
                   3.0e-23
E value
                   86
Match length
% identity
                   (AC000132) Similar to N. tabacum salt-inducible protein
NCBI Description
                   (gb_U08285). [Arabidopsis thaliana]
                   28972
Seq. No.
                   184150 1.R1040
Contig ID
5'-most EST
                   pxt700941132.hl
                   28973
Seq. No.
                   184152 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400026a02a1
                   28974
Seq. No.
                   184165 1.R1040
Contig ID
5'-most EST
                   fde700875776.h1
```

184193 1.R1040 Contig ID

uC-qmrominsoy162f07b1 5'-most EST

Method BLASTX q1946371 NCBI GI BLAST score 227 1.0e-18 E value



```
73
Match length
% identity
                  56
                  (U93215) regulatory protein Viviparous-1 isolog
NCBI Description
                   [Arabidopsis thaliana]
                  28976
Seq. No.
                  184206 1.R1040
Contig ID
                  fde700875834.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2245115
BLAST score
                  352
                   3.0e-33
E value
                  113
Match length
                   64
% identity
NCBI Description (Z97343) unnamed protein product [Arabidopsis thaliana]
                   28977
Seq. No.
                   184207 1.R1040
Contig ID
                   fde700875836.hl
5'-most EST
                   28978
Seq. No.
Contig ID
                   184272 1.R1040
                   jC-qmle01810080g05d1
5'-most EST
                   BLASTX
Method
                   q3242704
NCBI GI
                   406
BLAST score
E value
                   2.0e-39
                   134
Match length
% identity
                  (AC003040) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   28979
                   184280 1.R1040
Contig ID
                   zsq701118495.hl
5'-most EST
                   28980
Seq. No.
Contig ID
                   184304 1.R1040
                   fde700875979.h1
5'-most EST
                   28981
Seq. No.
                   184347 1.R1040
Contig ID
                   fde700876044.h1
5'-most EST
Seq. No.
                   28982
                   184382 1.R1040
Contig ID
                   hrw701058203.h1
5'-most EST
                   28983
Seq. No.
                   184402 1.R1040
Contig ID
                   g5509131
5'-most EST
                   BLASTX
Method
NCBI GI
                   g401213
```

5'-most EST g5509131
Method BLASTX
NCBI GI g401213
BLAST score 352
E value 3.0e-33
Match length 118
% identity 58

NCBI Description ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PRECURSOR >gi\_166792



(M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana] >gi\_445600\_prf\_\_1909347A phosphoribosylanthranilate transferase [Arabidopsis thaliana]

28984 Seq. No.

184404 1.R1040 Contig ID

jC-gmle01810086g04a1 5'-most EST

BLASTX Method q4572676 NCBI GI 387 BLAST score 2.0e-37 E value 129 Match length 60 % identity

(AC006954) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

28985 184414 1.R1040 Contig ID fde700876809.h1 5'-most EST

Seq. No.

184420 1.R1040 Contig ID fde700876155.hl 5'-most EST

28986

Seq. No. Contig ID 5'-most EST 28987 184421 1.R1040 fde700877225.hl

Seq. No. Contig ID 5'-most EST 28988 184422 1.R1040 epx701105813.h1

Seq. No. Contig ID

28989 184441 1.R1040 zhf700955464.h1

5'-most EST Seq. No.

28990

184445 1.R1040 Contig ID jC-qmf102220056a10a1

5'-most EST BLASTN Method q3243214 NCBI GI BLAST score 41 E value 1.0e-13

Match length 163 % identity 87

Arabidopsis thaliana BAC T19B17 from chromsome IV, near NCBI Description

19.3 cM, complete sequence [Arabidopsis thaliana]

28991 Seq. No.

184488 1.R1040 Contig ID fde700876250.h1 5'-most EST

Seq. No. 28992

184516 1.R1040 Contig ID fde700877171.hl 5'-most EST

BLASTX Method g1652609 NCBI GI



BLAST score 150 E value 5.0e-10 Match length 78 % identity 36

NCBI Description (D90906) 2-hydroxy-6-oxohepta-2,4-dienoate hydrolase

[Synechocystis sp.]

Seq. No. 28993

Contig ID 184528\_1.R1040 5'-most EST jC-gmle01810040d01a1

Method BLASTX
NCBI GI g4455278
BLAST score 115
E value 2.0e-13
Match length 156
% identity 25

NCBI Description (AL035527) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28994

Contig ID 184530\_1.R1040 5'-most EST fde700877123.h1

Seq. No. 28995

Contig ID 184545\_1.R1040 5'-most EST fde700876343.h1

Seq. No. 28996

Contig ID 184597\_1.R1040 5'-most EST fde700876433.h1

Seq. No. 28997

Contig ID 184604\_1.R1040 5'-most EST fde700876445.h1

Method BLASTX
NCBI GI g1279911
BLAST score 441
E value 3.0e-44
Match length 84
% identity 98

NCBI Description (U52963) mitogen-activated protein kinase [Nectria

haematococca var. brevicona]

Seq. No. 28998

Contig ID 184612\_1.R1040 5'-most EST fde700876454.h1

Method BLASTX
NCBI GI g3522948
BLAST score 357
E value 8.0e-34
Match length 143
% identity 54

NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28999

Contig ID 184628\_1.R1040 5'-most EST g5342489

Method BLASTX



```
g2137562
NCBI GI
                   130
BLAST score
                   2.0e-17
E value
Match length
                   181
% identity
                   35
                   mouse Dhm1 protein - mouse >gi_1060921_dbj_BAA07524_
NCBI Description
                   (D38517) Dhm1 protein [Mus musculus]
                   29000
Seq. No.
                   184629 1.R1040
Contig ID
                   fde700876476.h1
5'-most EST
                   BLASTX
Method
                   g133961
NCBI GI
BLAST score
                   311
E value
                   6.0e-29
Match length
                   83
                   70
% identity
                   40S RIBOSOMAL PROTEIN S4 (OMNIPOTENT SUPRESSOR PROTEIN
NCBI Description
                   SUP44) (RP12) (S2E) >gi_70888 pir R3BYS2 ribosomal protein
                   S2.e - yeast (Saccharomyces cerevisiae) >gi_172793 (M59375)
                   ribosomal protein S4 [Saccharomyces cerevisiae]
                   >gi_1322683_emb_CAA96831_ (Z72645) ORF YGL123w
                   [Saccharomyces cerevisiae] >gi_1628451_emb_CAA63835_
                   (X94106) SUP44 [Saccharomyces cerevisiae]
                   29001
Seq. No.
                   184665 1.R1040
Contig ID
5'-most EST
                   q5606302
Method
                   BLASTX
                   g1705651
NCBI GI
                   444
BLAST score
                   6.0e-44
E value
                   141
Match length
                   61
% identity
                   20 KD NUCLEAR CAP BINDING PROTEIN (NCBP 20 KD SUBUNIT)
NCBI Description
                   (CBP20) >gi_984139_emb_CAA58962_ (X84157) subunit of the dimeric cap binding complex CBC [Homo sapiens]
                   >gi 1582342_prf 2118330A cap-binding protein [Homo
                   sapiens]
                   29002
Seq. No.
                   184684 1.R1040
Contig ID
                   jC-qmst02400049d06a1
5'-most EST
                   29003
Seq. No.
                   184705 1.R1040
Contig ID
                   fde700876592.h1
5'-most EST
                   29004
Seq. No.
                   184708 1.R1040
Contig ID
5'-most EST
                   fde700877110.h1
Method
                   BLASTX
                   a3876337
NCBI GI
```

4476

270

72

69

4.0e-24

BLAST score E value

Match length

% identity



NCBI Description (Z79754) similar to nucleoside diphosphate kinase; cDNA EST CEMSG50F comes from this gene; cDNA EST EMBL:D71761 comes from this gene; cDNA EST EMBL:D72901 comes from this gene; cDNA EST EMBL:D72956 comes from this gene; cDNA ES

Seq. No. 29005

Contig ID 184713\_1.R1040 5'-most EST fde700876604.h1

Seq. No. 29006

Contig ID 184749\_1.R1040 5'-most EST sat701012630.h1

Method BLASTX
NCBI GI g2160692
BLAST score 863
E value 4.0e-93
Match length 193
% identity 83

NCBI Description (U73527) B' regulatory subunit of PP2A [Arabidopsis

thaliana]

Seq. No. 29007

Contig ID 184792\_1.R1040 5'-most EST fde700876732.h1

Method BLASTX
NCBI GI g3025189
BLAST score 178
E value 3.0e-13
Match length 69
% identity 57

NCBI Description HYPOTHETICAL 67.1 KD PROTEIN SLL1770

>gi\_1652753\_dbj\_BAA17672\_ (D90908) ABC1-like [Synechocystis

sp.]

Seq. No. 29008

Contig ID 184804\_1.R1040 5'-most EST zsg701119021.h1

Method BLASTX
NCBI GI g2344854
BLAST score 161
E value 1.0e-10
Match length 128
% identity 36

NCBI Description (Z98756) endopeptidase IV [Mycobacterium leprae]

Seq. No. 29009

Contig ID 184808\_1.R1040 5'-most EST zsg701118427.h1

Method BLASTX
NCBI GI g2842482
BLAST score 183
E value 1.0e-13
Match length 73
% identity 41

NCBI Description (AL021749) protein phosphatase 2C-like protein [Arabidopsis

thaliana]



184816 1.R1040 Contig ID zhf700955674.h1 5'-most EST

BLASTX Method q2262116 NCBI GI BLAST score 247 4.0e-21 E value 122 Match length % identity

NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]

29011 Seq. No.

184840 1.R1040 Contig ID jex700909913.h1 5'-most EST

29012 Seq. No.

184850 1.R1040 Contig ID 5'-most EST fde700877149.h1

29013 Seq. No.

184856 1.R1040 Contig ID fde700876844.hl 5'-most EST

BLASTX Method g1076334 NCBI GI 175 BLAST score 6.0e-13 E value 82 Match length % identity

hypothetical protein HYP1 - Arabidopsis thaliana NCBI Description

>gi\_499168\_emb\_CAA56145\_ (X79707) HYP1 [Arabidopsis

thaliana]

29014 Seq. No.

184860 1.R1040 Contig ID fua701041059.hl 5'-most EST

29015 Seq. No.

Contig ID 184869 1.R1040 fde700876880.hl 5'-most EST

29016 Seq. No.

184876 1.R1040 Contig ID 5'-most EST sat701011851.hl

29017 Seq. No.

184877 1.R1040 Contig ID dpv701102090.hl 5'-most EST

BLASTX Method g3355477 NCBI GI BLAST score 425 3.0e-42 E value Match length 91 % identity

(AC004218) putative P-glycoprotein, pgpl [Arabidopsis NCBI Description

thaliana]

29018 Seq. No.

NCBI Description



```
184878 1.R1040
Contig ID
                   fde700877003.hl
5'-most EST
                   29019
Seq. No.
                   184902 1.R1040
Contig ID
                   uC-gmflminsoy018h06b1
5'-most EST
                   29020
Seq. No.
                   184915 1.R1040
Contig ID
                   uC\text{-}gmrominsoy030h02b1
5'-most EST
Method
                   BLASTN
                   g4220643
NCBI GI
BLAST score
                   39
                   2.0e-12
E value
Match length
                   200
% identity
                   81
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MWD22, complete sequence [Arabidopsis thaliana]
                    29021
Seq. No.
                    184919 1.R1040
Contig ID
5'-most EST
                    zzp700836090.hl
                   BLASTX
Method
                    q3063455
NCBI GI
                    426
BLAST score
                    5.0e-42
E value
Match length
                    98
% identity
                   (AC003981) F22013.17 [Arabidopsis thaliana]
NCBI Description
                    29022
Seq. No.
Contig ID
                    184969 1.R1040
5'-most EST
                    q5057575
                    29023
Seq. No.
                    185038 1.R1040
Contig ID
                    fde700877132.h1
5'-most EST
                    BLASTX
Method
                    q1001541
NCBI GI
BLAST score
                    160
                    4.0e-11
E value
Match length
                    74
% identity
                    41
                    (D64000) ABC transporter [Synechocystis sp.]
NCBI Description
                    29024
Seq. No.
                    185045 1.R1040
Contig ID
                    \texttt{fC-gms}\overline{\texttt{t}}700894694\texttt{a}3
5'-most EST
                    BLASTX
Method
                    g4204303
NCBI GI
                    319
BLAST score
E value
                    1.0e-29
                    73
Match length
                    79
% identity
```

[Arabidopsis thaliana]

(AC003027) lcl prt seq No definition line found

Method

NCBI GI

BLAST score



```
29025
Seq. No.
                  185098 1.R1040
Contig ID
                  hrw701057980.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2880047
                   481
BLAST score
                   2.0e-48
E value
                   132
Match length
% identity
NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]
                   29026
Seq. No.
                   185110 1.R1040
Contig ID
                   jC-gmle01810024e05a1
5'-most EST
                   BLASTX
Method
                   g3928543
NCBI GI
                   196
BLAST score
                   8.0e-15
E value
                   139
Match length
                   35
% identity
                   (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   29027
Seq. No.
                   185147 1.R1040
Contig ID
                   fde700877282.hl
5'-most EST
Method
                   BLASTX
                   q3341693
NCBI GI
                   163
BLAST score
                   2.0e-11
E value
                   74
Match length
                   45
% identity
                   (AC003672) unknown protein [Arabidopsis thaliana]
NCBI Description
                    29028
Seq. No.
                    185191 1.R1040
Contig ID
                    leu701\overline{1}56146.h1
 5'-most EST
 Seq. No.
                    29029
                    185202 2.R1040
 Contig ID
                    gsv701047468.hl
 5'-most EST
                    BLASTX
 Method
                    q3024871
 NCBI GI
                    357
 BLAST score
                    4.0e-34
 E value
                    111
 Match length
                    57
 % identity
                    HYPOTHETICAL 77.3 KD PROTEIN SLL0005
 NCBI Description
                    >gi 1001579_dbj BAA10206_ (D64000) ABC1-like [Synechocystis
                    sp.]
                    29030
 Seq. No.
                    185205_1.R1040
 Contig ID
                    xzm700763756.h1
 5'-most EST
                    BLASTX
```

4480

g1707642



```
7.0e-33
E value
Match length
                  141
                  52
% identity
NCBI Description (Y07748) TMK [Oryza sativa]
Seq. No.
                  29031
Contig ID
                  185233 1.R1040
5'-most EST
                  gsv701053512.h1
Seq. No.
                  29032
                  185236 1.R1040
Contig ID
5'-most EST
                  xzm700763802.h1
                  29033
Seq. No.
Contig ID
                  185246 1.R1040
5'-most EST
                  uC-gmropic112d05b1
                  BLASTX
Method
NCBI GI
                  g961450
BLAST score
                  153
                  5.0e-10
E value
Match length
                  69
                  39
% identity
NCBI Description (D63879) KIAA0156 gene product is related to Xenopus
                  nucleolin. [Homo sapiens]
                  29034
Seq. No.
                  185258 1.R1040
Contig ID
5'-most EST
                  fC-qmle7000763827f1
Method
                  BLASTX
NCBI GI
                  g3192042
BLAST score
                  404
                  1.0e-39
E value
Match length
                  117
                  62
% identity
NCBI Description (AL023796) phosphoglucomutase [Schizosaccharomyces pombe]
Seq. No.
                  29035
                  185315 1.R1040
Contig ID
5'-most EST
                  xzm700763896.h1
Seq. No.
                  29036
Contig ID
                  185318 1.R1040
5'-most EST
                  fC-qmro7000763905f1
Method
                  BLASTX
NCBI GI
                  q3892866
BLAST score
                  173
                  5.0e-12
E value
                  146
Match length
% identity
NCBI Description (X56958) ankyrin (brank-2) [Homo sapiens]
                  29037
Seq. No.
```

185346 1.R1040 Contig ID 5'-most EST kl1701204634.h1

Method BLASTX NCBI GI q4539347 BLAST score 104



```
4.0e-11
E value
Match length
                  94
% identity
                  (AL035539) putative growth regulator protein [Arabidopsis
NCBI Description
                  thaliana]
                  29038
Seq. No.
                  185351 1.R1040
Contig ID
                  jC-gmro02910069d03a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2213602
BLAST score
                  293
                  2.0e-26
E value
                  125
Match length
% identity
                  (AC000348) T7N9.22 [Arabidopsis thaliana]
NCBI Description
                   29039
Seq. No.
                   185366 1.R1040
Contig ID
                   pmv700894654.hl
5'-most EST
                   BLASTN
Method
NCBI GI
                   q3695060
BLAST score
                   162
                   4.0e-86
E value
                   286
Match length
                   90
% identity
                   Lotus japonicus rac GTPase activating protein 2 mRNA,
NCBI Description
                   partial cds
                   29040
Seq. No.
                   185376 1.R1040
Contig ID
                   sat701006641.h1
5'-most EST
                   BLASTX
Method
                   g2129956
NCBI GI
                   255
BLAST score
                   3.0e-22
E value
                   74
Match length
                   68
% identity.
                   photoassimilate-responsive protein PAR-1c precursor -
NCBI Description
                   common tobacco >gi_871489_emb_CAA58732_ (X83852) mRNA
                   inducible by sucrose and salicylic acid and potato virus Y
                   expressed in sugar-accumulating plants [Nicotiana tabacum]
                   29041
Seq. No.
                   185394 1.R1040
Contig ID
                   yza700764023.h1
5'-most EST
                   BLASTX
Method
                   g3873408
NCBI GI
                   214
BLAST score
                   5.0e-17
E value
                   138
Match length
                   31
 % identity
                   (L76926) putative zinc finger protein [Arabidopsis
NCBI Description
```

NCBI Description

29042

thaliana]

Contig ID

Seq. No.

185407\_1.R1040



epx701103845.hl 5'-most EST BLASTX Method NCBI GI g3063706 BLAST score 345 E value 2.0e-32 173 Match length % identity (AL022537) putative protein [Arabidopsis thaliana] NCBI Description 29043 Seq. No. 185410 1.R1040 Contig ID pxt700941214.hl 5'-most EST BLASTX Method

NCBI GI g1491617
BLAST score 749
E value 1.0e-79
Match length 193
% identity 75

NCBI Description (X99952) peroxidase [Arabidopsis thaliana]

Seq. No. 29044

Contig ID 185424\_1.R1040 5'-most EST zsg701117471.h1

Method BLASTX
NCBI GI g2979555
BLAST score 227
E value 7.0e-19
Match length 97
% identity 45

NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]

Seq. No. 29045

Contig ID 185450\_1.R1040 5'-most EST fua701039269.h1

Method BLASTX
NCBI GI g3236246
BLAST score 526
E value 9.0e-54
Match length 106
% identity 87

NCBI Description (AC004684) putative expansin protein [Arabidopsis thaliana]

Seq. No. 29046

Contig ID 185461 1.R1040 5'-most EST zzp700829558.h1

Seq. No. 29047

Contig ID 185465\_1.R1040 5'-most EST zzp700832744.h1

Seq. No. 29048

Contig ID 185471\_1.R1040 5'-most EST pmv700889702.h1

Method BLASTX
NCBI GI g2244898
BLAST score 492
E value 1.0e-49



Match length 146 % identity 63

NCBI Description (Z97338) strong similarity to protein phosphatase 2A

regulatory chain, 74K [Arabidopsis thaliana]

Seq. No. 29049

Contig ID 185480 1.R1040 5'-most EST asn701139454.h1

Seq. No. 29050

Contig ID 185483\_1.R1040 5'-most EST zhf700963571.h1

Seq. No. 29051

Contig ID 185486\_1.R1040 5'-most EST zzp700829606.h1

Method BLASTX
NCBI GI g2493318
BLAST score 265
E value 2.0e-23
Match length 76
% identity 74

NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963

(Z25471) blue copper protein [Pisum sativum]

>gi\_1098264\_prf\_\_2115352A blue Cu protein [Pisum sativum]

Seq. No. 29052

Contig ID 185527\_1.R1040 5'-most EST jex700905589.h1

Seq. No. 29053

Contig ID 185547\_1.R1040 5'-most EST zzp700832556.h1

Method BLASTX
NCBI GI g1076715
BLAST score 172
E value 1.0e-12
March length 57
% identity 53

NCBI Description abscisic acid-induced protein HVA22 - barley >gi\_404589

(L19119) A22 [Hordeum vulgare]

Seq. No. 29054

Contig ID 185557 1.R1040 5'-most EST jex700903613.h1

Method BLASTX
NCBI GI g1710663
BLAST score 392
E value 2.0e-38
Match length 90
% identity 77

NCBI Description PUTATIVE DNA-DIRECTED RNA POLYMERASE III 130 KD POLYPEPTIDE

(RNA POLYMERASE III SUBUNIT 2) >gi\_1204209\_emb\_CAA93558\_(Z69727) putative DNA-directed RNA polymerase III 130 kd

subunit [Schizosaccharomyces pombe]

Seq. No. 29055



Contig ID 185558 1.R1040 5'-most EST dpv701102174.hl

Seq. No. 29056

185581 1.R1040 Contig ID 5'-most EST jC-gmf102220073a03a1

Method BLASTX NCBI GI q2760839 BLAST score 241 3.0e-20 E value Match length 93 53 % identity

NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.

29057

Contig ID

185604 1.R1040

5'-most EST

uC-gmrominsoy177a06b1

Seq. No.

29058

Contig ID 5'-most EST 185612 1.R1040 zzp700829884.h1

Seq. No.

29059

Contig ID 5'-most EST 185627 1.R1040 zzp700834172.h1

Seq. No.

29060

Contig ID

185660 1.R1040

5'-most EST

uC-gmrominsoy073c05b1

Seq. No.

29061

Contig ID 5'-most EST 185661 1.R1040

Method

zzp700833292.h1 BLASTX

NCBI GI

q2317717

BLAST score E value

250 8.0e-22

Match length % identity

75 56

NCBI Description (AF012943) RblA [Dictyostelium discoideum]

Seq. No.

29062

Contig ID

185667\_1.R1040

5'-most EST

zzp700829991.hl

Seq. No.

29063

Contig ID

185678 1.R1040

5'-most EST

jC-gmro02910048g11d1

Method

BLASTX

NCBI GI

g3243234

BLAST score

162

E value Match length 4.0e-11

% identity

38 79

NCBI Description

(AF071477) isoflavone reductase related protein [Pyrus

communis



404

Seq. No. 29064 Contig ID

185679 1.R1040 jsh701070177.hl

5'-most EST Method NCBI GI BLAST score

BLASTX g349379

E value 8.0e-40 87 Match length % identity 91

NCBI Description (L22847) HAHB-1 [Helianthus annuus]

Seq. No.

29065

Contig ID 5'-most EST 185683 1.R1040 sat701009239.h1

Seq. No.

29066

Contig ID 5'-most EST 185684 1.R1040 asn701132976.h1

Seq. No.

29067

Contig ID 5'-most EST 185694 1.R1040 zzp700830049.h1

Method BLASTX NCBI GI q3688177 BLAST score 479 E value 6.0e-48 Match length 128 % identity 70

NCBI Description

(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.

29068

BLASTX

Contig ID 5'-most EST 185754 1.R1040 zzp700830288.h1

Method NCBI GI BLAST score E value

q4097522 586

Match length % identity

2.0e-60 142

NCBI Description

(U63534) cinnamyl alcohol dehydrogenase [Fragaria x

<u>.</u>

ananassa]

Seq. No.

29069

Contig ID 5'-most EST 185765 1.R1040 zzp700830201.h1

Seq. No.

29070

Contig ID 5'-most EST 185786 1.R1040 jC-gmro02910052f11a1

Seq. No.

29071

Contig ID 5'-most EST 185800 1.R1040

jC-gmst02400044h01a1

Seq. No.

29072

Contig ID

185812 1.R1040 zzp700830276.h1

5'-most EST



```
Seq. No.
                  29073
                  185824 1.R1040
Contig ID
5'-most EST
                  sat701007490.h2
Method
                  BLASTX
                  q3548806
NCBI GI
                  260
BLAST score
                  3.0e-22
E value
                  123
Match length
% identity
                  39
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
                   29074
Seq. No.
                   185884 1.R1040
Contig ID
                  hrw701060967.hl
5'-most EST
Seq. No.
                   29075
                   185901 1.R1040
Contig ID
                   zzp700830441.h1
5'-most EST
                   BLASTX
Method
                   q4309698
NCBI GI
BLAST score
                   244
                   8.0e-21
E value
                   101
Match length
% identity
                   (AC006266) putative glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   29076
Seq. No.
                   185911 1.R1040
Contig ID
                   zsq701123782.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4539301
                   275
BLAST score
                   4.0e-24
E value
                   111
Match length
% identity
                   (AL049480) putative mitochondrial protein [Arabidopsis]
NCBI Description
                   thaliana]
                   29077
Seq. No.
                   185920 1.R1040
Contig ID
                   zzp700830472.hl
5'-most EST
                   BLASTX
Method
                   q4558678
NCBI GI
                   181
BLAST score
                   8.0e-13
E value
Match length
                   86
 % identity
                   42
                   (AC006586) unknown protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   29078
```

Contig ID 5'-most EST

185928 1.R1040 jsh701068871.h1

Seq. No. 29079

Contig ID 185971\_1.R1040



```
zzp700830562.h1
5'-most EST
                  29080
Seq. No.
                  185976 1.R1040
Contig ID
                  zzp700830758.hl
5'-most EST
                  BLASTX
Method
                  q4567265
NCBI GI
BLAST score
                  141
                  6.0e-20
E value
                  77
Match length
% identity
                  (AC006841) putative kinesin protein [Arabidopsis thaliana]
NCBI Description
                  29081
Seq. No.
                  185983 1.R1040
Contig ID
5'-most EST
                  fua701039571.h1
                  29082
Seq. No.
                   185994 1.R1040
Contig ID
                   uC-gmropic035h11b1
5'-most EST
                   29083
Seq. No.
                   185994 2.R1040
Contig ID
                   zzp700830606.hl
5'-most EST
                   29084
Seq. No.
                   186007 1.R1040
Contig ID
                   uC-gmrominsoy246d04b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3135273
BLAST score
                   308
E value
                   4.0e-28
Match length
                   120
                   53
% identity
                   (AC003058) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4191773 (AC005917) putative WD-40 repeat protein
                   [Arabidopsis thaliana]
                   29085
Seq. No.
                   186011 1.R1040
Contig ID
                   uC-gmropic102h03b1
5'-most EST
                   BLASTX
Method
                   q3319349
NCBI GI
                   246
BLAST score
                   6.0e-21
E value
                   119
Match length
                   43
 % identity
                   (AF077407) No definition line found [Arabidopsis thaliana]
NCBI Description
                   29086
 Seq. No.
                   186029 1.R1040
 Contig ID
                   zzp700830656.h1
 5'-most EST
```

29087

186035 1.R1040

zzp700830663.hl

Seq. No.

Contig ID

5'-most EST



```
29088
Seq. No.
                  186043 1.R1040
Contig ID
                  g5126618
5'-most EST
Method
                  BLASTX
                  g2832661
NCBI GI
                  179
BLAST score
                  5.0e-13
E value
                  73
Match length
% identity
                  51
                  (AL021710) pherophorin - like protein [Arabidopsis
NCBI Description
                  thaliana]
                   29089
Seq. No.
                   186051 1.R1040
Contig ID
5'-most EST
                   leu701151237.h1
                   29090
Seq. No.
                   186061 1.R1040
Contig ID
                   sat701009937.h2
5'-most EST
                   BLASTX
Method
                   g571484
NCBI GI
BLAST score
                   378
                   1.0e-36
E value
Match length
                   91
                   81
% identity
NCBI Description (U16727) peroxidase precursor [Medicago truncatula]
                   29091
Seq. No.
                   186079 1.R1040
Contig ID
                   zzp700830727.h1
5'-most EST
                   29092
Seq. No.
                   186090 1.R1040
Contig ID
                   sat701004872.hl
5'-most EST
                   29093
Seq. No.
                   186116_1.R1040
Contig ID
                   zhf700959735.h1
5'-most EST
                   BLASTX
Method
                   q3746060
NCBI GI
                   290
BLAST score
                   5.0e-26
E value
Match length
                   60
                   83
% identity
NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]
                   29094
Seq. No.
                   186134 1.R1040
 Contig ID
                   zzp700830813.h1
 5'-most EST
                   BLASTX
Method
                   g2344894
NCBI GI
                   453
 BLAST score
                   2.0e-45
 E value
                   98
Match length
```

NCBI Description (AC002388) hypothetical protein [Arabidopsis thaliana]

27

% identity



Contig ID 186146\_1.R1040 5'-most EST zzp700830930.h1

Method BLASTX
NCBI GI g3004556
BLAST score 390
E value 3.0e-38
Match length 84
% identity 86

NCBI Description (AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29096

Contig ID 186174\_1.R1040 5'-most EST zzp700830882.h1

Method BLASTX
NCBI GI g4314391
BLAST score 270
E value 5.0e-28
Match length 88
% identity 71

NCBI Description (AC006232) unknown protein [Arabidopsis thaliana]

Seq. No. 29097

Contig ID 186180\_1.R1040 5'-most EST uC-gmropic120c12b1

Method BLASTN
NCBI GI g4220633
BLAST score 52
E value 3.0e-20
Match length 200
% identity 81

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K7J8, complete sequence [Arabidopsis thaliana]

Seq. No. 29098

Contig ID 186181\_1.R1040 5'-most EST zzp700830892.h1

Seq. No. 29099

Contig ID 186194\_1.R1040 5'-most EST zzp700830922.h1

Method BLASTX
NCBI GI g3080448
BLAST score 212
E value 2.0e-17
Match length 61
% identity 64

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 29100

Contig ID 186196\_1.R1040 5'-most EST zzp700830925.h1

Seq. No. 29101

Contig ID 186201\_1.R1040 5'-most EST zhf700953126.h1



186206 1.R1040 Contig ID 5'-most EST zzp700830940.hl

Method BLASTX g2827638 NCBI GI BLAST score 166 E value 8.0e-12 Match length 93 43 % identity

(AL021636) Cytochrome P450-like protein [Arabidopsis NCBI Description

thaliana]

Seq. No.

29103 Contig ID 186233 1.R1040 5'-most EST zzp700830985.hl

Seq. No. 29104

Contig ID 186234 1.R1040 5'-most EST zzp700830986.h1

Seq. No.

29105 186278 1.R1040 Contig ID 5'-most EST gsv701045850.hl

Seq. No.

29106 186283 1.R1040 Contig ID 5'-most EST zzp700831073.hl

Seq. No.

29107 186329 1.R1040 Contig ID 5'-most EST jex700909430.hl

Seq. No.

29108 Contig ID 186331 1.R1040 5'-most EST zzp700831134.h1

29109 Seq. No. 186332 1.R1040 Contig ID

5'-most EST

jC-gmro02910001b06d1 Method BLASTX

NCBI GI g1652082 BLAST score 199 2.0e-15 E value Match length 67 % identity

(D90902) UDP-3-0-acyl N-acetylglcosamine deacetylase NCBI Description

[Synechocystis sp.]

Seq. No. 29110

Contig ID 186382 1.R1040 5'-most EST zzp700831205.h1

29111 Seq. No.

186398 1.R1040 Contig ID 5'-most EST zzp700831222.h1

Method BLASTX NCBI GI g2736286



```
BLAST score 412
E value 2.0e-40
Match length 84
% identity 90
```

NCBI Description (AF031079) isopentenyl diphosphate isomerase I [Camptotheca

acuminata]

Seq. No. 29112

Contig ID 186407\_1.R1040 5'-most EST awf700838333.h1

Method BLASTX
NCBI GI g3411152
BLAST score 352
E value 3.0e-33
Match length 95
% identity 69

NCBI Description (AF066050) thymidine kinase [Oryza sativa]

Seq. No.

Contig ID 186432\_1.R1040 5'-most EST zzp700831275.h1

29113

Seq. No. 29114

Contig ID 186475\_1.R1040 5'-most EST sat701005501.h1

Method BLASTX
NCBI GI g3738297
BLAST score 143
E value 5.0e-09
Match length 72
% identity 12

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 29115

Contig ID 186486 1.R1040 5'-most EST pxt700943302.h1

Method BLASTN
NCBI GI g1370200
BLAST score 55
E value 3.0e-22
Match length 79
% identity 92

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAC2

Seq. No. 29116

Contig ID 186503\_1.R1040 5'-most EST jsh701065671.h1

Seq. No. 29117

Contig ID 186517\_1.R1040 5'-most EST zzp700831429.h1

Method BLASTX
NCBI GI g2252827
BLAST score 403
E value 1.0e-39
Match length 100
% identity 75

Contig ID

29124

186656 1.R1040



```
(AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
                  29118
Seq. No.
Contig ID
                  186518 1.R1040
5'-most EST
                  zzp700831430.hl
Method
                  BLASTN
NCBI GI
                  g4159704
BLAST score
                  35
E value
                   6.0e-10
Match length
                  71
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MCB17, complete sequence [Arabidopsis thaliana]
                  29119
Seq. No.
                  186539 1.R1040
Contig ID
5'-most EST
                  zzp700831477.h1
Seq. No.
                  29120
                  186548 1.R1040
Contig ID
                  zzp700831491.h1
5'-most EST
Method
                  BLASTX
                  q3947735
NCBI GI
BLAST score
                  379
E value
                  2.0e-36
Match length
                  119
% identity
NCBI Description
                  (AJ009720) NL27 [Solanum tuberosum]
                  29121
Seq. No.
                  186556 1.R1040
Contig ID
                  hrw701060646.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2252631
BLAST score
                  312
E value
                  1.0e-28
Match length
                  115
% identity
                   61
NCBI Description
                  (U95973) hypothetical protein [Arabidopsis thaliana]
                   29122
Seq. No.
                  186574 1.R1040
Contig ID
5'-most EST
                   zzp700831529.h1
Method
                  BLASTX
NCBI GI
                  g4539321
BLAST score
                  271
                  8.0e-24
E value
Match length
                  69
                  70
% identity
                  (AL035679) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  29123
Contig ID
                  186584 1.R1040
5'-most EST
                  zzp700831550.h1
```



```
5'-most EST
                  uC-gmropic101e02b1
                  BLASTX
Method
NCBI GI
                  g4510401
BLAST score
                  371
                  1.0e-35
E value
Match length
                  85
% identity
NCBI Description
                  (AC006587) putative general negative regulator of
                  transcription [Arabidopsis thaliana]
Seq. No.
                  29125
Contig ID
                  186658 1.R1040
5'-most EST
                  jC-gmst02400033f02a1
Method
                  BLASTX
NCBI GI
                  q2529677
BLAST score
                  216
E value
                  2.0e-17
Match length
                  120
% identity
                  (AC002535) kinesin-like protein, heavy chain [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  29126
                  186662 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy083d10b1
Seq. No.
                  29127
Contig ID
                  186662 2.R1040
5'-most EST
                  leu701147412.h1
Seq. No.
                  29128
Contig ID
                  186677 1.R1040
5'-most EST
                  gsv701049260.hl
Seq. No.
                  29129
                  186697 1.R1040
Contig ID
5'-most EST
                  zzp700831730.hl
                  29130
Seq. No.
                  186734 1.R1040
Contig ID
5'-most EST
                  kl1701202390.h1
Seq. No.
                  29131
Contig ID
                  186756 1.R1040
5'-most EST
                  zzp700831811.h1
Seq. No.
                  29132
Contig ID
                  186789 1.R1040
5'-most EST
                  zzp700831860.hl
Method
                  BLASTN
NCBI GI
                  g2828183
BLAST score
                  46
```

BLAST score 46
E value 8.0e-17
Match length 82
% identity 89
NCBI Description Arabidons

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                   29133
                  186835 1.R1040
Contig ID
                  kl1701213194.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3047075
BLAST score
                  214
E value
                  1.0e-17
                  72
Match length
                   53
% identity
                  (AF058914) contains similarity to SRF-type transcription
NCBI Description
                   factors DNA-binding and dimerization domains (PFam:
                  transcript fact.hmm, score 58.97) [Arabidopsis thaliana]
Seq. No.
                   29134
Contig ID
                   186836 1.R1040
5'-most EST
                   fjq700968457.h1
                   29135
Seq. No.
Contig ID
                  186859 1.R1040
5'-most EST
                  zzp700833807.h1
Seq. No.
                   29136
Contig ID
                   186871 1.R1040
5'-most EST
                   gsv701051432.hl
Seq. No.
                   29137
Contig ID
                  186874 1.R1040
5'-most EST
                   g4284638
Method
                   BLASTX
NCBI GI
                   q4107099
BLAST score
                   393
                   4.0e-38
E value
Match length
                   136
% identity
                   57
                  (AB015141) AHP1 [Arabidopsis thaliana]
NCBI Description
                   >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis
                   thaliana]
÷ý
Seq. No.
                   29138
                   186887 1.R1040
Contig ID
5'-most EST
                   dpv701102773.h1
Seq. No.
                   29139
                   186901 1.R1040
Contig ID
5'-most EST
                   uC-gmropic064h06b1
Seq. No.
                   29140
```

Seq. No. 29140 Contig ID 186931\_1.R1040 5'-most EST zzp700832477.h1

Method BLASTX
NCBI GI g2244866
BLAST score 193
E value 4.0e-15
Match length 81
% identity 46

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]



Seq. No. 29141 Contig ID 18697

Contig ID 186976 1.R1040 5'-most EST leu701156322.h1

Seq. No. 29142

Contig ID 187004\_1.R1040 5'-most EST zzp700832146.h1

Seq. No. 29143

Contig ID 187007\_1.R1040 5'-most EST sat701009295.h1

Seq. No. 29144

Contig ID 187013\_1.R1040 5'-most EST zzp700832162.h1

Seq. No. 29145

Contig ID 187021 1.R1040 5'-most EST pmv700892075.h1

Seq. No. 29146

Contig ID 187041\_1.R1040 5'-most EST uC-gmropic041d04b1

Method BLASTX
NCBI GI g4335751
BLAST score 480
E value 2.0e-48
Match length 102
% identity 83

NCBI Description (AC006284) putative methyltransferase [Arabidopsis

thaliana]

Seq. No. 29147

Contig ID 187079\_1.R1040 5'-most EST zzp700832247.h1

Seq. No. 29148

Contig ID 187092 1.R1040

5'-most EST jC-gmfl02220072h05a1

Method BLASTN
NCBI GI g914860
BLAST score 178
E value 2.0e-95
Match length 404
% identity 86

NCBI Description M.varia mRNA for mitotic cyclin

Seq. No. 29149

Contig ID 187100\_1.R1040 5'-most EST bth700849008.h1

Seq. No. 29150

Contig ID 187105\_1.R1040

5'-most EST uC-gmrominsoy123e01b1

Seq. No. 29151



Contig ID 187108\_1.R1040 5'-most EST fua701040291.h1 Method BLASTX

NCBI GI g416922
BLAST score 337
E value 1.0e-31
Match length 81
% identity 78

NCBI Description DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE) (DUTP PYROPHOSPHATASE) (P18) >gi\_282947\_pir\_\_JQ1599 dUTP

pyrophosphatase (EC 3.6.1.23) - tomato

>gi\_251897\_bbs\_109276 (S40549) deoxyuridine triphosphatase,

dUTPase, P18 (EC 3.6.1.23) [tomatoes, Tint Tim cultivar

LA154, Peptide, 169 aa] [Lycopersicon esculentum]

Seq. No. 29152

Contig ID 187133\_1.R1040

5'-most EST g5688128

Seq. No. 29153

Contig ID 187134\_1.R1040 5'-most EST zzp700832368.h1

Method BLASTX
NCBI GI g1091678
BLAST score 144
E value 3.0e-09
Match length 100
% identity 33

NCBI Description activator-like transposable element [Pennisetum glaucum]

Seq. No.

Contig ID 187135\_1.R1040

29154

5'-most EST g4313562
Method BLASTN
NCBI GI g4115370
BLAST score 55
E value 9.0e-22
Match length 127
% identity 86

NCBI Description Arabidopsis thaliana chromosome II BAC F27D4 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.

29155 187155 1.

Contig ID 187155\_1.R1040 5'-most EST kll701206753.h1

Seq. No. 29156

Contig ID 187161\_1.R1040 5'-most EST zzp700832411.h1

Method BLASTX
NCBI GI g4580462
BLAST score 231
E value 3.0e-19
Match length 127
% identity 46

NCBI Description (AC006081) hypothetical protein [Arabidopsis thaliana]



Contig ID 187176\_1.R1040 5'-most EST jC-gmle01810090c06d1

Method BLASTX
NCBI GI g2388585
BLAST score 262
E value 1.0e-22
Match length 109
% identity 56

NCBI Description (AC000098) Similar to Caenorhabditis unknown protein

T03F1.1 (gb U88169). [Arabidopsis thaliana]

Seq. No. 29158

Contig ID 187188\_1.R1040 5'-most EST jC-gmst02400047e04d1

Method BLASTX
NCBI GI 94539324
BLAST score 294
E value 1.0e-26
Match length 140
% identity 50

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 29159

Contig ID 187282\_1.R1040 5'-most EST zzp700832571.h1

Seq. No. 29160

Contig ID 187287\_1.R1040 5'-most EST fC-gmro700877049d1

Method BLASTN
NCBI GI g1806139
BLAST score 43
E value 9.0e-15
Match length 151
% identity 89

NCBI Description M.sativa mRNA for cdc2 kinase homologue, cdc2MsC

Seq. No. 29161

Contig ID 187329 1.R1040

5'-most EST uC-gmrominsoy140d09b1

Seq. No. 29162

Contig ID 187335 1.R1040 5'-most EST bth700849582.h1

Method BLASTX
NCBI GI g1922242
BLAST score 249
E value 2.0e-21
Match length 66
% identity 76

NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29163

Contig ID 187351\_1.R1040 5'-most EST zzp700833703.h1



Contig ID 187355 1.R1040 5'-most EST dpv701103408.h1

Seq. No. 29165

Contig ID 187392\_1.R1040 5'-most EST zhf700953442.h1

Seq. No. 29166

Contig ID 187411\_1.R1040 5'-most EST pmv700892727.h1

Seq. No. 29167

Contig ID 187468\_1.R1040

5'-most EST g4290412

Seq. No. 29168

Contig ID 187485\_1.R1040 5'-most EST zzp700832828.h1

Seq. No. 29169

Contig ID 187501\_1.R1040 5'-most EST jC-gmro02910061d07a1

Seq. No. 29170

Contig ID 187515\_1.R1040 5'-most EST zzp700832864.h1

Method BLASTX
NCBI GI g3021270
BLAST score 371
E value 2.0e-35
Match length 122
% identity 59

NCBI Description (AL022347) serine/threonine kinase -like protein

[Arabidopsis thaliana]

Seq. No. 29171

Contig ID 187527\_1.R1040 5'-most EST zzp700832881.h1

Method BLASTX
NCBI GI g3608495
BLAST score 339
E value 4.0e-32
Match length 82
% identity 82

NCBI Description (AF089738) plastid division protein FtsZ [Arabidopsis thaliana] >gi\_4510351\_gb\_AAD21440.1\_ (AC006921) plastid

division protein FtsZ [Arabidopsis thaliana]

Seq. No. 29172

Contig ID 187535\_1.R1040 5'-most EST zzp700832890.h1

Method BLASTX
NCBI GI g3335341
BLAST score 204
E value 3.0e-16
Match length 84



% identity 55

NCBI Description (AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No.

29173

Contig ID 5'-most EST

187537\_1.R1040 asn701135218.h1

Seq. No.

29174

Contig ID

187547\_1.R1040

5'-most EST

uC-gmrominsoy171e09b1

Seq. No.

29175

Contig ID 5'-most EST

187594\_1.R1040 zzp700833073.h1

Seq. No.

29176

Contig ID

187598\_1.R1040

5'-most EST

uC-gmrominsoy117g12b1

Method NCBI GI BLASTX q4337174

BLAST score

g4337174 246

E value

5.0e-21

Match length % identity

117 50

NCBI Description

(AC006416) Similar to gi\_1573829 HI0816 aminopeptidase P

homolog (pepP) from Haemophilus influenzae genome

gb\_U32764. [Arabidopsis thaliana]

Seq. No.

29177

Contig ID 5'-most EST 187602\_1.R1040 fua701037621.h1

Seq. No.

29178

Contig ID 5'-most EST

187621\_1.R1040 uC-gmropic004a03b1

Seq. No.

29179

Contig ID 5'-most EST

187622\_1.R1040 zzp700833005.h1

Seq. No.

29180

Contig ID 5'-most EST

187631\_1.R1040 sat701014046.h1

Seq. No.

29181

Contig ID 5'-most EST

187656\_1.R1040 zzp700833048.h1

Seq. No.

29182

Contig ID 5'-most EST

187712\_1.R1040 hrw701058357.h1

Method NCBI GI BLAST score E value

Match length

% identity

g3236235 357 3.0e-34

BLASTX

77 81



NCBI Description (AC004684) unknown protein [Arabidopsis thaliana] >gi\_4056501 (AC005896) unknown protein [Arabidopsis

thaliana)

Seq. No. 29183

Contig ID 187724\_1.R1040 5'-most EST zzp700833130.h1

Seq. No. 29184

Contig ID 187737 1.R1040 5'-most EST bth700844156.h1

Method BLASTX
NCBI GI g1168719
BLAST score 313
E value 2.0e-28
Match length 108
% identity 57

NCBI Description C6.1A PROTEIN >gi 2135176 pir I38167 gene C6.1A protein -

human >gi 36088 emb CAA45917 (X64643) C6.1A [Homo sapiens]

Seq. No. 29185

Contig ID 187761 1.R1040

5'-most EST uC-gmrominsoy057d02b1

Method BLASTX
NCBI GI g4206210
BLAST score 554
E value 2.0e-56
Match length 232
% identity 50

NCBI Description (AF071527) putative calcium channel [Arabidopsis thaliana]

>gi 4263043 gb AAD15312 (AC005142) putative calcium

channel [Arabidopsis thaliana]

Seq. No. 29186

Contig ID 187842\_1.R1040 5'-most EST uC-gmropic022c04b1

Seq. No. 29187

Contig ID 187845\_1.R1040

5'-most EST uC-gmrominsoy128h04b1

Method BLASTX
NCBI GI g3250697
BLAST score 601
E value 2.0e-62
Match length 136
% identity 84

NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 29188

Contig ID 187845 2.R1040 5'-most EST fua701039548.h1

Seq. No. 29189

Contig ID 187849\_1.R1040 5'-most EST zzp700833293.h1

Method BLASTN NCBI GI 94580454



BLAST score 6.0e-11 E value Match length 88 85 % identity

Arabidopsis thaliana chromosome II BAC T2G17 genomic NCBI Description

sequence, complete sequence

29190 Seq. No.

Contig ID 187853 1.R1040 5'-most EST zhf700960325.h1

Method BLASTX NCBI GI g3157942 BLAST score 149 E value 6.0e-10 Match length 73 49 % identity

(AC002131) Similar to style development-specific protein NCBI Description

9612 precursor gb X55193 and pectate lyase P59 precursor

gb X15499 from Lycopersicon esculentum. [Arabidopsis

thaliana]

Seq. No. 29191

Contig ID 187858 1.R1040 5'-most EST zzp700833309.h1

Seq. No. 29192

Contig ID 187870 1.R1040 5'-most EST zhf700952319.h1

29193 Seq. No.

Contig ID 187870 2.R1040 5'-most EST jex700908277.hl

Seq. No. 29194

187878 1.R1040 Contig ID 5'-most EST zzp700833333.hl

Seq. No. 29195

Contig ID 187882 1.R1040 5'-most EST zzp700833337.h1

Method BLASTX NCBI GI g3608263 BLAST score 322 E value 6.0e-30 Match length 82 76 % identity

NCBI Description (AB017565) Dof zinc finger protein [Arabidopsis thaliana]

Seq. No. 29196

187898 1.R1040 Contig ID 5'-most EST zzp700833362.h1

29197 Seq. No.

187904 1.R1040 Contig ID 5'-most EST zzp700833369.h1

Seq. No. 29198



Contig ID 187917\_1.R1040 5'-most EST zzp700833386.h1

Seq. No. 29199

Contig ID 187922 1.R1040 5'-most EST uC-gmropic101d01b1

Method BLASTX
NCBI GI g3063449
BLAST score 511
E value 7.0e-52
Match length 137
% identity 70

NCBI Description (AC003981) F22013.11 [Arabidopsis thaliana]

Seq. No. 29200

Contig ID 187929 1.R1040 5'-most EST sat701003791.h1

Seq. No. 29201

Contig ID 187955\_1.R1040 5'-most EST zzp700836295.h1

Method BLASTN
NCBI GI g4432829
BLAST score 33
E value 4.0e-09
Match length 41
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC T1B3 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 29202

Contig ID 187970\_1.R1040 5'-most EST zhf700954165.h1

Method BLASTX
NCBI GI g3128192
BLAST score 794
E value 5.0e-85
Match length 190
% identity 78

NCBI Description (AC004521) axi 1-like protein [Arabidopsis thaliana]

Seq. No. 29203

Contig ID 187997\_1.R1040

5'-most EST uC-gmrominsoy224g06b1

Seq. No. 29204

Contig ID 188021\_1.R1040 5'-most EST uC-gmropic089h09b1

Seq. No. 29205

Contig ID 188026\_1.R1040

5'-most EST sat701008619.h1

Seq. No. 29206

Contig ID 188093\_1.R1040 5'-most EST fC-gmse7000764839f1



Seq. No. 29207

Contig ID 188105 1.R1040

5'-most EST jC-gmst02400060e10d1

Seq. No. 29208

Contig ID 188118\_1.R1040 5'-most EST zzp700833677.h1

Method BLASTX
NCBI GI g4567279
BLAST score 353
E value 3.0e-33
Match length 142
% identity 52

NCBI Description (AC006841) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 29209

Contig ID 188119\_1.R1040 5'-most EST gsv701053208.h1

Seq. No. 29210

Contig ID 188126\_1.R1040 5'-most EST pxt700945449.h1

Seq. No. 29211

Contig ID 188128\_1.R1040 5'-most EST gsv701048757.h1

Method BLASTX
NCBI GI g4538961
BLAST score 937
E value 1.0e-101
Match length 205
% identity 80

NCBI Description (AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis

thaliana]

Seq. No. 29212

Contig ID 188156\_1.R1040-5'-most EST bth700848590.h1

Method BLASTX
NCBI GI g4262224
BLAST score 159
E value 3.0e-14
Match length 67
% identity 64

NCBI Description (AC006200) putative amino acid or GABA permease

[Arabidopsis thaliana]

Seq. No. 29213

Contig ID 188172\_1.R1040 5'-most EST zzp700833757.h1

Seq. No. 29214

Contig ID 188183 1.R1040 5'-most EST zzp700833768.h1

Seq. No. 29215



Contig ID 188190\_1.R1040 5'-most EST zzp700833776.h1

Method BLASTX
NCBI GI g3043612
BLAST score 275
E value 2.0e-24
Match length 131
% identity 40

NCBI Description (AB011116) KIAA0544 protein [Homo sapiens]

Seq. No. 29216

Contig ID 188204 1.R1040

5'-most EST uC-gmrominsoy158c08b1

Seq. No. 29217

Contig ID 188204\_3.R1040 5'-most EST pmv700890839.h1

Seq. No. 29218

Contig ID 188211\_1.R1040 5'-most EST zzp700833804.h1

Method BLASTX
NCBI GI g3377941
BLAST score 194
E value 8.0e-15
Match length 82
% identity 38

NCBI Description (AL021960) putative protein (fragment) [Arabidopsis

thaliana]

Seq. No. 29219

Contig ID 188231 1.R1040 5'-most EST leu701150952.h1

Method BLASTX
NCBI GI g4455371
BLAST score 324
E value 2.0e-30
Match length 90
% identity 70

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 29220

Contig ID 188240 1.R1040 5'-most EST zzp700833839.h1

Seq. No. 29221

Contig ID 188247\_1.R1040 5'-most EST jsh701064965.h1

Seq. No. 29222

Contig ID 188248 1.R1040 5'-most EST zzp700833848.h1

Method BLASTX
NCBI GI g3482979
BLAST score 332
E value 6.0e-31
Match length 87



% identity

NCBI Description

(AL031369) putative protein [Arabidopsis thaliana] >gi\_4567258 gb\_AAD23672.1\_AC007070 21 (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.

29223

Contig ID 5'-most EST

188249\_1.R1040 bth700848866.h1

Method NCBI GI BLASTX q1076486

BLAST score E value 231 1.0e-19

Match length % identity

74 64

NCBI Description

cim1 protein - soybean >gi\_555616 (U03860) cytokinin

induced message [Glycine max]

Seq. No.

29224

Contig ID

188280\_1.R1040

5'-most EST

jC-gmle01810045f07a1

Method NCBI GI BLASTX g3152566

BLAST score E value 147 2.0e-09

Match length % identity

109 58

NCBI Description

(AC002986) Similar to hypothetical protein YLR002c,

gb Z7314 from S. cerevisiae. [Arabidopsis thaliana]

Seq. No.

29225

Contig ID 5'-most EST

188281\_1.R1040 zzp700833886.h1

Seq. No.

29226

Contig ID

188285\_1.R1040 zhf700957450.h1

5'-most EST Method

BLASTN

NCBI GI BLAST score g3894098 213

BLAST sco E value

1.0e-116

Match length

388 89

% identity NCBI Description

Pisum sativum mRNA for protein encoded by MCM3 gene,

partial

Seq. No.

29227

Contig ID 5'-most EST

188296\_1.R1040 pmv700891237.h1

Seq. No.

29228

Contig ID 5'-most EST

188329 1.R1040 k11701213764.h1

Seq. No.

29229

Contig ID 5'-most EST 188334\_1.R1040 zzp700833950.h1

Method

BLASTX



NCBI GI g129021 BLAST score 266 E value 2.0e-23 Match length 109 % identity 51

NCBI Description SPOOB-ASSOCIATED GTP-BINDING PROTEIN >gi\_98326\_pir\_B32804 GTP-binding protein, spoOB 3'-region - Bacillus subtilis >gi\_508979 (M24537) GTP-binding protein [Bacillus subtilis]

>gi\_2635257\_emb\_CAB14752\_ (Z99118) GTPase activity

[Bacillus subtilis]

Seq. No. 29230

Contig ID 188350 1.R1040 5'-most EST zzp700833967.h1

Method BLASTX
NCBI GI g2642433
BLAST score 230
E value 2.0e-19
Match length 83
% identity 63

NCBI Description (AC002391) putative receptor protein kinase [Arabidopsis

thalianal

Seq. No. 29231

Contig ID 188397 1.R1040 5'-most EST sat701004442.h1 Method BLASTX

NCBI GI g3941448
BLAST score 423
E value 5.0e-42
Match length 87
% identity 85

NCBI Description (AF062878) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 29232

Contig ID 188403\_1.R1040 5'-most EST fua701037879.h1

Method BLASTN
NCBI GI g2739003
BLAST score 132
E value 4.0e-68
Match length 272
% identity 88

NCBI Description Glycine max cytochrome P450 monooxygenase CYP82Clp

(CYP82C1) mRNA, complete cds

Seq. No. 29233

Contig ID 188407 1.R1040 5'-most EST zzp700834038.h1

Seq. No. 29234

Contig ID 188414\_1.R1040 5'-most EST zzp700834045.h1

Seq. No. 29235

Contig ID 188430 1.R1040



5'-most EST jex700907604.h1

Method BLASTX
NCBI GI g3881761
BLAST score 158
E value 2.0e-10
Match length 123
% identity 35

NCBI Description (Z37093) alternative splicing in ZK669.1a; cDNA EST

EMBL:D36754 comes from this gene [Caenorhabditis elegans] >gi\_3881779\_emb\_CAA86848\_ (Z46812) alternative splicing in

ZK669.1a; cDNA EST EMBL: D36754 comes from this gene

[Caenorhabditis elegans]

Seq. No. 29236

Contig ID 188447\_1.R1040 5'-most EST fC-gmse700646582g1

Seq. No. 29237

Contig ID 188469\_1.R1040 5'-most EST gsv701056189.h1

Seq. No. 29238

Contig ID 188509\_1.R1040 5'-most EST zzp700834153.h1

Seq. No. 29239

Contig ID 188517\_1.R1040

5'-most EST uC-gmrominsoy035f10b1

Seq. No. 29240

Contig ID 188542\_1.R1040 5'-most EST zhf700954428.h1

Method BLASTX
NCBI GI g4510339
BLAST score 251
E value 1.0e-21
Match length 75
% identity 44

NCBI Description (AC006921) putative ABC transporter protein [Arabidopsis

thaliana]

Seq. No. 29241

Contig ID 188548\_1.R1040 5'-most EST pxt700946279.h1

Seq. No. 29242

Contig ID 188568 1.R1040

5'-most EST uC-gmflminsoy075h06b1

Method BLASTX
NCBI GI g2224695
BLAST score 552
E value 9.0e-57
Match length 150
% identity 68

NCBI Description (AB002375) KIAA0377 [Homo sapiens]

Seq. No. 29243

% identity

44



```
Contig ID
                  188579 1.R1040
5'-most EST
                  uC-gmrominsoy260h06b1
                  {\tt BLASTX}
Method
NCBI GI
                  g3360291
BLAST score
                  314
E value
                  8.0e-29
Match length
                  77
% identity
                  44
NCBI Description
                  (AF023165) leucine-rich repeat transmembrane protein kinase
                  2 [Zea mays]
                  29244
Seq. No.
Contig ID
                  188584 1.R1040
5'-most EST
                  zzp700834242.h1
Seq. No.
                  29245
Contig ID
                  188606 1.R1040
5'-most EST
                  zzp700834266.h1
Method
                  BLASTX
NCBI GI
                  g4039155
                  202
BLAST score
                  2.0e-15
E value
Match length
                  121
% identity
                  31
NCBI Description (AF104258) putative copper-inducible 35.6 kDa protein
                   [Festuca rubra]
                  29246
Seq. No.
Contig ID
                  188614 1.R1040
5'-most EST
                  zzp700834277.h1
Seq. No.
                   29247
Contig ID
                  188625 1.R1040
5'-most EST
                   zzp700834289.h1
Method
                  BLASTX
NCBI GI
                  g1491931
BLAST score
                  572
E value
                   4.0e-59
Match length
                  147
% identity
                  76
NCBI Description (U52078) kinesin-like protein [Nicotiana tabacum]
Seq. No.
                   29248
Contig ID
                   188640 1.R1040
5'-most EST
                   zzp700834310.h1
                  29249
Seq. No.
                  188658 1.R1040
Contig ID
5'-most EST
                  fua701037533.h1
Method
                  BLASTX
                  g2262099
NCBI GI
BLAST score
                  173
E value
                  1.0e-12
Match length
                  82
```

NCBI Description (AC002343) thaumatin isolog [Arabidopsis thaliana]



```
29250
Seq. No.
                   188663_1.R1040
Contig ID
                   uC-gmf\overline{l}minsoy022f09b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4049353
BLAST score
                   340
                   3.0e-37
E value
                   162
Match length
                   47
% identity
                   (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
                   29251
Seq. No.
                   188676 1.R1040
Contig ID
                   k11701\overline{2}06281.h1
5'-most EST
                    29252
Seq. No.
                    188695 1.R1040
Contig ID
                    k11701\overline{2}02629.h1
5'-most EST
                    29253
Seq. No.
                    188750 1.R1040
Contig ID
                    jsh701070358.hl
5'-most EST
                    29254
Seq. No.
                    188751 1.R1040
Contig ID
                    dpv701101342.hl
5'-most EST
                    BLASTX
Method
                    q3724087
NCBI GI
                    392
BLAST score
                    5.0e-38
E value
                    115
Match length
                    66
% identity
                   (AJ011840) 1-deoxyxylulose 5-phosphate synthase
NCBI Description
                    [Catharanthus roseus]
                    29255
Seq. No.
                    188751 2.R1040
Contig ID
                    jC-gmr002910006h07a1
 5'-most EST
                    BLASTX
Method
                    g3724087
NCBI GI
 BLAST score
                    235
                    1.0e-19
 E value
 Match length
                    89
                    57
 % identity
                    (AJ011840) 1-deoxyxylulose 5-phosphate synthase
 NCBI Description
                     [Catharanthus roseus]
                    29256
 Seq. No.
                    188761 1.R1040
 Contig ID
                    epx701\overline{106429.h1}
 5'-most EST
                     29257
 Seq. No.
                     188793 1.R1040
```

Contig ID zzp700834573.h1 5'-most EST

BLASTX Method g2347188 NCBI GI 187 BLAST score



E value 2.0e-14 Match length 53 % identity 64

NCBI Description (AC002338) laccase isolog [Arabidopsis thaliana] >gi 3150401 (AC004165) putative laccase [Arabidopsis

thaliana]

Seq. No. 29258

Contig ID 188798\_1.R1040 5'-most EST uC-gmropic109g12b1

Method BLASTX
NCBI GI g3790593
BLAST score 286
E value 2.0e-25
Match length 92
% identity 59

NCBI Description (AF079185) RING-H2 finger protein RHY1a [Arabidopsis

thaliana]

Seq. No. 29259

Contig ID 188804\_1.R1040 5'-most EST zzp700834584.h1

Seq. No. 29260

Contig ID 188817\_1.R1040 5'-most EST uC-gmropic116h02b1

Method BLASTX
NCBI GI g3080439
BLAST score 200
E value 1.0e-15
Match length 75
% identity 48

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 29261

Contig ID 188843\_1.R1040 5'-most EST zzp700834638.h1

Method BLASTX
NCBI GI g2632252
BLAST score 260
E value 1.0e-22
Match length 125
% identity 46

NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No. 29262

Contig ID 188896 1.R1040 5'-most EST pmv700889915.h1

Seq. No. 29263

Contig ID 188898 1.R1040 5'-most EST zsg701120708.h1

Seq. No. 29264

Contig ID 188899\_1.R1040 5'-most EST kl1701205278.h1

Method BLASTX



NCBI GI g1871158 BLAST score 170 3.0e-12 E value 62 Match length 50 % identity

NCBI Description (U52364) SMCY [Equus caballus]

Seq. No.

29265 Contig ID 188951 1.R1040 5'-most EST zzp700834840.hl

Seq. No. 29266

188952 1.R1040 Contig ID 5'-most EST jC-qmf102220070g01d1

Method BLASTX NCBI GI g3913437 BLAST score 479 4.0e-48 E value Match length 111 % identity 80

PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA NCBI Description

HELICASE >qi 1402875 emb CAA66825 (X98130) RNA helicase [Arabidopsis thaliana] >gi 1495271 emb CAA66613 (X97970)

RNA helicase [Arabidopsis thaliana]

Seq. No. 29267

Contig ID 189011 1.R1040

5'-most EST jC-gmle01810094a04d1

Seq. No. 29268

189012\_1.R1040 Contig ID

5'-most EST uC-gmrominsoy283h11b1

Method BLASTX NCBI GI g3249105 BLAST score 191 2.0e-27 E value Match length 108 % identity 60

NCBI Description (AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 29269

Contig ID 189019 1.R1040 5'-most EST sat701003223.hl

Method BLASTX NCBI GI q3834318 149 BLAST score E value 1.0e-09 Match length 92 % identity 35

(AC005679) Similar to gi\_2244754 heat shock transcription NCBI Description

factor HSF30 homolog from Arabidopsis thaliana chromosome 4

contig gb Z97335. [Arabidopsis thaliana]

Seq. No. 29270

189019 2.R1040 Contig ID kl1701213812.hl 5'-most EST



Seq. No. 29271

Contig ID 189024 1.R1040 5'-most EST zzp700834874.h1

Method BLASTX
NCBI GI g4567279
BLAST score 455
E value 2.0e-45
Match length 140
% identity 63

NCBI Description (AC006841) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 29272

Contig ID 189062 1.R1040

5'-most EST jC-gmf102220064g02a1

Seq. No. 29273

Contig ID 189077\_1.R1040 5'-most EST zzp700834944.h1

Seq. No. 29274

Contig ID 189082\_1.R1040 5'-most EST zzp700834949.h1

Method BLASTX
NCBI GI g119640
BLAST score 163
E value 2.0e-11
Match length 74
% identity 42

NCBI Description 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN

E8) >gi\_82109\_pir\_\_S01642 ripening protein E8 - tomato >gi\_19199\_emb\_CAA31789\_ (X13437) E8 protein [Lycopersicon

esculentum]

Seq. No. 29275

Contig ID 189091\_1.R1040 5'-most EST jC-gmst02400055c07a1

Seq. No. 29276

Contig ID 189100\_1.R1040 5'-most EST uC-gmropic022b04b1

Method BLASTX
NCBI GI g1854443
BLAST score 585
E value 2.0e-60
Match length 132
% identity 83

NCBI Description (D83970) CPRD8 protein [Vigna unguiculata]

Seq. No. 29277

Contig ID 189103 1.R1040 5'-most EST zzp700834976.h1

Seq. No. 29278

Contig ID 189120\_1.R1040 5'-most EST jC-gmle01810012a03a1

NCBI GI

BLAST score



```
29279
Seq. No.
                  189126 1.R1040
Contig ID
                   jC-gmle01810004e12d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4538987
BLAST score
                  182
                  2.0e-13
E value
                  47
Match length
                   68
% identity
NCBI Description (AJ133777) gamma-adaptin 2 [Arabidopsis thaliana]
                  29280
Seq. No.
Contig ID
                  189173 1.R1040
5'-most EST
                  kl1701206401.hl
Seq. No.
                  29281
Contig ID
                  189202 1.R1040
5'-most EST
                  g4397430
Seq. No.
                  29282
                  189207 1.R1040
Contig ID
5'-most EST
                  zzp700835112.h1
Seq. No.
                  29283
Contig ID
                  189235 1.R1040
5'-most EST
                  zzp700835146.hl
                   29284
Seq. No.
                   189248 1.R1040
Contig ID
5'-most EST
                   zzp700835167.h1
Method
                   BLASTX
NCBI GI
                   g3402704
BLAST score
                   177
E value
                   8.0e-13
Match length
                  83
% identity
                   41
NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   29285
                   189279 1.R1040
Contig ID
                   g4292541
5'-most EST
Method
                   BLASTX
NCBI GI
                   q559237
BLAST score
                   351
E value
                   2.0e-33
Match length
                   110
% identity
                   65
                  (L36982) tyrosine-rich hydroxyproline-rich glycoprotein
NCBI Description
                   [Petroselinum crispum]
                   29286
Seq. No.
                   189286 1.R1040
Contig ID
5'-most EST
                   zzp700835214.h1
                  BLASTX
Method
```

g1170626

448



E value 8.0e-45
Match length 103
% identity 84
NCBI Description CALCIUM

CALCIUM/CALMODULIN-DEPENDENT SERINE/THREONINE PROTEIN KINASE >gi\_478408\_pir\_\_JQ2251 calcium/calmodulin-binding protein kinase - apple tree >gi\_311320\_emb\_CAA78961\_(Z17313) calcium/calmodulin-dependent serine/threonine protein kinase [Malus domestica] >gi\_984160\_emb\_CAA86286\_

(Z38126) calmodulin-binding protein kinase [Malus

domestica]

Seq. No. 29287

Contig ID 189295\_1.R1040 5'-most EST zzp700835225.h1

Method BLASTX
NCBI GI g4432860
BLAST score 166
E value 3.0e-11
Match length 120
% identity 8

NCBI Description (AC006300) putative glucose-induced repressor protein

[Arabidopsis thaliana]

Seq. No. 29288

Contig ID 189325\_1.R1040 5'-most EST zzp700835263.h1

Seq. No. 29289

Contig ID 189344 1.R1040 5'-most EST zzp700835285.h1

Seq. No. 29290

Contig ID 189349\_1.R1040 5'-most EST uC-gmropic074c08b1

Seq. No. 29291

Contig ID 189375 1.R1040 5'-most EST zzp700835330.h1

Seq. No. 29292

Contig ID 189382 1.R1040 5'-most EST dpv701098653.h1

Seq. No. 29293

Contig ID 189395 1.R1040

5'-most EST jC-gmle01810069h03d1

Seq. No. 29294

Contig ID 189399\_1.R1040 5'-most EST zzp700835359.h1

Method BLASTX
NCBI GI g2829912
BLAST score 308
E value 2.0e-28
Match length 72
% identity 82

NCBI Description (AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis

E value

Match length



```
thaliana]
Seq. No.
                   29295
Contig ID
                   189406 1.R1040
5'-most EST
                   zzp700835367.h1
                   BLASTX
Method
                   g4510344
NCBI GI
BLAST score
                   210
E value
                   9.0e-17
Match length
                   50
% identity
                   78
NCBI Description
                  (AC006921) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   29296
                   189432 1.R1040
Contig ID
                   jC-gms\(\overline{t}\)02400071a12a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3641845
BLAST score
                   172
```

% identity 49
NCBI Description (AJ223358) stelar K+ outward rectifying channel

[Arabidopsis thaliana]

74

4.0e-12

 Seq. No.
 29297

 Contig ID
 189460\_1.R1040

 5'-most EST
 asj700967492.h1

Seq. No. 29298

Contig ID 189481\_1.R1040 5'-most EST zzp700835461.h1

Method BLASTX
NCBI GI g2335096
BLAST score 164
E value 8.0e-12
Match length 55
% identity 62

NCBI Description (AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29299

Contig ID 189519\_1.R1040 5'-most EST 2hf700961719.h1

Seq. No. 29300

Contig ID 189532\_1.R1040 5'-most EST dpv701101315.h1

Method BLASTX
NCBI GI g3023519
BLAST score 210
E value 7.0e-29
Match length 113
% identity 58

NCBI Description ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT

(ENDOPEPTIDASE CLP) >gi\_2384690 (AF013216) proteosome major

subunit [Myxococcus xanthus]



29301 Seq. No.

189548 1.R1040 Contig ID uC-gmropic022a06b1 5'-most EST

Seq. No. 29302

189557 1.R1040 Contig ID q5175508 5'-most EST

29303 Seq. No.

189565 1.R1040 Contig ID jC-gmle01810005b06a1 5'-most EST

29304 Seq. No.

189575 1.R1040 Contig ID jC-gmle01810080a08d1 5'-most EST

29305 Seq. No.

189589 1.R1040 Contig ID 5'-most EST dpv701103654.hl

29306 Seq. No.

189638 1.R1040 Contig ID zzp700835668.hl 5'-most EST

29307 Seq. No.

189641 1.R1040 Contig ID

uC-qmrominsoy219d04b1 5'-most EST

29308 Seq. No.

189643 1.R1040 Contig ID 5'-most EST zzp700835673.h1

29309 Seq. No.

189650 1.R1040 Contig ID uC-gmropic056e01b1 5'-most EST

29310 Seq. No.

189653 1.R1040 Contig ID jC-gmst02400031c10a1 5'-most EST

BLASTX Method q4567304 NCBI GI 583 BLAST score 6.0e-60 E value 238 Match length

% identity

NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]

29311 Seq. No.

189670 1.R1040 Contig ID zzp700835712.hl 5'-most EST

29312 Seq. No.

189678 1.R1040 Contig ID  $\verb"jC-gml" \overline{e}01810010g04a1"$ 5'-most EST

29313 Seq. No.

189725\_1.R1040 Contig ID



```
5'-most EST
                  zsg701125908.h1
Seq. No.
                  29314
Contig ID
                  189729 1.R1040
5'-most EST
                  fC-gmse700854605a1
Method
                  BLASTX
                  q3482919
NCBI GI
BLAST score
                  657
                  5.0e-69
E value
                  135
Match length
% identity
NCBI Description (AC003970) Putative protein kinase [Arabidopsis thaliana]
                  29315
Seq. No.
Contig ID
                  189748 1.R1040
5'-most EST
                  jC-gmro02910024g04a1
                  BLASTX
Method
NCBI GI
                  g3461845
BLAST score
                  460
                  9.0e-46
E value
Match length
                  163
                  59
% identity
NCBI Description (AC005315) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  29316
Contig ID
                  189748 2.R1040
5'-most EST
                  bth700848410.h1
                  29317
Seq. No.
Contig ID
                  189775 1.R1040
5'-most EST
                  zzp700835838.hl
                  BLASTX
Method
NCBI GI
                  g3153889
BLAST score
                  513
E value
                   4.0e-52
Match length
                  118
% identity
                  81
NCBI Description (AF065444) root iron transporter protein [Pisum sativum]
Seq. No.
                  29318
                  189803 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220079b06a1
                  BLASTX
Method
NCBI GI
                  q4510427
                  232
BLAST score
                  2.0e-19
E value
Match length
                  124
% identity
                  50
NCBI Description (AC006929) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  29319
```

Contig ID 189857\_1.R1040 5'-most EST pmv700889134.h1

Method BLASTX NCBI GI g3021355 BLAST score 542 E value 2.0e-55



Match length 133 % identity 78

NCBI Description (AJ005081) UDP-galactose 4-epimerase [Cyamopsis

tetragonoloba]

Seq. No. 29320

Contig ID 189888\_1.R1040 5'-most EST zzp700835984.h1

Method BLASTX
NCBI GI g3395439
BLAST score 191
E value 1.0e-14
Match length 94
% identity 41

NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29321

Contig ID 189917\_1.R1040 5'-most EST zzp700836026.h1

Seq. No. 29322

Contig ID 189936\_1.R1040 5'-most EST zzp700836048.h1

Method BLASTX
NCBI GI g3281849
BLAST score 830
E value 4.0e-89
Match length 193
% identity 79

NCBI Description (AL031004) methyltransferase - like protein [Arabidopsis

thaliana]

Seq. No. 29323

Contig ID 189945\_1.R1040 5'-most EST zzp700836163.h1

Seq. No. 29324

Contig ID 189953\_1.R1040 5'-most EST sat701004288.h1

Method BLASTX
NCBI GI g1420936
BLAST score 293
E value 1.0e-26
Match length 91
% identity 66

NCBI Description (U61396) Vigna unguiculata aspartic proteinase mRNA,

complete cds. [Vigna unguiculata]

Seq. No. 29325

Contig ID 189959 1.R1040 5'-most EST zzp700836078.h1

Seq. No. 29326

Contig ID 190014\_1.R1040 5'-most EST jC-gmle01810004e05a1

Seq. No. 29327



```
190037 1.R1040
Contig ID
                     crh700855395.h1
  5'-most EST
                     BLASTX
  Method
                     g2688822
  NCBI GI
                     518
  BLAST score
                     2.0e-52
  E value
                     132
  Match length
                     73
  % identity
                     (U93272) pyrophosphate-dependent phosphofructo-1-kinase
  NCBI Description
                     [Prunus armeniaca]
                     29328
  Seq. No.
                     190066 1.R1040
  Contig ID
                     zzp700836223.hl
  5'-most EST
  Method
                     BLASTX
  NCBI GI
                     q4056403
  BLAST score
                     191
                     9.0e-15
  E value
                     72
  Match length
                     62
  % identity
                     (AD001673) lipoxygenase [Persea americana]
  NCBI Description
                     29329
  Seq. No.
                     190069 1.R1040
  Contig ID
  5'-most EST
                     zzp700836236.hl
                     BLASTX
  Method
                     q3402675
  NCBI GI
  BLAST score
                     248
  E value
                     8.0e-21
                     137
  Match length
   % identity
                     40
                     (AC004697) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
                     29330
   Seq. No.
                     190078 1.R1040
   Contig ID
                     zzp700836239.h1
   5'-most EST
                     29331
   Seq. No.
                     190081 1.R1040
   Contig ID
                     zzp700836243.h1
   5'-most EST
                      29332
   Seq. No.
                      190088 1.R1040
   Contig ID
                     uC-gmrominsoy028d10b1
   5'-most EST
                      29333
   Seq. No.
                      190214 1.R1040
   Contig ID
                      uC-gmrominsoy099e05b1
   5'-most EST
                      29334
   Seq. No.
                      190220 1.R1040
   Contig ID
                      sat701002720.h2
   5'-most EST
```

BLASTX

431

119

g3819699

2.0e-42

Method

NCBI GI

E value Match length

BLAST score



% identity NCBI Description (AJ009609) BnMAP4K alpha2 [Brassica napus]

29335 Seq. No.

190226 1.R1040 Contig ID

5'-most EST g4301764 Method BLASTX NCBI GI g4091080 BLAST score 224 2.0e-18 E value 75 Match length

NCBI Description (AF045571) nucleic acid binding protein [Oryza sativa]

Seq. No.

% identity

29336 Contig ID 190237 1.R1040 5'-most EST sat701002744.h2

59

Seq. No. 29337

Contig ID 190244 1.R1040 5'-most EST sat701002754.h2

Method BLASTX NCBI GI g2244940 BLAST score 329 E value 2.0e-30 Match length 128 % identity 61

NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]

29338 Seq. No.

Contig ID 190246 1.R1040 5'-most EST jC-gmro02800035d05a1

Seq. No. 29339

190246\_2.R1040 Contig ID 5'-most EST asn701133567.h2

Seq. No. 29340

190258 1.R1040 Contig ID gsv701053458.h1 5'-most EST

Seq. No. 29341

Contig ID 190303 1.R1040 5'-most EST sat701002823.hl

Seq. No. 29342

190327 1.R1040 Contig ID 5'-most EST yz1700967050.h1

29343 Seq. No.

Contig ID 190344 1.R1040 5'-most EST uC-gmropic023b02b1

Method BLASTX NCBI GI q2809253 BLAST score 228 E value 1.0e-18 Match length 120



% identity 42 NCBI Description (AC002560) F21B7.22 [Arabidopsis thaliana]

Seq. No. 29344

Contig ID 190395 1.R1040 5'-most EST gsv701050433.h1

Method BLASTX
NCBI GI g1532167
BLAST score 192
E value 2.0e-14
Match length 65
% identity 49

NCBI Description (U63815) localized according to blastn similarity to EST

sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis

thaliana]

Seq. No. 29345

Contig ID 190399 1.R1040 5'-most EST jC-gmf102220094a02a1

5'-most EST jC-gmf102
Method BLASTX
NCBI GI g3242715
BLAST score 183
E value 2.0e-13
Match length 139
% identity 39

NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29346

Contig ID 190421\_1.R1040

5'-most EST jC-gmf\overline{1}02220052h06a1

Method BLASTX
NCBI GI g2618698
BLAST score 587
E value 6.0e-61
Match length 134
% identity 91

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 29347

Contig ID 190446\_1.R1040 5'-most EST pmv700891419.h1

Method BLASTX
NCBI GI g2598575
BLAST score 224
E value 2.0e-18
Match length 117
% identity 41

NCBI Description (Y15293) MtN21 [Medicago truncatula]

Seq. No. 29348

Contig ID 190448\_1.R1040

5'-most EST uC-gmflminsoy069d04b1

Seq. No. 29349

Contig ID 190485\_1.R1040

4522



```
sat701003065.hl
5'-most EST
                   29350
Seq. No.
                   190516 1.R1040
Contig ID
                   sat701003104.hl
5'-most EST
                   29351
Seq. No.
                   190522 1.R1040
Contig ID
                   sat701\overline{0}03112.h1
5'-most EST
                  BLASTN
Method
                   g1619601
NCBI GI
BLAST score
                   112
                   3.0e-56
E value
                   188
Match length
                   90
% identity
NCBI Description M.truncatula mRNA for MtN3 gene
                   29352
Seq. No.
                   190526 1.R1040
Contig ID
                   jC-gmst02400063h04a1
5'-most EST
                   29353
Seq. No.
                   190534 1.R1040
Contig ID
                   sat701\overline{0}03129.h1
5'-most EST
                   BLASTX
Method
                   q4455232
NCBI GI
BLAST score
                   167
                   2.0e-11
E value
                   164
Match length
% identity
                   34
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
                   29354
Seq. No.
                   190556 1.R1040
Contig ID
                   sat701003164.hl
5'-most EST
                   BLASTN
Method
                   g2224910
NCBI GI
                   58
BLAST score
                   5.0e-24
E value
                   170
Match length
                   84
 % identity
NCBI Description Daucus carota somatic embryogenesis receptor-like kinase
                   mRNA, complete cds
                   29355
 Seq. No.
                   190592 1.R1040
 Contig ID
                   sat701003209.hl
 5'-most EST
                    29356
 Seq. No.
                    190599 1.R1040
 Contig ID
                    pmv700894036.h1
 5'-most EST
```

BLASTX

Method g3834306 NCBI GI 165 BLAST score 2.0e-11 E value 90 Match length 42 % identity



NCBI Description (AC005679) EST gb\_R65024 comes from this gene. [Arabidopsis thaliana]

Seq. No. 29357

Contig ID 190615\_1.R1040 5'-most EST sat701003239.h1

Method BLASTX
NCBI GI g3805960
BLAST score 260
E value 3.0e-33
Match length 91
% identity 79

NCBI Description (Y13771) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No. 29358

Contig ID 190646\_1.R1040 5'-most EST zsg701120890.h1

Method BLASTX
NCBI GI g3176709
BLAST score 285
E value 2.0e-25
Match length 162
% identity 36

NCBI Description (AC002392) putative anthranilate

N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis

thaliana]

Seq. No. 29359

Contig ID 190700\_1.R1040 5'-most EST sat701003354.h1

Method BLASTX
NCBI GI g2464905
BLAST score 207
E value 4.0e-16
Match length 95
% identity 52

NCBI Description (Z99708) minor allergen [Arabidopsis thaliana]

Seq. No. 29360

Contig ID 190704 1.R1040

5'-most EST jC-gmf102220103g10d1

Seq. No. 29361

Contig ID 190746\_1.R1040 5'-most EST sat701006016.h2

Method BLASTX
NCBI GI g3805956
BLAST score 537
E value 9.0e-55
Match length 100
% identity 91

NCBI Description (Y13769) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No. 29362

Contig ID 190763\_1.R1040 5'-most EST bth700847786.h1



Seq. No. 29363

Contig ID 190774\_1.R1040 5'-most EST sat701004372.h1

Seq. No. 29364

Contig ID 190782\_1.R1040

5'-most EST uC-gmrominsoy058b04b1

Seq. No. 29365

Contig ID 190782\_2.R1040 5'-most EST sat701004554.h1

Seq. No. 29366

Contig ID 190794\_1.R1040 5'-most EST zhf700953746.h1

Seq. No. 29367

Contig ID 190815\_1.R1040 5'-most EST sat701003537.h1

Method BLASTX
NCBI GI g1402879
BLAST score 104
E value 9.0e-09
Match length 65
% identity 49

NCBI Description (X98130) unknown [Arabidopsis thaliana]

>gi 1495247\_emb\_CAA66220\_ (X97616) orf 05 [Arabidopsis

thaliana]

Seq. No. 29368

Contig ID 190817\_1.R1040 5'-most EST sat701003539.h1

Seq. No. 29369

Contig ID 190822\_1.R1040 5'-most EST bth700846694.h1

Method BLASTX
NCBI GI g3242717
BLAST score 145
E value 2.0e-09
Match length 55
% identity 56

NCBI Description (AC003040) putative APG protein [Arabidopsis thaliana]

Seq. No. 29370

Contig ID 190824 1.R1040 5'-most EST pxt700944659.h1

Seq. No. 29371

Contig ID 190841\_1.R1040

5'-most EST uC-gmflminsoy063a12b1

Seq. No. 29372

Contig ID 190843 1.R1040 5'-most EST zhf700959449.h1

Seq. No. 29373



Contig ID 190873 1.R1040 5'-most EST sat701003613.h1

Seq. No. 29374

Contig ID 190882\_1.R1040 5'-most EST sat701003623.h1 Method BLASTX

Method BLASTX
NCBI GI g2795804
BLAST score 178
E value 3.0e-13
Match length 74
% identity 53

NCBI Description (AC003674) unknown protein [Arabidopsis thaliana]

>gi\_3355492 (AC004218) unknown protein [Arabidopsis

thaliana]

Seq. No. 29375

Contig ID 190899 1.R1040 5'-most EST sat701003647.h1

Seq. No. 29376

Contig ID 190920 1.R1040

5'-most EST jC-gmr002910027e08a1

Method BLASTX
NCBI GI g114974
BLAST score 1742
E value 0.0e+00
Match length 484
% identity 67

NCBI Description NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR

>gi\_67491\_pir\_\_GLJY31 beta-glucosidase (EC 3.2.1.21)

precursor (clone TRE361) - white clover

>gi 21955 emb CAA40058.1 (X56734) beta-glucosidase

[Trifolium repens]

Seq. No. 29377

Contig ID 190926\_1.R1040 5'-most EST leu701147471.h1

Seq. No. 29378

Contig ID 190926 2.R1040 5'-most EST leu701154868.h1

Seq. No. 29379

Contig ID 190967\_1.R1040 5'-most EST asn701142641.h1

Method BLASTX
NCBI GI 94455359
BLAST score 721
E value 2.0e-76
Match length 201
% identity 73

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 29380

Contig ID 190977\_1.R1040 5'-most EST sat701003770.h1



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Seq. No. 29381
```

Contig ID 191020\_1.R1040

5'-most EST uC-gmflminsoy074g01b1

Method BLASTX
NCBI GI g4056496
BLAST score 263
E value 6.0e-23
Match length 68
% identity 76

NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 29382

Contig ID 191043\_1.R1040 5'-most EST kl1701202887.h1

Seq. No. 29383

Contig ID 191054\_1.R1040 5'-most EST sat701003880.h1

Seq. No. 29384

Contig ID 191063\_1.R1040

5'-most EST g5175467
Method BLASTX
NCBI GI g3080401
BLAST score 480
E value 5.0e-48
Match length 140
% identity 64

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

>qi 4455265 emb CAB36801.1 (AL035527) putative protein

[Arabidopsis thaliana]

Seq. No. 29385

Contig ID 191143 1.R1040 5'-most EST sat701004031.h1

Seq. No. 29386

Contig ID 191147\_1.R1040 5'-most EST pxt700944436.h1

Method BLASTX
NCBI GI g1841464
BLAST score 390
E value 1.0e-37
Match length 109
% identity 39

NCBI Description (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No. 29387

Contig ID 191153 1.R1040 5'-most EST sat701004047.h1

Seq. No. 29388

Contig ID 191172\_1.R1040 5'-most EST jC-gmle01810020g12a1

Method BLASTX NCBI GI g2335096



BLAST score 281 E value 5.0e-25 Match length 63 % identity 81

NCBI Description (AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29389

Contig ID 191172\_2.R1040 5'-most EST sat701005843.h1

Seq. No. 29390

Contig ID 191187\_1.R1040 5'-most EST leu701751195.h1

Method BLASTX
NCBI GI g2213594
BLAST score 356
E value 6.0e-34
Match length 108
% identity 63

NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No. 29391

Contig ID 191219\_1.R1040 5'-most EST sat701004140.h1

Seq. No. 29392

Contig ID 191253\_1.R1040 5'-most EST awf700842935.h1

Method BLASTN
NCBI GI g2564050
BLAST score 35
E value 3.0e-10
Match length 135
% identity 81

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUA22, complete sequence [Arabidopsis thaliana]

Seq. No. 29393

Contig ID 191271\_1.R1040 5'-most EST sat701012823.h1

Seq. No. 29394

Contig ID 191344\_1.R1040 5'-most EST zsg701118002.h2

Method BLASTX
NCBI GI g4530126
BLAST score 241
E value 2.0e-20
Match length 81
% identity 52

NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1

[Phaseolus vulgaris]

Seq. No. 29395

Contig ID 191350\_1.R1040 5'-most EST sat701004324.h1

E value



```
29396
Seq. No.
                  191377 1.R1040
Contig ID
                   jC-qmst02400072h03a1
5'-most EST
Method
                  BLASTX
                   g3522942
NCBI GI
                   397
BLAST score
                   2.0e-38
E value
                   120
Match length
% identity
                  (AC004411) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   29397
Seq. No.
                   191427 1.R1040
Contig ID
                   sat701004421.hl
5'-most EST
Seq. No.
                   29398
                   191441 1.R1040
Contig ID
                   jC-gmle01810002d05d1
5'-most EST
                   29399
Seq. No.
                   191442 1.R1040
Contig ID
                   sat701004440.h1
5'-most EST
                   BLASTX
Method
                   q4006829
NCBI GI
BLAST score
                   468
                   9.0e-47
E value
Match length
                   136
% identity
                   69
                  (AC005970) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   29400
Seq. No.
                   191461 1.R1040
Contig ID
                   kl1701209210.hl
5'-most EST
                   BLASTX
Method
                   g3402679
NCBI GI
                   408
BLAST score
                   3.0e-40
E value
                   95
Match length
                   81
% identity
                  (AC004697) unknown protein [Arabidopsis thaliana]
NCBI Description
                   29401
Seq. No.
                   191494 1.R1040
Contig ID
                   sat701\overline{0}08312.h1
5'-most EST
                   29402
Seq. No.
                   191514_1.R1040
Contig ID
                   hrw701061533.hl
5'-most EST
                   BLASTX
Method
                   q1709358
NCBI GI
BLAST score
                   206
```

57 Match length 74 % identity NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE NCBI Description PHOSPHOHYDROLASE) (NTPASE) >gi\_629638\_pir\_\_S48859

2.0e-16

nucleoside triphosphatase - garden pea



>gi\_2129890\_pir\_\_S65147 nucleoside triphosphatase
precursor, chromatin-associated - garden pea
>gi\_563612\_emb\_CAA83655\_ (Z32743) nucleoside triphosphatase
[Pisum sativum] >gi\_4519173\_dbj\_BAA75506.1\_ (AB022319)
nucleoside triphosphatase (NTPase) [Pisum sativum]

 Seq. No.
 29403

 Contig ID
 191527\_1.R1040

 5'-most EST
 rlr700897515.h1

 Method
 BLASTX

 NCBI GI
 g544134

NCBI GI g544134 BLAST score 321 E value 1.0e-29 Match length 113 % identity 54

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi\_99720\_pir\_S22863 hypothetical protein - Arabidopsis thaliana >gi\_421844\_pir\_A46260 RecA functional analog

DRT100 - Arabidopsis thaliana (fragment)

Seq. No. 29404

Contig ID 191561 1.R1040

5'-most EST uC-gmflminsoy089e08b1

Seq. No. 29405

Contig ID 191575\_1.R1040 5'-most EST rlr700899927.h1

Method BLASTX
NCBI GI g2498732
BLAST score 208
E value 3.0e-18
Match length 104
% identity 46

NCBI Description PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2

>gi\_1362014\_pir\_\_S57612 zeta-crystallin homolog Arabidopsis thaliana >gi\_886430\_emb\_CAA89262\_ (Z49268)

zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No. 29406

Contig ID 191594\_1.R1040

5'-most EST g4405621
Method BLASTX
NCBI GI g4467156
BLAST score 390
E value 1.0e-37
Match length 99
% identity 69

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 29407

Contig ID 191600 1.R1040

5'-most EST jC-gmro02910008h08a1

Seq. No. 29408

Contig ID 191603\_1.R1040 5'-most EST pxt700943255.h1

Method BLASTX

```
g1076274
NCBI GI
BLAST score
                  333
                  3.0e-31
E value
                  121
Match length
                  59
% identity
                  cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)
NCBI Description
                  29409
Seq. No.
                  191605 1.R1040
Contig ID
                  uC-gmrominsoy224a09b1
5'-most EST
                  BLASTX
Method
                  g2224933
NCBI GI
                  171
BLAST score
                  5.0e-12
E value
Match length
                  56
% identity
                  61
                  (AF004216) ethylene-insensitive3 [Arabidopsis thaliana]
NCBI Description
                  >gi 2224935 (AF004217) ethylene-insensitive3 [Arabidopsis
                  thaliana]
Seq. No.
                  29410
                  191625 1.R1040
Contig ID
                  sat701004679.h1
5'-most EST
                  BLASTX
Method
                  g2129859
NCBI GI
BLAST score
                  534
                  1.0e-54
E value
Match length
                  141
% identity
                   69
                  vestitone reductase - alfalfa >gi_973249 (U28213) vestitone
NCBI Description
                  reductase [Medicago sativa subsp. sativa]
                  29411
Seq. No.
                   191633 1.R1040
Contig ID
                   sat701004688.hl
5'-most EST
                   29412
Seq. No.
                   191646 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810061h01a1
                   29413
Seq. No.
                   191655 1.R1040
Contig ID
                   fua701037394.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3668085
                   171
BLAST score
                   1.0e-11
E value
Match length
                   124
                   52
% identity
NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]
                   29414
Seq. No.
```

Contig ID 191655\_2.R1040 5'-most EST gsv701044364.h1

Method BLASTX
NCBI GI g3668085
BLAST score 151



1.0e-09 E value 95 Match length 41 % identity

(AC004667) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 29415

191659 1.R1040 Contig ID sat701009643.hl 5'-most EST

Method BLASTX q4538934 NCBI GI BLAST score 288 3.0e-26 E value 91 Match length 37 % identity

(AL049483) putative leucine-rich-repeat protein NCBI Description

[Arabidopsis thaliana]

29416 Seq. No.

191700 1.R1040 Contig ID sat701004787.hl 5'-most EST

29417 Seq. No.

191737 1.R1040 Contig ID gsv701051086.hl 5'-most EST

29418 Seq. No.

191779 1.R1040 Contig ID

jC-qmfl02220138g07a1 5'-most EST

BLASTX Method NCBI GI g1076664 BLAST score 356 9.0e-34 E value 150 Match length 53 % identity

leucine zipper transcription factor - potato NCBI Description

>qi 575418 emb CAA57894\_ (X82544) leucine zipper

transcription factor [Solanum tuberosum]

29419 Seq. No.

191811 1.R1040 Contig ID sat701004943.h1 5'-most EST

BLASTX Method q3426039 NCBI GI 234 BLAST score 2.0e-19 E value 101 Match length 50 % identity

(AC005168) unknown protein [Arabidopsis thaliana] NCBI Description

29420 Seq. No.

191825 1.R1040 Contig ID

jC-gmro02910023e02d1 5'-most EST

BLASTX Method g2827992 NCBI GI 587 BLAST score 7.0e-61 E value 145 Match length



% identity 76
NCBI Description (AF034743) UDP-glucuronosyltransferase [Pisum sativum]

Seq. No. 29421

Contig ID 191835\_1.R1040 5'-most EST sat701004975.h1

Seq. No. 29422

Contig ID 191869\_1.R1040 5'-most EST sat701005029.h1

Method BLASTX
NCBI GI g3242717
BLAST score 230
E value 2.0e-19
Match length 79
% identity 62

NCBI Description (AC003040) putative APG protein [Arabidopsis thaliana]

Seq. No. 29423

Contig ID 191878\_1.R1040 5'-most EST uC-gmronoir071f04b1

Method BLASTX
NCBI GI g3176662
BLAST score 1155
E value 1.0e-127
Match length 325
% identity 66

NCBI Description (AC004393) Similar to mannosyl-oligosaccharide glucosidase

gb\_X87237 from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 29424

Contig ID 191898\_1.R1040 5'-most EST sat701014033.h1

Method BLASTX
NCBI GI g3242062
BLAST score 264
E value 6.0e-23
Match length 80
% identity 64

NCBI Description (Z97058) NRT2;1p [Arabidopsis thaliana] >gi\_3608362

(AF019748) high-affinity nitrate transporter ACH1 [Arabidopsis thaliana] >gi\_3747058 (AF093754)

trans-membrane nitrate transporter protein AtNRT2:1

[Arabidopsis thaliana]

Seq. No. 29425

Contig ID 191901\_1.R1040 5'-most EST zhf700956811.h1

Method BLASTX
NCBI GI g1418990
BLAST score 199
E value 3.0e-15
Match length 136
% identity 30

NCBI Description (275524) unknown [Lycopersicon esculentum]

Seq. No. 29426



```
191913 1.R1040
Contig ID
                   sat701005116.hl
5'-most EST
Seq. No.
                   29427
                   191931 1.R1040
Contig ID
                   sat701005170.hl
5'-most EST
Method
                   BLASTX
                   q2961385
NCBI GI
BLAST score
                   183
E value
                   8.0e-14
Match length
                   73
                   52
% identity
                  (AL022141) putative protein [Arabidopsis thaliana]
NCBI Description
                   29428
Seq. No.
Contig ID
                   191944 1.R1040
                   sat701005164.hl
5'-most EST
Method
                   BLASTX
                   g4455328
NCBI GI
BLAST score
                   154
E value
                   2.0e-10
Match length
                   42
                   69
% identity
                  (AL035525) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   29429
Seq. No.
                   191978 1.R1040
Contig ID
                   jC-gmro02910067b11a1
5'-most EST
Method
                   BLASTX
                   g2739008
NCBI GI
                   378
BLAST score
E value
                   4.0e-36
                   145
Match length
                   50
% identity
                  (AF022463) CYP78A3p [Glycine max]
NCBI Description
                   29430
Seq. No.
                   192004 1.R1040
Contig ID
                   jex700908551.h1
5'-most EST
                   29431
Seq. No.
                   192014 1.R1040
Contig ID
                   g56881<u>9</u>2
5'-most EST
                   29432
Seq. No.
                   192016 1.R1040
Contig ID
                   sat701\overline{0}05301.h1
5'-most EST
                   29433
Seq. No.
                   192046 1.R1040
Contig ID
5'-most EST
                   sat701005365.hl
```

Seq. No. 29434

Contig ID 192052\_1.R1040 5'-most EST uC-gmropic107f07b1

Method BLASTX NCBI GI g3461820



```
BLAST score
                   3.0e-22
E value
Match length
                   75
% identity
                   59
```

(AC004138) unknown protein [Arabidopsis thaliana] NCBI Description

29435 Seq. No.

192070 1.R1040 Contiq ID awf700841401.hl 5'-most EST

Method BLASTX g2914703 NCBI GI BLAST score 337 2.0e-31 E value Match length 104 % identity 62

(AC003974) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 29436

192078 1.R1040 Contig ID sat701005415.hl 5'-most EST

29437 Seq. No.

192082 1.R1040 Contig ID  $sat701\overline{0}05419.h1$ 5'-most EST

Seq. No. 29438

192104 1.R1040 Contig ID 5'-most EST sat701005451.h1

29439 Seq. No.

192119 1.R1040 Contig ID bth700845486.h1 5'-most EST

BLASTN Method g2245682 NCBI GI 127 BLAST score 6.0e-65 E value 243 Match length 88 % identity

Glycine max peroxidase precursor (GMIPER1) mRNA, complete NCBI Description

29440 Seq. No.

192131 1.R1040 Contig ID zhf700959074.h1 5'-most EST

BLASTX Method g2829895 NCBI GI 146 BLAST score 1.0e-09 E value 55 Match length 58 % identity

(AC002311) hypothetical protein [Arabidopsis thaliana] NCBI Description

29441 Seq. No.

192138 1.R1040 Contig ID 5'-most EST rlr700900359.hl

29442 Seq. No.



Contig ID 192139\_1.R1040 5'-most EST jC-gmst02400014c07d1

Seq. No. 29443

Contig ID 192196\_1.R1040 5'-most EST sat701006082.h2

Seq. No. 29444

Contig ID 192207\_1.R1040 5'-most EST zsg701119825.h1

Method BLASTX
NCBI GI g4455286
BLAST score 151
E value 8.0e-10
Match length 91
% identity 46

NCBI Description (AL035527) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29445

Contig ID 192216\_1.R1040 5'-most EST sat701005901.h1

Seq. No. 29446

Contig ID 192259\_1.R1040 5'-most EST sat701005847.h1

Method BLASTX
NCBI GI g4508076
BLAST score 186
E value 1.0e-13
Match length 70
% identity 46

NCBI Description (AC005882) 55659 [Arabidopsis thaliana]

Seq. No. 29447

Contig ID 192326\_1.R1040 5'-most EST epx701109214.h1

Method BLASTX
NCBI GI g4406780
BLAST score 232
E value 2.0e-19
Match length 63
% identity 67

NCBI Description (AC006532) putative multispanning membrane protein

[Arabidopsis thaliana]

Seq. No. 29448

Contig ID 192346\_1.R1040 5'-most EST sat701005981.h1

Method BLASTN
NCBI GI g3005575
BLAST score 160
E value 1.0e-84
Match length 356
% identity 86

NCBI Description Glycine max putative high affinity nitrate transporter

(NRT2) mRNA, complete cds



```
29449
Seq. No.
Contig ID
                  192376 1.R1040
                  bth700844904.h1
5'-most EST
                  BLASTX
Method
                  g3063471
NCBI GI
                  279
BLAST score
                  5.0e-25
E value
Match length
                  80
% identity
                  64
                  (AC003981) F22013.33 [Arabidopsis thaliana]
NCBI Description
                  29450
Seq. No.
                  192383 1.R1040
Contig ID
5'-most EST
                  sat701\overline{0}06027.h2
                  BLASTX
Method
                  g4567227
NCBI GI
                  273
BLAST score
                  3.0e-24
E value
                  83
Match length
                   64
% identity
                  (AC007119) putative transport protein [Arabidopsis
NCBI Description
                  thaliana]
                   29451
Seq. No.
Contig ID
                   192405 1.R1040
                  uC-gmrominsoy070b12b1
5'-most EST
                   29452
Seq. No.
                   192437 1.R1040
Contig ID
                   sat701006110.h1
5'-most EST
                   BLASTX
Method
                   g2275218
NCBI GI
BLAST score
                   492
                   7.0e-50
E value
Match length
                   114
                   82
% identity
                   (AC002337) G-beta-repeat containing protein isolog
NCBI Description
                   [Arabidopsis thaliana]
                   29453
Seq. No.
Contig ID
                   192444 1.R1040
                   epx701106795.hl
5'-most EST
                   29454
Seq. No.
Contig ID
                   192446 1.R1040
                   uC-gmronoir008h08b1
5'-most EST
                   BLASTX
Method
                   q2388580
NCBI GI
BLAST score
                   174
                   2.0e-12
E value
Match length
                   56
                   54
```

% identity

NCBI Description

192449\_1.R1040 Contig ID

(gb 1253956). [Arabidopsis thaliana]

(AC000098) Similar to Sequence 10 from patent 5477002



5'-most EST

q4290719

Seq. No.

29456

Contig ID 5'-most EST 192475 1.R1040 sat701015349.h1

Seq. No. Contig ID 29457

5'-most EST

192508 1.R1040 sat701006191.hl

Seq. No. Contig ID 29458

5'-most EST

192518 1.R1040 fua701040190.h1

Seq. No. Contig ID 29459

5'-most EST

192520 1.R1040  $k11701\overline{2}12647.h1$ 

Seq. No.

29460

29461

Contig ID 5'-most EST 192532 1.R1040 sat701006225.h2

BLASTN Method g2104674 NCBI GI BLAST score 72 3.0e-32E value Match length 171 % identity 86

NCBI Description V.faba mRNA for transcription factor containing bZIP

Seq. No.

Contig ID

192565 1.R1040

5'-most EST

jC-qmf102220063g08a1

BLASTX Method g2738982 NCBI GI 316 BLAST score 4.0e-29 E value 96 Match length 61 % identity

NCBI Description (AF022157) CYP71A10 [Glycine max]

Seq. No.

Contig ID 5'-most EST 192568 1.R1040 sat701006272.h2

Seq. No.

29463

29462

Contig ID 5'-most EST 192588 1.R1040 sat701006401.hl

Seq. No.

29464

Contig ID

192596\_1.R1040

5'-most EST

g4302555

Seq. No. Contig ID 29465

5'-most EST

192598 1.R1040 sat701006326.h1

Seq. No.

29466



```
Contig ID 192599_1.R1040
5'-most EST uC-gmronoir053c02b1
Method BLASTX
```

NCBI GI g1360088
BLAST score 336
E value 4.0e-31
Match length 76
% identity 72

NCBI Description (X97947) In finger protein [Nicotiana tabacum]

Seq. No. 29467

Contig ID 192608\_1.R1040 5'-most EST sat701006345.h1

Seq. No. 29468

Contig ID 192611\_1.R1040 5'-most EST sat701006353.h1

Method BLASTX
NCBI GI g2281627
BLAST score 151
E value 4.0e-10
Match length 40
% identity 60

NCBI Description (AF003094) AP2 domain containing protein RAP2.1

[Arabidopsis thaliana]

Seq. No. 29469

Contig ID 192614\_1.R1040 5'-most EST sat701006358.h1

Seq. No. 29470

Contig ID 192616 1.R1040 5'-most EST sat701006371.h1

Seq. No. 29471

Contig ID 192620\_1.R1040 5'-most EST sat701006375.h1

Seq. No. 29472

Contig ID 192621 1.R1040 5'-most EST sat701006376.h1

Seq. No. 29473

Contig ID 192639\_1.R1040 5'-most EST sat701006407.h1

Method BLASTX
NCBI GI g3176687
BLAST score 515
E value 3.0e-74
Match length 164
% identity 78

NCBI Description (AC003671) Strong similarity to trehalose-6-phosphate synthase homolog from A. thaliana chromosome 4 contig

gb\_Z97344. ESTs gb\_H37594, gb\_R65023, gb\_H37578 and gb\_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No. 29474



```
192694 1.R1040
Contig ID
                   uC-gmrominsoy217b04b1
5'-most EST
                   {\tt BLASTX}
Method
NCBI GI
                   g2292921
BLAST score
                   419
                   2.0e-52
E value
                   152
Match length
                   73
% identity
                  (Y10252) pantoate--beta-alanine ligase [Lotus japonicus]
NCBI Description
                   29475
Seq. No.
                   192722 1.R1040
Contig ID
                   uC-gmropic032c09b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4530585
BLAST score
                   208
                   2.0e-16
E value
Match length
                   51
                   71
% identity
                   (AF130978) B12D protein [Ipomoea batatas]
NCBI Description
Seq. No.
                   29476
                   192722 2.R1040
Contig ID
                   sat701006550.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4530585
BLAST score
                   354
E value
                   2.0e-33
Match length
                   87
                   70
% identity
                   (AF130978) B12D protein [Ipomoea batatas]
NCBI Description
                   29477
Seq. No.
                   192730 1.R1040
Contig ID
                   zsg701128511.h1
5'-most EST
                   {\tt BLASTX}
Method
                   g3201627
NCBI GI
                   363
BLAST score
                   2.0e-40
E value
                   114
Match length
% identity
                   68
                   (AC004669) putative SWH1 protein [Arabidopsis thaliana]
NCBI Description
                   29478
Seq. No.
                   192760 1.R1040
Contig ID
                   sat701006609.h1
5'-most EST
                   BLASTX
Method
                   g3688173
NCBI GI
                    454
BLAST score
```

3.0e-45 E value Match length 134 % identity

(AL031804) putative protein [Arabidopsis thaliana] NCBI Description

29479 Seq. No.

192777 1.R1040 Contig ID 5'-most EST sat701006632.hl



```
29480
Seq. No.
                  192784_1.R1040
Contig ID
                   jC-gmro02910067a10d1
5'-most EST
Method
                   BLASTN
                   g728482
NCBI GI
BLAST score
                   119
                   3.0e-60
E value
                   263
Match length
                   86
% identity
                  Pisum sativum endo-1,4-beta-glucanase (EGL1) gene, complete
NCBI Description
                   29481
Seq. No.
                   192788 1.R1040
Contig ID
5'-most EST
                   zsq701118194.hl
Method
                   BLASTX
NCBI GI
                   g2947063
                   227
BLAST score
                   1.0e-18
E value
                   82
Match length
% identity
                   (AC002521) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   29482
Seq. No.
                   192790 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400014e12d1
Seq. No.
                   29483
                   192846 1.R1040
Contig ID
                   sat701006802.h1
5'-most EST
Seq. No.
                   29484
                   192865 1.R1040
Contig ID
                   jC-gmf\overline{1}02220148f04a1
5'-most EST
                   29485
Seq. No.
                   192903 1.R1040
Contig ID
                   asn701142412.hl
5'-most EST
                   BLASTX
Method
                   q3402746
NCBI GI
                   241
BLAST score
                   4.0e-20
E value
                   76
Match length
                   58
% identity
                   (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3402762_emb_CAA20208.1_ (AL031187) putative protein
                    [Arabidopsis thaliana]
```

Seq. No. 29486 Contig ID 192909\_1.R1040

5'-most EST sat701007001.h1
Method BLASTX
NCBI GI g2392895
BLAST score 151
E value 4.0e-10



Match length 47 % identity

(AF017056) brassinosteroid insensitive 1 [Arabidopsis NCBI Description

thaliana]

29487 Seq. No.

192917 1.R1040 Contig ID sat701007016.hl 5'-most EST

29488 Seq. No.

192945 1.R1040 Contig ID  $k11701\overline{2}07211.h1$ 5'-most EST

29489 Seq. No.

192952 1.R1040 Contig ID sat701007114.hl 5'-most EST

29490 Seq. No.

193009 1.R1040 Contig ID dpv701098378.hl 5'-most EST

29491 Seq. No.

193029 1.R1040 Contig ID  $sat701\overline{0}07212.h2$ 5'-most EST

BLASTX Method q416651 NCBI GI 314 BLAST score 9.0e-29 E value Match length 92

% identity 63

PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN NCBI Description PCNT103) >gi\_100301\_pir\_\_S16269 auxin-induced protein

(clone pCNT103) - common tobacco >gi 19791 emb CAA39704

(X56263) auxin-induced protein [Nicotiana tabacum]

29492 Seq. No.

193077 1.R1040 Contig ID sat701007277.h2 5'-most EST

29493 Seq. No.

193080 1.R1040 Contig ID sat701007280.h2 5'-most EST

29494 Seq. No.

193108 1.R1040 Contig ID zsg701127564.hl 5'-most EST

29495 Seq. No.

193118 1.R1040 Contig ID

uC-gmflminsoy022c01b1 5'-most EST

29496 Seq. No.

193128 1.R1040 Contig ID epx701104056.hl 5'-most EST

29497 Seq. No.

193147\_1.R1040 Contig ID



```
sat701007370.h2
5'-most EST
                  29498
Seq. No.
                  193153 1.R1040
Contig ID
                  sat701007377.h2
5'-most EST
                  29499
Seq. No.
                  193161_1.R1040
Contig ID
                  uC-gmropic069h12b1
5'-most EST
                  29500
Seq. No.
                  193166 1.R1040
Contig ID
                  jC-gmst02400029f06a1
5'-most EST
Seq. No.
                   29501
                   193180 1.R1040
Contig ID
                   k11701\overline{2}07080.h1
5'-most EST
                   29502
Seq. No.
                   193209 1.R1040
Contig ID
5'-most EST
                   g4314091
                   BLASTX
Method
                   g3822223
NCBI GI
                   1022
BLAST score
                   1.0e-111
E value
                   255
Match length
                   73
% identity
                   (AF077955) branched-chain alpha keto-acid dehydrogenase E1
NCBI Description
                   alpha subunit [Arabidopsis thaliana]
                   29503
Seq. No.
                   193214 1.R1040
Contig ID
                   sat701007463.h2
5'-most EST
                   BLASTX
Method
                   g1495804
NCBI GI
                   497
BLAST score
                   4.0e-50
E value
                   161
Match length
% identity
                   63
                  (X96406) 13-lipoxygenase [Solanum tuberosum]
NCBI Description
                   29504
Seq. No.
                   193302 1.R1040
Contig ID
                   sat701007613.hl
5'-most EST
                   BLASTX
Method
                   g3170230
NCBI GI
                   185
BLAST score
                   7.0e-14
E value
                   78
Match length
                   55
% identity
                   (AF041848) fructose-6-phosphate 2-kinase
NCBI Description
                   /fructose-2,6-bisphosphatase [Spinacia oleracea]
```

Contig ID 193348\_1.R1040 5'-most EST jC-gmst02400014b05d1

Method BLASTX

```
q4490310
NCBI GI
BLAST score
                  185
                   1.0e-13
E value
                   62
Match length
% identity
                  (AL035678) somatic embryogenesis receptor-like kinase-like
NCBI Description
                  protein [Arabidopsis thaliana]
                   29506
Seq. No.
                   193352 1.R1040
Contig ID
5'-most EST
                  gsv701054114.hl
                   BLASTX
Method
                   q3367574
NCBI GI
                   168
BLAST score
                   6.0e-12
E value
Match length
                   117
% identity
                  (AL031135) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   29507
Seq. No.
                   193369 1.R1040
Contig ID
5'-most EST
                   awf700841301.hl
                   BLASTX
Method
                   q2894594
NCBI GI
                   155
BLAST score
                   1.0e-09
E value
                   46
Match length
                   59
% identity
                  (AL021889) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   29508
Seq. No.
                   193371 1.R1040
Contig ID
                   asn701133458.h1
5'-most EST
                   29509
Seq. No.
                   193395 1.R1040
Contig ID
                   sat701007806.h1
5'-most EST
                   BLASTX
Method
                   g2346988
NCBI GI
BLAST score
                   141
E value
                   8.0e-09
Match length
                   52
% identity
                   40
                   (AB006606) ZPT4-4 [Petunia x hybrida]
NCBI Description
                   29510
Seq. No.
                   193431 1.R1040
Contig ID
                   fua701040268.hl
5'-most EST
                   BLASTX
Method
```

Method BLASTX
NCBI GI g2598575
BLAST score 159
E value 5.0e-11
Match length 51
% identity 63

NCBI Description (Y15293) MtN21 [Medicago truncatula]

Seq. No. 29511



```
193450 1.R1040
Contig ID
                  sat701008113.h1
5'-most EST
                  BLASTX
Method
                  g3643085
NCBI GI
                  228
BLAST score
                  4.0e-19
E value
                  85
Match length
                  56
% identity
                  (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum
NCBI Description
                  crystallinum]
                  29512
Seq. No.
                  193467_1.R1040
Contig ID
                  sat701007943.h1
5'-most EST
Method
                  BLASTX
                  q2499882
NCBI GI
BLAST score
                  141
                  1.0e-08
E value
                   51
Match length
                   49
% identity
                  PROTEASE IV HOMOLOG (ENDOPEPTIDASE IV)
NCBI Description
                   >gi 1652816 dbj BAA17735_ (D90908) protease IV
                   [Synechocystis sp.]
                   29513
Seq. No.
                   193468 1.R1040
Contig ID
                   jC-gmle01810011f08a1
5'-most EST
                   BLASTX
Method
                   q4335751
NCBI GI
                   476
BLAST score
                   8.0e-48
E value
                   157
Match length
                   57
% identity
                  (ACO06284) putative methyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   29514
Seq. No.
                   193482 1.R1040
Contig ID
                   sat701008130.hl
5'-most EST
                   BLASTX
Method
                   g3548806
NCBI GI
BLAST score
                   166
                   3.0e-19
E value
                   75
Match length
                   77
% identity
                  (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                   29515
Seq. No.
                   193486 1.R1040
Contig ID
5'-most EST
                   gsv701054389.h1
Seq. No.
                   29516
                   193538 1.R1040
```

Contig ID sat701008054.hl 5'-most EST

BLASTX Method NCBI GI g2749982 351 BLAST score



4.0e-33 E value Match length 139 53 % identity

(AF036705) Similar to phytoene desaturase; coded for by C. NCBI Description

elegans cDNA CEESX74F; coded for by C. elegans cDNA

yk303f4.3; coded for by C. elegans cDNA yk257d4.3; coded for by C. elegans cDNA yk303f4.5; coded for by C. elegans

cDNA yk257d4.5;

29517 Seq. No.

193542 1.R1040 Contig ID sat701008061.hl 5'-most EST

BLASTX Method q1707412 NCBI GI 235 BLAST score E value 6.0e-20 Match length 65 60 % identity

(X95906) Cleavage and Polyadenylation Specifity Factor NCBI Description

protein [Bos taurus]

29518 Seq. No.

193558 1.R1040 Contig ID zsq701123432.hl 5'-most EST

Method BLASTX q1087073 NCBI GI BLAST score 240 1.0e-20 E value 62 Match length

% identity

(S79243) calmodulin-binding heat-shock protein, CaMBP NCBI Description [Nicotiana tabacum=tobacco, Wisconsin-38, Peptide, 449 aa]

[Nicotiana tabacum]

29519 Seq. No.

Contig ID 193559 1.R1040 sat701008090.hl 5'-most EST

BLASTX Method q2244902 NCBI GI 174 BLAST score 1.0e-12 E value 59 Match length % identity 47

(Z97339) allene oxide synthase [Arabidopsis thaliana] NCBI Description

29520 Seq. No.

193565 1.R1040 Contig ID sat701008102.h1 5'-most EST

29521 Seq. No.

193569 1.R1040 Contig ID

uC-gmflminsoy077g05b1 5'-most EST

29522 Seq. No.

193586 1.R1040 Contig ID jsh701070376.hl 5'-most EST

Method BLASTX

NCBI GI g3551956
BLAST score 406
E value 9.0e-40
Match length 88
% identity 77

NCBI Description (AF082031) senescence-associated protein 6 [Hemerocallis hybrid cultivar]

Seq. No. 29523

Contig ID 193588\_1.R1040 5'-most EST sat701010616.h1

Seq. No. 29524

Contig ID 193596\_1.R1040

NCBI Description (AC003040) putative APG protein [Arabidopsis thaliana]

Seq. No. 29525

Contig ID 193597\_1.R1040

5'-most EST jC-gmst02400052e03d1

Method BLASTN
NCBI GI g2252848
BLAST score 39
E value 2.0e-12
Match length 143
% identity 82

NCBI Description Arabidopsis thaliana BAC TM018A10

Seq. No. 29526

Contig ID 193598\_1.R1040 5'-most EST sat701008164.h1

Seq. No. 29527

Contig ID 193624\_1.R1040 5'-most EST pmv700890406.h1

Seq. No. 29528

Contig ID 193629\_1.R1040 5'-most EST pmv700890281.h1

Method BLASTX
NCBI GI g3540182
BLAST score 193
E value 8.0e-15
Match length 79
% identity 53

NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 29529

Contig ID 193665\_1.R1040 5'-most EST fua701037777.h1

```
29530
Seq. No.
```

193666 1.R1040 Contig ID epx701109858.hl 5'-most EST

Method BLASTX g3114968 NCBI GI 300 BLAST score 1.0e-27 E value Match length 83 % identity 67

(Y14997) prolidase [Suberites domuncula] NCBI Description

29531 Seq. No.

193678 1.R1040 Contig ID sat701008303.hl 5'-most EST

BLASTN Method NCBI GI g19506 BLAST score 132 E value 3.0e-68 208 Match length 91 % identity

NCBI Description L.polyphyllus mRNA for pPLZ02 protein

Seq. No. Contig ID

29532 193694 1.R1040

uC-gmrominsoy145b02b1 5'-most EST

Seq. No. 29533

193727 1.R1040 Contig ID sat701008405.h1 5'-most EST

Method BLASTX g3335349 NCBI GI BLAST score 658 4.0e-69 E value 177 Match length % identity 69

(AC004512) Similar to gb\_U46691 putative chromatin NCBI Description

structure regulator (SUPT6H) from Homo sapiens. ESTs gb T42908, gb\_AA586170 and gb\_AA395125 come from this gene.

[Arabidopsis thaliana]

Seq. No. 29534

193738 1.R1040 Contig ID sat701008420.h1 5'-most EST

29535 Seq. No.

193739 1.R1040 Contiq ID

jC-gmle01810045d06a1 5'-most EST BLASTX Method

g2191171 NCBI GI 259 BLAST score 1.0e-22 E value 81 Match length % identity 48

(AF007270) similar to A. thaliana DI19 mRNA (NID:g469110) NCBI Description

[Arabidopsis thaliana]

29536 Seq. No.

4548



Contig ID 193795\_1.R1040 5'-most EST uC-gmrominsoy276e05b1

Seq. No. 29537

Contig ID 193816\_1.R1040 5'-most EST sat701008663.h1

Seq. No. 29538

Contig ID 193828\_1.R1040 5'-most EST sat701008568.h1

Seq. No. 29539

Contig ID 193831\_1.R1040 5'-most EST rlr700900159.h1

Method BLASTX
NCBI GI g3152579
BLAST score 225
E value 1.0e-27
Match length 98
% identity 72

NCBI Description (AC002986) YUP8H12R.9 [Arabidopsis thaliana]

Seq. No. 29540

Contig ID 193855\_1.R1040 5'-most EST kl1701212568.h1

Method BLASTX
NCBI GI g2723496
BLAST score 244
E value 3.0e-25
Match length 128
% identity 52

NCBI Description (AB009972) beta-1,4-xylosidase [Aspergillus oryzae]

Seq. No. 29541

Contig ID 193859\_1.R1040 5'-most EST sat701008602.h1

Method BLASTX
NCBI GI g3647355
BLAST score 301
E value 1.0e-27
Match length 105
% identity 58

NCBI Description (Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w), Human hypothetical protein KIAA0249-related protein len:

1160 aa; Similarity to 2 human and an yeast hypothetical gene. Human hypothetical protein KIAA0249 (SW:Y249 HUMA

Seq. No. 29542

Contig ID 193868\_1.R1040 5'-most EST sat701008613.h1

Seq. No. 29543

Contig ID 193870 1.R1040

5'-most EST g5057567

Seq. No. 29544

Contig ID 193929\_1.R1040



```
zhf700965246.h1
5'-most EST
                  29545
Seq. No.
                  193951 1.R1040
Contig ID
                  bth700845382.h1
5'-most EST
                  BLASTX
Method
                  q3241943
NCBI GI
                  677
BLAST score
                  2.0e-71
E value
Match length
                  152
% identity
                  80
                  (AC004625) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  29546
                  193969 1.R1040
Contig ID
5'-most EST
                  g5057839
                   29547
Seq. No.
                   193990 1.R1040
Contig ID
                   sat701008819.h1
5'-most EST
                   29548
Seq. No.
                   193995 1.R1040
Contig ID
                   epx701109276.hl
5'-most EST
                   BLASTX
Method
                   g4544451
NCBI GI
BLAST score
                   163
                   2.0e-11
E value
Match length
                   72
                   46
% identity
                  (AC006592) unknown protein [Arabidopsis thaliana]
NCBI Description
                   29549
Seq. No.
                   194008 1.R1040
Contig ID
                   jC-gmro02910067h09a1
5'-most EST
                   BLASTX
Method
                   g2245032
NCBI GI
                   234
BLAST score
                   3.0e-19
E value
                   106
Match length
                   51
 % identity
                  (Z97342) gibberellin oxidase homolog [Arabidopsis thaliana]
NCBI Description
                   29550
 Seq. No.
                   194016 1.R1040
 Contig ID
                   sat701008859.h1
 5'-most EST
                   29551
 Seq. No.
                   194045 1.R1040
 Contig ID
                   kl1701209619.hl
 5'-most EST
                   BLASTX
 Method
 NCBI GI
                   g2827556
                   169
 BLAST score
                   3.0e-15
 E value
                   127
 Match length
                   44
 % identity
 NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]
```



```
29552
Seq. No.
                  194051 1.R1040
Contig ID
                  uC-gmrominsoy111f07b1
5'-most EST
                  29553
Seq. No.
                  194066 1.R1040
Contig ID
                  uC-gmronoir030b03b1
5'-most EST
                  29554
Seq. No.
                  194073 1.R1040
Contig ID
                  sat701008951.hl
5'-most EST
                  29555
Seq. No.
Contig ID
                  194089 1.R1040
                  sat701008972.h1
5'-most EST
                  BLASTX
Method
                  g2944423
NCBI GI
                  183
BLAST score
                  1.0e-13
E value
Match length
                  116
% identity
                   41
                  (AF049850) hypothetical protein [Mus musculus]
NCBI Description
                   29556
Seq. No.
                   194097_1.R1040
Contig ID
                   sat701009149.hl
5'-most EST
Seq. No.
                   29557
                   194107 1.R1040
Contig ID
                   fua701042312.hl
5'-most EST
                   BLASTX
Method
                   q3402684
NCBI GI
                   183
BLAST score
                   6.0e-14
E value
                   51
Match length
                   63
% identity
                  (AC004697) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   29558
Seq. No.
                   194109 1.R1040
Contig ID
                   awf700838967.h1
5'-most EST
                   BLASTX
Method
                   q3021409
NCBI GI
BLAST score
                   497
                   4.0e-50
E value
                   139
Match length
% identity
                   20
```

NCBI Description

(Y12781) transducin (beta) like 1 protein [Homo sapiens]

29559 Seq. No.

194126 1.R1040 Contig ID pxt700943384.hl 5'-most EST

BLASTX Method g3482929 NCBI GI BLAST score 301 1.0e-27 E value



Match length 67 % identity 79

NCBI Description (AC003970) Putative transcription factor [Arabidopsis

thaliana]

Seq. No. 29560

Contig ID 194127\_1.R1040 5'-most EST sat701009961.h2

Method BLASTN
NCBI GI g2293067
BLAST score 49
E value 3.0e-18
Match length 281
% identity 89

NCBI Description S.rostrata mRNA for early nodulin

Seq. No. 29561

Contig ID 194157\_1.R1040 5'-most EST pxt700944035.h1

Seq. No. 29562

Contig ID 194202\_1.R1040

5'-most EST jC-gmle01810094g08d1

Seq. No. 29563

Contig ID 194217\_1.R1040

5'-most EST jC-gmro02910004a07a1

Seq. No. 29564

Contig ID 194247\_1.R1040 5'-most EST sat701009196.h1

Method BLASTX
NCBI GI 9461812
BLAST score 232
E value 3.0e-19
Match length 128
% identity 34

NCBI Description CYTOCHROME P450 72 (CYPLXXII) (PROBABLE

GERANIOL-10-HYDROXYLASE) (GE10H) >gi\_167484 (L10081)

Cytochrome P-450 protein [Catharanthus roseus]

>gi 445604 prf 1909351A cytochrome P450 [Catharanthus

roseus]

Seq. No. 29565

Contig ID 194256\_1.R1040 5'-most EST sat701009212.h1

Method BLASTX
NCBI GI g4115379
BLAST score 223
E value 1.0e-18
Match length 80
% identity 56

NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis

thaliana]

Seq. No. 29566

Contig ID 194276\_1.R1040



```
jC-gmst02400057g06a1
5'-most EST
                  29567
Seq. No.
                  194289 1.R1040
Contig ID
                  sat701009252.hl
5'-most EST
                  29568
Seq. No.
                  194294 2.R1040
Contig ID
                  gsv701\overline{0}56852.h1
5'-most EST
                  29569
Seq. No.
                  194333 1.R1040
Contig ID
                  sat701009314.hl
5'-most EST
Seq. No.
                   29570
                   194337 1.R1040
Contig ID
                  uC-gmronoir062f12b1
5'-most EST
                   29571
Seq. No.
                   194339 1.R1040
Contig ID
                   pmv700892839.hl
5'-most EST
                   BLASTX
Method
                   g1076274
NCBI GI
                   188
BLAST score
                   1.0e-26
E value
Match length
                   129
% identity
                   52
NCBI Description cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)
                   29572
Seq. No.
                   194381 1.R1040
Contig ID
                   sat701009375.hl
5'-most EST
                   BLASTX
Method
                   g4490736
NCBI GI
                   345
BLAST score
                   1.0e-32
E value
                   114
Match length
% identity
                   65
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
                   29573
Seq. No.
                   194384 1.R1040
Contig ID
                   sat701009378.h1
5'-most EST
                   BLASTX
Method
                   g125415
NCBI GI
BLAST score
                   214
                   3.0e-17
E value
                   110
Match length
                   42
```

% identity

KINESIN HEAVY CHAIN >gi 102714\_pir\_\_A35075 kinesin heavy NCBI Description chain - longfin squid >gi 161290 (J05258) kinesin heavy

chain [Loligo pealii]

29574 Seq. No.

194385 1.R1040 Contig ID 5'-most EST sat701009379.hl



Contig ID 194394\_1.R1040 5'-most EST sat701009392.h1

Seq. No. 29576

Contig ID 194414\_1.R1040 5'-most EST zhf700953808.h1

Method BLASTX
NCBI GI g2832686
BLAST score 519
E value 6.0e-53
Match length 139
% identity 63

NCBI Description (AL021712) putative protein [Arabidopsis thaliana]

Seq. No. 29577

Contig ID 194463\_2.R1040 5'-most EST pxt700945306.h1

Method BLASTX
NCBI GI g3033389
BLAST score 147
E value 2.0e-09
Match length 70
% identity 24

NCBI Description (AC004238) Cf-2.1-like protein [Arabidopsis thaliana]

Seq. No. 29578

Contig ID 194466\_1.R1040 5'-most EST sat701009506.h1

Seq. No. 29579

Contig ID 194468\_1.R1040 5'-most EST sat701009512.h1

Seq. No.

Contig ID 194482\_1.R1040 5'-most EST bth700849483.h1

Seq. No. 29581

Contig ID 194499\_1.R1040

5'-most EST jC-gmro02910063b03a1

29580

Seq. No. 29582

Contig ID 194546\_1.R1040 5'-most EST pxt700943786.h1

Seq. No. 29583

Contig ID 194553\_1.R1040

5'-most EST jC-gmst02400065d04a2

Seq. No. 29584

Contig ID 194575\_1.R1040 5'-most EST gsv701047130.h1

Seq. No. 29585

Contig ID 194623\_1.R1040 5'-most EST sat701009739.h1



Contig ID 194731\_1.R1040 5'-most EST sat701009879.h1

Seq. No. 29587

Contig ID 194735\_1.R1040 5'-most EST sat701009886.h1

Seq. No. 29588

Contig ID 194735 2.R1040

5'-most EST uC-gmflminsoy078c02b1

Seq. No. 29589

Contig ID 194747\_1.R1040 5'-most EST bth700846381.h1

Method BLASTX
NCBI GI g3367594
BLAST score 222
E value 4.0e-18
Match length 88
% identity 47

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 29590

Contig ID 194760\_1.R1040 5'-most EST sat701009926.h2

Seq. No. 29591

Contig ID 194789\_1.R1040 5'-most EST sat701009960.h2

Method BLASTN
NCBI GI g298018
BLAST score 141
E value 2.0e-73
Match length 225
% identity 94

NCBI Description M.sativa mRNA msk7 for map kinase

Seq. No. 29592

Contig ID 194793 1.R1040 5'-most EST uC-gmropic033d02b1

Seq. No. 29593

Contig ID 194813\_1.R1040 5'-most EST kl1701212812.h1

Seq. No. 29594

Contig ID 194814 1.R1040 5'-most EST sat701009994.h2

Seq. No. 29595

Contig ID 194816\_1.R1040 5'-most EST hrw701061964.h1

Seq. No. 29596

Contig ID 194833\_1.R1040

4555

```
uC-qmrominsoy272c09b1
5'-most EST
                  BLASTX
Method
                  q3413704
NCBI GI
BLAST score
                  560
E value
                  2.0e-57
Match length
                  147
% identity
                  70
                  (AC004747) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  29597
Seq. No.
                  194833 2.R1040
Contig ID
                  uC-gmrominsoy109c12b1
5'-most EST
                   BLASTX
Method
                   g3413704
NCBI GI
BLAST score
                   272
E value
                   7.0e-24
Match length
                   82
% identity
                   65
                  (AC004747) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   29598
                   194858 1.R1040
Contig ID
                   sat701010054.h2
5'-most EST
                   BLASTX
Method
                   q2507229
NCBI GI
BLAST score
                   297
                   6.0e-27
E value
                   90
Match length
                   66
% identity
                   40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE)
NCBI Description
                   (ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED
                   PROTEIN) (ESTROGEN RECEPTOR BINDING CYCLOPHILIN)
                   >gi_423247_pir__A46579 estrogen receptor-binding
                   cyclophilin - bovine >gi_393300_dbj_BAA03159_ (D14074)
                   cyclophilin [Bos taurus]
                   29599
Seq. No.
                   194860 1.R1040
Contig ID
                   sat701010057.h2
5'-most EST
                   BLASTN
Method
                   g312988
NCBI GI
                   127
BLAST score
                   3.0e-65
E value
                   227
Match length
                   89
 % identity
NCBI Description G.max mRNA for beta-tubulin, partial cds
                   29600
 Seq. No.
                   194870 1.R1040
 Contig ID
                   leu701148749.hl
 5'-most EST
                   BLASTX
 Method
                   q4249380
 NCBI GI
                   252
 BLAST score
                   1.0e-21
 E value
                   90
 Match length
 % identity
                   52
 NCBI Description (AC005966) ESTs gb_Z37637, gb_AA042498 and gb_AA042269 come
```



from this gene. [Arabidopsis thaliana]

Seq. No. 29601

Contig ID 194875\_1.R1040 5'-most EST sat701010075.h2

Seq. No. 29602

Contig ID 194900\_1.R1040

5'-most EST jC-gmst02400029f07d1

Method BLASTX
NCBI GI g2623297
BLAST score 192
E value 2.0e-14
Match length 59
% identity 56

NCBI Description (AC002409) unknown protein [Arabidopsis thaliana]

 $>gi_3790583$  (AF079180) RING-H2 finger protein RHC1a

[Arabidopsis thaliana]

Seq. No. 29603

Contig ID 194900\_2.R1040 5'-most EST jC-gmro02910071b07d1

Method BLASTX
NCBI GI g2982466
BLAST score 155
E value 3.0e-10
Match length 39
% identity 59

NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 29604

Contig ID 194904\_1.R1040 5'-most EST jsh701066235.h1

Method BLASTX
NCBI GI g3540180
BLAST score 232
E value 2.0e-19
Match length 104
% identity 49

NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 29605

Contig ID 194930\_1.R1040 5'-most EST sat701010158.h2

Seq. No. 29606

Contig ID 194936\_1.R1040 5'-most EST sat701010170.h2

Seq. No. 29607

Contig ID 194946\_1.R1040 5'-most EST sat701010189.h2

Method BLASTX
NCBI GI g3695019
BLAST score 297
E value 3.0e-27
Match length 92

```
% identity
                   (AF055848) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
                   29608
Seq. No.
                   194957 1.R1040
Contig ID
                   jC-gms\overline{t}02400027d10a1
5'-most EST
```

194970 1.R1040 Contig ID sat701010228.h2 5'-most EST

29610 Seq. No.

194982 1.R1040 Contig ID pmv700889887.h1 5'-most EST

Seq. No. 29611

195033 1.R1040 Contig ID q5677757

5'-most EST BLASTX Method q3600049 NCBI GI BLAST score 378 E value 2.0e-36 123 Match length 64 % identity

(AF080120) similar to initiation factor IF2-beta (Pfam: NCBI Description

GTP EFTU.hmm, score: 226.67) [Arabidopsis thaliana]

Seq. No. 29612

195062 1.R1040 Contig ID  $sat701\overline{0}10365.h1$ 5'-most EST

BLASTX Method g3600032 NCBI GI 378 BLAST score 1.0e-36 E value 102 Match length 61 % identity

(AF080119) contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam: NCBI Description ATP-synt\_B.hmm, score: 10.89) [Arabidopsis thaliana]

29613 Seq. No.

195094 1.R1040 Contig ID

 $g56060\overline{4}4$ 5'-most EST BLASTX Method g4559333 NCBI GI 182 BLAST score 9.0e-17 E value 122 Match length 49 % identity

(AC007087) unknown protein [Arabidopsis thaliana] NCBI Description

29614 Seq. No.

195207 1.R1040 Contig ID sat701010565.hl 5'-most EST

29615 Seq. No.

195227\_1.R1040 Contig ID

Match length

% identity

54 57



```
jex700904394.h1
5'-most EST
                   29616
Seq. No.
                   195290 1.R1040
Contig ID
                   sat701010670.hl
5'-most EST
                   29617
Seq. No.
                   195299 1.R1040
Contig ID
                   uC-gmropic019a01b1
5'-most EST
                   29618
Seq. No.
                   195313 1.R1040
Contig ID
                   asn701137390.hl
5'-most EST
                   BLASTX
Method
                   g3249105
NCBI GI
BLAST score
                   396
                   1.0e-38
E value
Match length
                   98
                   69
% identity
                   (AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                   (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
                   29619
Seq. No.
                   195326 1.R1040
Contig ID
                   sat701\overline{0}10719.h1
5'-most EST
                   29620
Seq. No.
                   195354 1.R1040
Contig ID
                   asn701\overline{1}38694.h1
5'-most EST
                   BLASTX
Method
                   g2342423
NCBI GI
BLAST score
                   274
                   2.0e-24
E value
                   101
Match length
% identity
                   (AB000797) NPK1-related protein kinase 1S [Arabidopsis
NCBI Description
                   thaliana]
                   29621
Seq. No.
                   195465 1.R1040
Contig ID
                   sat701010931.hl
5'-most EST
                   29622
Seq. No.
                   195499 1.R1040
Contig ID
                   sat701\overline{0}10979.h1
5'-most EST
                    29623
Seq. No.
                    195533_1.R1040
Contig ID
                    sat701011065.hl
5'-most EST
                    BLASTX
Method
NCBI GI
                    q4539314
                    161
BLAST score
                    1.0e-11
E value
```

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]



```
Seq. No.
                  195555 1.R1040
Contig ID
5'-most EST
                  sat701011073.hl
Seq. No.
                  29625
                  195587 1.R1040
Contig ID
                  sat701011116.hl
5'-most EST
                  BLASTX
Method
                  q4432835
NCBI GI
BLAST score
                  196
E value
                   2.0e-15
                   54
Match length
% identity
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   29626
Seq. No.
                   195588 1.R1040
Contig ID
5'-most EST
                   sat701011117.hl
                   BLASTN
Method
                   q2598586
NCBI GI
                   152
BLAST score
E value
                   4.0e-80
                   272
Match length
% identity
                   89
NCBI Description Medicago truncatula mRNA for cycloartenol synthase, partial
                   29627
Seq. No.
                   195612 1.R1040
Contig ID
                   sat701011145.hl
5'-most EST
                   BLASTX
Method
                   q4220535
NCBI GI
BLAST score
                   369
                   1.0e-35
E value
                   85
Match length
% identity
                   (AL035356) clathrin coat assembly like protein [Arabidopsis
NCBI Description
                   thaliana]
                   29628
Seq. No.
                   195622 1.R1040
Contig ID
5'-most EST
                   asn701139014.h1
                   29629
Seq. No.
                   195663 1.R1040
Contig ID
                   leu701146071.hl
 5'-most EST
                   BLASTX
Method
                   g1651736
NCBI GI
```

241 BLAST score 3.0e-20 E value 69 Match length 65 % identity

NCBI Description (D90899) cysteine synthase [Synechocystis sp.]

Seq. No.

29630

Contig ID 5'-most EST 195667 1.R1040  $jsh701\overline{0}66652.h1$ 

BLASTX Method



NCBI GI g4432855 BLAST score 392 E value 5.0e-38 Match length 140 % identity 68

NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]

Seq. No. 29631

Contig ID 195670\_1.R1040 5'-most EST sat701011220.h1

Seq. No. 29632

Contig ID 195692\_1.R1040 5'-most EST zsg701127909.h1

Seq. No. 29633

Contig ID 195710\_1.R1040 5'-most EST sat701011269.h1

Seq. No. 29634

Contig ID 195715\_1.R1040 5'-most EST sat701011275.h1

Seq. No. 29635

Contig ID 195739\_1.R1040 5'-most EST sat701011311.h1

Seq. No. 29636

Contig ID 195761\_1.R1040 5'-most EST fua701036962.h1

Method BLASTX
NCBI GI g3269296
BLAST score 145
E value 5.0e-09
Match length 76
% identity 41

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 29637

Contig ID 195771\_1.R1040

5'-most EST jC-gmle01810093d04d1

Seq. No. 29638

Contig ID 195772\_1.R1040

 5'-most EST
 g4292625

 Method
 BLASTX

 NCBI GI
 g4512681

 BLAST score
 372

 E value
 1.0e-35

 Match length
 160

 % identity
 52

NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29639

Contig ID 195775\_1.R1040 5'-most EST gsv701050635.h1



```
Seq. No.
                  195791 1.R1040
Contig ID
                  gsv701045616.h1
5'-most EST
Seq. No.
                  29641
Contig ID
                  195810 1.R1040
5'-most EST
                  jC-qmst02400040d05a1
                  BLASTX
Method
NCBI GI
                  q2135172
BLAST score
                  186
E value
                  1.0e-13
Match length
                  133
% identity
                  32
NCBI Description gene anonymous protein - human >gi 388012 (L18972)
                  anonymous [Homo sapiens]
                  >gi 4505829 ref NP 003669.1 pPK1.3 gene from
                  NF2/meningioma region of 22q12
                  29642
Seq. No.
                  195824 1.R1040
Contig ID
5'-most EST
                  yz1700966927.h1
Method
                  BLASTX
NCBI GI
                  g2344890
BLAST score
                  244
                  5.0e-27
E value
                  83
Match length
% identity
                  76
NCBI Description (AC002388) TINY transcription factor isolog [Arabidopsis
                  thaliana]
                  29643
Seq. No.
Contig ID
                  195832 1.R1040
5'-most EST
                  sat701011429.h1
                  29644
Seq. No.
                  195846 1.R1040
Contig ID
5'-most EST
                  leu701145620.h1
                  BLASTX
Method
                  g2739372
NCBI GI
BLAST score
                  180
E value
                  2.0e-13
                  66
Match length
% identity
NCBI Description (AC002505) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  29645
                  195849 1.R1040
```

Contig ID

5'-most EST epx701105188.h1

29646 Seq. No.

195857 1.R1040 Contig ID 5'-most EST sat701011463.hl

Seq. No. 29647

195867 1.R1040 Contig ID 5'-most EST zhf700965170.h1



Contig ID 195880\_1.R1040 5'-most EST sat701011503.h1

Seq. No. 29649

Contig ID 195983\_1.R1040 5'-most EST leu701155819.h1

Method BLASTX
NCBI GI g1223579
BLAST score 305
E value 3.0e-28
Match length 85
% identity 68

NCBI Description (X96481) cDNA101 [Arabidopsis thaliana]

Seq. No. 29650

Contig ID 196011 1.R1040

5'-most EST uC-gmrominsoy168c03b1

Method BLASTX
NCBI GI g3355640
BLAST score 477
E value 3.0e-48
Match length 120
% identity 81

NCBI Description (AJ009684) IVR-like protein [Nicotiana tabacum]

Seq. No. 29651

Contig ID 196036\_1.R1040 5'-most EST sat701011749.h1

Method BLASTX
NCBI GI g3080435
BLAST score 637
E value 2.0e-66
Match length 147
% identity 82

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 29652

Contig ID 196068 1.R1040 5'-most EST jex700907228.h1

Seq. No. 29653

Contig ID 196101 1.R1040 5'-most EST sat701011846.h1

Seq. No. 29654

Contig ID 196144\_1.R1040 5'-most EST sat701012096.h1

Seq. No. 29655

Contig ID 196150\_1.R1040

5'-most EST uC-gmflminsoy010a02b1

Method BLASTX
NCBI GI g3033392
BLAST score 723
E value 1.0e-76
Match length 186



% identity 72

NCBI Description (AC004238) putative translation initiation factor EIF-2B-epsilon subunit [Arabidopsis thaliana]

Seq. No. 29656

Contig ID 196152\_1.R1040 5'-most EST jC-gmle01810062d11a1

Method BLASTX
NCBI GI g2864618
BLAST score 605
E value 8.0e-63
Match length 191
% identity 61

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 29657

Contig ID 196202\_1.R1040 5'-most EST sat701012010.h1

Method BLASTX
NCBI GI g4544399
BLAST score 296
E value 8.0e-27
Match length 133
% identity 68

NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 29658

Contig ID 196209\_1.R1040 5'-most EST sat701012020.h1

Method BLASTX
NCBI GI g927575
BLAST score 112
E value 4.0e-11
Match length 125
% identity 40

NCBI Description (U12926) alpha galactosidase [Glycine max]

Seq. No. 29659

Contig ID 196216\_1.R1040 5'-most EST pxt700946306.h1

Method BLASTX
NCBI GI g2244792
BLAST score 342
E value 1.0e-32
Match length 75
% identity 85

NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No. 29660

Contig ID 196233\_1.R1040

5'-most EST uC-gmflminsoy089g03b1

Seq. No. 29661

Contig ID 196234 1.R1040 5'-most EST jC-gmfI02220053g12a1

Method BLASTX

4564



NCBI GI g3152582 BLAST score 361 E value 2.0e-34 Match length 151 % identity 50

NCBI Description (AC002986) YUP8H12R.20 [Arabidopsis thaliana]

Seq. No. 29662

Contig ID 196243 1.R1040

5'-most EST uC-gmflminsoy021h04b1

Seq. No. 29663

Contig ID 196251\_1.R1040 5'-most EST zsg701130316.h1

Method BLASTX
NCBI GI g2190548
BLAST score 186
E value 5.0e-14
Match length 69
% identity 55

NCBI Description (AC001229) EST gb\_ATTS1121 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 29664

Contig ID 196277\_1.R1040 5'-most EST sat701012132.h1

Method BLASTX
NCBI GI g3176690
BLAST score 325
E value 4.0e-30
Match length 75
% identity 83

NCBI Description (AC003671) Similar to ubiquitin ligase gb\_D63905 from S.

cerevisiae. EST gb\_R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 29665

Contig ID 196282\_1.R1040 5'-most EST jsh701065685.h1

Method BLASTN
NCBI GI g2627180
BLAST score 241
E value 1.0e-133
Match length 453
% identity 88

NCBI Description Pisum sativum mRNA for cycloartenol synthase, complete cds

Seq. No. 29666

Contig ID 196303\_1.R1040 5'-most EST uC-gmronoir033g10b1

Seq. No. 29667

Contig ID 196326\_1.R1040 5'-most EST zhf700957964.h1

Seq. No. 29668

Contig ID 196395\_1.R1040

Contig ID



```
jC-gmro02910029f11d1
5'-most EST
                  29669
Seq. No.
                  196421 1.R1040
Contig ID
                  sat701012409.h1
5'-most EST
Method
                  BLASTX
                  g1865721
NCBI GI
BLAST score
                  348
                  4.0e-33
E value
                  80
Match length
% identity
                  (Y08067) mitochondrial single-subunit DNA-dependent RNA
NCBI Description
                  polymerase [Chenopodium album]
                   29670
Seq. No.
Contig ID
                   196426 1.R1040
                   zhf700959816.h1
5'-most EST
                   29671
Seq. No.
                   196442 1.R1040
Contig ID
                   iC-qmst02400055e08a1
5'-most EST
Method
                   BLASTX
                   q2827556
NCBI GI
                   192
BLAST score
                   1.0e-14
E value
                   79
Match length
% identity
NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]
                   29672
Seq. No.
                   196453 1.R1040
Contig ID
                   sat701012406.hl
5'-most EST
Method
                   BLASTN
                   q4115338
NCBI GI
BLAST score
                   112
                   3.0e-56
E value
                   220
Match length
% identity
                   22
NCBI Description Pisum sativum (Alaska) ubuquitin (PUB4) gene, complete cds
Seq. No.
                   29673
                   196651 1.R1040
Contig ID
5'-most EST
                   gsv701046508.hl
Seq. No.
                   29674
                   196699 1.R1040
Contig ID
                   g5752704
 5'-most EST
Method
                   BLASTX
                   g4322940
NCBI GI
                   384
BLAST score
                   7.0e-37
E value
                   113
Match length
 % identity
                   37
                   (AF096299) DNA-binding protein 2 [Nicotiana tabacum]
 NCBI Description
                   29675
```

196730 1.R1040



```
dpv701100906.h1
 5'-most EST
                    29676
 Seq. No.
                    196753 1.R1040
 Contig ID
                    uC-gmronoir007e01b1
 5'-most EST
                    29677
 Seq. No.
                    196755 1.R1040
 Contig ID
                    zhf700\overline{9}51721.h1
 5'-most EST
 Method
                    BLASTX
                    g2959781
 NCBI GI
 BLAST score
                    676
                    5.0e-90
 E value
                    192
 Match length
 % identity
 NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]
                    29678
 Seq. No.
                    196758 1.R1040
 Contig ID
                    sat701012844.hl
 5'-most EST
                    29679
 Seq. No.
                    196763 1.R1040
 Contig ID
                    sat701012849.hl
5'-most EST
                    29680
 Seq. No.
                    196801 1.R1040
 Contig ID
                    sat701012906.h1
 5'-most EST
                    BLASTX
 Method
                    g4539324
 NCBI GI
                    175
 BLAST score
                    9.0e-13
 E value
                    60
 Match length
                    60
  % identity
                    (AL035679) kinesin like protein [Arabidopsis thaliana]
  NCBI Description
                    29681
  Seq. No.
                    196816 1.R1040
  Contig ID
                    hrw701062093.hl
  5'-most EST
                    29682
  Seq. No.
                    196827 1.R1040
  Contig ID
                     sat701012935.h1
  5'-most EST
                    BLASTX
  Method
                     q4204259
  NCBI GI
                     211
  BLAST score
                     4.0e-17
  E value
                     51
  Match length
                     76
  % identity
                    (AC005223) 18074 [Arabidopsis thaliana]
  NCBI Description
                     29683
  Seq. No.
                     196841 1.R1040
  Contig ID
                     sat701012958.hl
  5'-most EST
```

4567

BLASTX

208

g3287270

Method

NCBI GI BLAST score



E value 1.0e-16
Match length 86
% identity 56

NCBI Description (Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No. 29684

Contig ID 196912 1.R1040 5'-most EST jsh701066923.h1

Method BLASTX
NCBI GI g482404
BLAST score 145
E value 6.0e-09
Match length 160
% identity 11

NCBI Description T-complex-associated-testes-expressed-1 protein - mouse

>gi\_201910 (M28821) Tcte-1 peptide [Mus musculus]

Seq. No. 29685

Contig ID 196940 1.R1040 5'-most EST bth700849266.h1

Method BLASTX
NCBI GI g1402918
BLAST score 404
E value 2.0e-39
Match length 106
% identity 71

NCBI Description (X98320) peroxidase [Arabidopsis thaliana]

>gi\_1429215\_emb\_CAA67310\_ (X98774) peroxidase ATP6a

[Arabidopsis thaliana]

Seq. No. 29686

Contig ID 196952\_1.R1040 5'-most EST sat701013110.h1

Seq. No. 29687

Contig ID 196976\_1.R1040 5'-most EST sat701013323.h1

Seq. No. 29688

Contig ID 197022\_1.R1040 5'-most EST leu701155607.h1

Seq. No. 29689

Contig ID 197029\_1.R1040 5'-most EST rlr700897547.h1

Method BLASTX
NCBI GI 94417287
BLAST score 185
E value 7.0e-14
Match length 78
% identity 51

NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]

Seq. No. 29690

Contig ID 197032\_1.R1040 5'-most EST sat701013224.h1

Method BLASTX



q4056460 NCBI GI 257 BLAST score 3.0e-22E value Match length 89 % identity (AC005990) Contains similarity to gb\_L26505 Met30p from NCBI Description Saccharomyces cerevisiae. ESTs gb\_F14133, gb\_T46217, gb AA404758 and gb\_Z37647 come from this gene. [Arabidopsis thaliana] 29691 Seq. No. 197142 1.R1040 Contig ID sat701013408.h1 5'-most EST

Seq. No. 29692 Contig ID 197147\_1.R1040

5'-most EST jC-gmro02910071h01d1

 Seq. No.
 29693

 Contig ID
 197160\_1.R1040

 5'-most EST
 dpv701101082.h1

 Seq. No.
 29694

 Contig ID
 197161\_1.R1040

 5'-most EST
 fC-gmse700838708c1

 Method
 BLASTX

Method BLASTX
NCBI GI g1877397
BLAST score 187
E value 6.0e-14
Match length 46
% identity 74

NCBI Description (Y11591) shaggy-like kinase [Ricinus communis]

 Seq. No.
 29695

 Contig ID
 197170\_1.R1040

 5'-most EST
 jC-gmle01810082e07a1

Seq. No. 29696 Contig ID 197228\_1.R1040 5'-most EST g4298019

Seq. No. 29697 Contig ID 197233\_1.R1040

5'-most EST fua701038023.h1
Seq. No. 29698

197235 1.R1040

5'-most EST fC-gmro700845003f1
Method BLASTX
NCBI GI g1246403
BLAST score 237
E value 1.0e-29
Match length 91

Contig ID



Seq. No. 29699 Contin ID 197236

Contig ID 197236\_1.R1040 5'-most EST bth700849379.h1

Method BLASTX
NCBI GI g3128176
BLAST score 373
E value 1.0e-35
Match length 118
% identity 55

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 29700

Contig ID 197237\_1.R1040 5'-most EST gsv701046729.h1

Seq. No. 29701

Contig ID 197355\_1.R1040 5'-most EST sat701013738.h1

Seq. No. 29702

Contig ID 197357\_1.R1040 5'-most EST jC-gmro02910071e07d1

Method BLASTX
NCBI GI g2344894
BLAST score 152
E value 7.0e-10
Match length 60
% identity 52

NCBI Description (AC002388) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29703

Contig ID 197382\_1.R1040 5'-most EST g5606452 Method BLASTX NCBI GI g2275213

NCBI GI g2275213 BLAST score 473 E value 3.0e-47 Match length 182 % identity 56

NCBI Description (AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29704

Contig ID 197403\_1.R1040 5'-most EST uC-gmropic041h04b1

Seq. No. 29705

Contig ID 197406\_1.R1040

5'-most EST jC-gmf $\overline{1}$ 022220053f04a1

Seq. No. 29706

Contig ID 197406\_2.R1040 5'-most EST pxt700944637.h1

Seq. No. 29707

Contig ID 197411\_1.R1040

5'-most EST g5509811 Method BLASTX



```
NCBI GI
                  g4006886
BLAST score
                  460
E value
                  9.0e-46
                  131
Match length
                  67
% identity
NCBI Description (299708) putative protein [Arabidopsis thaliana]
                  29708
Seq. No.
                  197434 1.R1040
Contig ID
                  bth700845640.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q2245682
                  145
```

BLAST score 145
E value 1.0e-75
Match length 305
% identity 87
NCBI Description Glycine max

NCBI Description Glycine max peroxidase precursor (GMIPER1) mRNA, complete

cds

Seq. No. 29709

Contig ID 197444\_1.R1040 5'-most EST sat701013865.h1

Seq. No. 29710

Contig ID 197454\_1.R1040 5'-most EST sat701013877.h1

Seq. No. 29711

Contig ID 197484\_1.R1040 5'-most EST sat701013920.h1

Method BLASTX
NCBI GI g2558516
BLAST score 206
E value 2.0e-16
Match length 84
% identity 45

NCBI Description (AJ001119) Rab5 GDP/GTP exchange factor, Rabex5 [Bos

taurus]

Seq. No. 29712

Contig ID 197554 1.R1040 5'-most EST kl1701211259.h1

Seq. No. 29713

Contig ID 197564 1.R1040 5'-most EST sat701014050.h1

Seq. No. 29714

Contig ID 197607\_1.R1040 5'-most EST sat701014106.h1

Method BLASTN
NCBI GI g1396053
BLAST score 74
E value 6.0e-34
Match length 142
% identity 88

NCBI Description Pisum sativum mRNA for phosphoribosylanthranilate



## transferase, partial cds

29715 Seq. No. 197627 1.R1040 Contig ID sat701014139.hl 5'-most EST BLASTX Method g4115383 NCBI GI 300 BLAST score 1.0e-27 E value 92 Match length 58 % identity (ACO05967) receptor-like protein kinase [Arabidopsis NCBI Description thaliana] 29716 Seq. No. 197632 1.R1040 Contig ID  $sat701\overline{0}14146.h1$ 5'-most EST BLASTX Method q2827699 NCBI GI 147 BLAST score 4.0e-09 E value 182 Match length 25 % identity (AL021684) predicted protein [Arabidopsis thaliana] NCBI Description 29717 Seq. No. 197661 1.R1040 Contig ID fC-gmse700660311r5 5'-most EST 29718 Seq. No. 197689 1.R1040 Contig ID bth700844437.h1 5'-most EST 29719 Seq. No. 197725\_4.R1040 Contig ID zsg701126981.h1 5'-most EST 29720 Seq. No. 197747 1.R1040 Contig ID asn701137866.hl 5'-most EST 29721 Seq. No. 197748 1.R1040 Contig ID  $jsh701\overline{0}67605.h1$ 5'-most EST 29722 Seq. No. 197764 1.R1040 Contig ID jC-gmf102220096c03d1 5'-most EST BLASTX Method q1161167 NCBI GI BLAST score 220 1.0e-17 E value 80 Match length 44 % identity

Seq. No. 29723

NCBI Description (L42466) ethylene-forming enzyme [Picea glauca]



197797 1.R1040 Contig ID dpv701101334.hl 5'-most EST

29724 Seq. No.

Contig ID 197832 1.R1040  $sat701\overline{0}14423.h1$ 5'-most EST

BLASTX Method q4063751 NCBI GI 160 BLAST score 6.0e-11 E value Match length 118 33 % identity

(AC005851) putative white protein [Arabidopsis thaliana] NCBI Description

>gi 4510409\_gb\_AAD21495.1\_ (AC006929) putative white

protein [Arabidopsis thaliana]

Seq. No. 29725

Contig ID 197891 1.R1040 sat701014510.hl 5'-most EST

29726 Seq. No.

Contig ID 197893 1.R1040 sat701014593.h1 5'-most EST

29727 Seq. No.

197943 1.R1040 Contig ID

5'-most EST jC-gmle01810029c10d1

BLASTX Method q3236255 NCBI GI BLAST score 147 E value 4.0e-09 89 Match length

% identity

(AC004684) hypothetical protein [Arabidopsis thaliana] NCBI Description

29728 Seq. No.

Contig ID 197965 1.R1040

jC-gmf102220130d06a1 5'-most EST

29729 Seq. No.

197986 1.R1040 Contig ID zhf700958990.h1 5'-most EST

29730 Seq. No.

198008 1.R1040 Contig ID  $jex700\overline{9}06491.h1$ 5'-most EST

Seq. No. 29731

198012 1.R1040 Contig ID zsg701119896.hl 5'-most EST

29732 Seq. No.

198110 1.R1040 Contig ID sat701014822.hl 5'-most EST

BLASTX Method g3924598 NCBI GI BLAST score 228



E value 1.0e-18 Match length 167 % identity 31

NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 29733

Contig ID 198111\_1.R1040 5'-most EST sat701014823.h1

Seq. No. 29734

Contig ID 198125\_1.R1040 5'-most EST kl1701207269.h1

Seq. No. 29735

Contig ID 198139 1.R1040 5'-most EST sat701014863.h1

Method BLASTX
NCBI GI g1418331
BLAST score 593
E value 2.0e-61
Match length 169
% identity 66

NCBI Description (X95909) receptor like protein kinase [Arabidopsis

thaliana]

Seq. No. 29736

Contig ID 198142 1.R1040

5'-most EST g4303640
Method BLASTX
NCBI GI g1853968
BLAST score 391
E value 2.0e-41
Match length 150
% identity 62

NCBI Description (D88121) CPRD12 protein [Vigna unguiculata]

Seq. No. 29737

Contig ID 198152\_1.R1040 5'-most EST zsg701127620.h1

Seq. No. 29738

Contig ID 198299 1.R1040 5'-most EST sat701015140.h1

Seq. No. 29739

Contig ID 198306\_1.R1040

5'-most EST uC-gmflminsoy042d09b1

Seq. No. 29740

Contig ID 198309\_1.R1040 5'-most EST leu701153759.h1

Method BLASTX
NCBI GI g4128133
BLAST score 141
E value 8.0e-09
Match length 56
% identity 45



```
NCBI Description (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]
                   29741
Seq. No.
                   198316 1.R1040
Contig ID
                   sat701\overline{0}15161.h1
5'-most EST
                   29742
Seq. No.
                   198427 1.R1040
Contig ID
                   sat701\overline{0}15304.h1
5'-most EST
Method
                   BLASTX
                   q4099090
NCBI GI
                   572
BLAST score
                   9.0e-59
E value
                   137
Match length
                   75
% identity
NCBI Description (U83178) unknown [Arabidopsis thaliana]
                   29743
Seq. No.
                   198434_1.R1040
Contig ID
                   asn701141557.h1
5'-most EST
                   29744
Seq. No.
                   198451 1.R1040
Contig ID
                   pxt700945140.hl
5'-most EST
                   BLASTX
Method
                   q3927836
NCBI GI
                   212
BLAST score
                   3.0e-17
E value
                   47
Match length
                   79
% identity
                   (AC005727) unknown protein [Arabidopsis thaliana]
NCBI Description
                   29745
Seq. No.
                   198453 1.R1040
Contig ID
                   sat701015335.hl
5'-most EST
                   29746
Seq. No.
                   198458 1.R1040
Contig ID
                    sat701015342.h1
5'-most EST
                    29747
Seq. No.
                    198461 1.R1040
Contig ID
 5'-most EST
                    rlr700901985.hl
Method
                    BLASTX
                    q3068713
NCBI GI
BLAST score
                    253
                    5.0e-22
 E value
Match length
                    87
 % identity
                    60
                   (AF049236) unknown [Arabidopsis thaliana]
 NCBI Description
                    29748
 Seq. No.
```

Contig ID 5'-most EST

198515\_1.R1040 sat701015414.h1

Seq. No. 29749

Contig ID 198519\_1.R1040



```
uC-gmrominsoy209a04b1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4455260
BLAST score
                   819
E value
                   1.0e-87
Match length
                   173
% identity
                   (AL035353) protein kinase-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   29750
                   198553 1.R1040
Contig ID
                   sat701015458.hl
5'-most EST
                   BLASTX
Method
                   g1931652
NCBI GI
BLAST score
                   147
E value
                   3.0e-09
Match length
                   39
% identity
                   22
                   (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
NCBI Description
                   [Arabidopsis thaliana]
                   29751
Seq. No.
                   198556 1.R1040
Contig ID
                   jC-gmro02910036b05d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4490736
BLAST score
                   479
E value
                   3.0e-48
Match length
                   112
% identity
                   64
                   (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                   29752
Seq. No.
                   198577 1.R1040
Contig ID
                   sat701\overline{0}15493.h1
5'-most EST
                   29753
Seq. No.
                   198633 1.R1040
Contig ID
                   awf700836368.hl
5'-most EST
                   29754
Seq. No.
                   198663 1.R1040
Contig ID
                   q5058327
5'-most EST
                   BLASTX
Method
NCBI GI
                   g710465
                   309
BLAST score
                   3.0e-28
E value
                   142
Match length
                   51
% identity
NCBI Description OEP86=outer envelope protein [Peas, Peptide Chloroplast,
                   878 aa]
```

5'-most EST awf700836424.h1

Seq. No.

Contig ID

29755

198672 1.R1040



Seq. No. 29756

Contig ID 198681\_1.R1040 5'-most EST awf700836435.h1

Method BLASTN
NCBI GI g609343
BLAST score 101
E value 2.0e-49
Match length 342
% identity 85

% identity 85
NCBI Description Pisum sativum Wando aspartate carbamoyltransferase (pyrB3)

mRNA, complete cds

Seq. No. 29757

Contig ID 198729\_1.R1040 5'-most EST awf700836507.h1

Method BLASTX
NCBI GI g2947070
BLAST score 213
E value 6.0e-19
Match length 160
% identity 44

NCBI Description (AC002521) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 29758

Contig ID 198749\_1.R1040

5'-most EST jC-gmf\overline{1}02220090g03a1

Method BLASTX
NCBI GI g2130210
BLAST score 156
E value 5.0e-10
Match length 70
% identity 44

NCBI Description hypothetical protein - fission yeast (Schizosaccharomyces

pombe)

Seq. No. 29759

Contig ID 198749\_2.R1040

5'-most EST g4286231

Seq. No. 29760

Contig ID 198758\_1.R1040 5'-most EST awf700836543.h1

Seq. No. 29761

Contig ID 198818\_1.R1040 5'-most EST awf700836625.h1

Seq. No. 29762

Contig ID 198835\_1.R1040

5'-most EST uC-gmflminsoy001c03b1

Seq. No. 29763

Contig ID 198862 1.R1040 5'-most EST awf700842302.h1

Method BLASTX NCBI GI g3063444



BLAST score 174 E value 3.0e-12 Match length 60 % identity 57

NCBI Description (AC003981) F22013.5 [Arabidopsis thaliana]

Seq. No. 29764

Contig ID 198933\_1.R1040 5'-most EST awf700836778.h1

Seq. No. 29765

Contig ID 198949\_1.R1040 5'-most EST awf700836802.h1

Method BLASTN
NCBI GI g13384
BLAST score 169
E value 3.0e-90
Match length 278
% identity 90

NCBI Description Pea mitochondrial coxI gene for cytochrome oxidase subunit

Ι

Seq. No. 29766

Contig ID 198997\_1.R1040 5'-most EST all700863227.h1

Seq. No. 29767

Contig ID 199013\_1.R1040

5'-most EST uC-gmrominsoy261d11b1

Seq. No. 29768

Contig ID 199020\_1.R1040 5'-most EST awf700836913.h1

Method BLASTN
NCBI GI g3868723
BLAST score 44
E value 1.0e-15
Match length 192
% identity 81

NCBI Description Arabidopsis thaliana chromosome V map 60.5 cM, complete

sequence [Arabidopsis thaliana]

Seq. No. 29769

Contig ID 199035 1.R1040 5'-most EST awf700836932.h1

Seq. No. 29770

Contig ID 199038\_1.R1040 5'-most EST awf700836937.h1

Method BLASTX
NCBI GI g4106395
BLAST score 294
E value 2.0e-26
Match length 111
% identity 55

NCBI Description (AF073744) raffinose synthase [Cucumis sativus]



29771 Seq. No.

199039 1.R1040 Contig ID 5'-most EST awf700842414.hl

Seq. No. Contig ID 5'-most EST

29772 199056 1.R1040 awf700836959.h1

Seq. No. Contig ID 29773 199075 1.R1040

5'-most EST

 $jC-gms\overline{t}02400026d02a1$ 

Seq. No. Contig ID 29774 199081 1.R1040

5'-most EST

zhf700953761.h1

Seq. No. Contig ID 5'-most EST

29775 199151 1.R1040 uC-gmropic113a07b1

Seq. No. Contig ID 5'-most EST 29776 199167 1.R1040 awf700837156.h1

Seq. No. Contig ID 5'-most EST 29777 199186 1.R1040 awf700837147.hl

Seq. No. Contig ID 5'-most EST 29778 199260 1.R1040 awf700837255.h1

Seq. No. Contig ID 5'-most EST

29779 199274 1.R1040 awf700837280.hl

Seq. No. Contig ID 29780 199297 1.R1040

5'-most EST

jC-gmst02400016e07a1

BLASTX Method g4490708 NCBI GI 214 BLAST score 2.0e-17 E value 51 Match length 80 % identity

NCBI Description (AL035680) putative protein [Arabidopsis thaliana]

Seq. No.

29781

Contig ID 5'-most EST 199312 1.R1040 jC-gmf102220104h04d1

BLASTN Method g18731 NCBI GI 194 BLAST score 1.0e-105 E value 218 Match length 97

% identity

NCBI Description Soybean RPB1-B1 gene for the largest subunit of RNA



## polymerase II (EC 2.7.7.6)

Seq. No. 29782

Contig ID 199313\_1.R1040 5'-most EST awf700837341.h1

Seq. No. 29783

Contig ID 199315\_1.R1040 5'-most EST crh700852559.h1

Method BLASTX
NCBI GI g1363749
BLAST score 152
E value 5.0e-10
Match length 93
% identity 35

NCBI Description probable membrane protein YLR418c - yeast (Saccharomyces

cerevisiae) >gi\_632679 (U20162) Cdc73p [Saccharomyces

cerevisiae]

Seq. No. 29784

Contig ID 199383\_1.R1040 5'-most EST awf700837445.h1

Seq. No. 29785

Contig ID 199443\_1.R1040 5'-most EST fC-gmse700841524f1

Seq. No. 29786

Contig ID 199451\_1.R1040 5'-most EST dpv701098501.h1

Seq. No. 29787

Contig ID 199455 1.R1040

5'-most EST uC-gmflminsoy066d02b1

Seq. No. 29788

Contig ID 199482\_1.R1040 5'-most EST hrw701059258.h1

Seq. No. 29789

Contig ID 199482\_3.R1040 5'-most EST bth700844906.h1

Seq. No. 29790

Contig ID 199498\_1.R1040 5'-most EST kl1701213363.h1

Seq. No. 29791

Contig ID 199515\_1.R1040

5'-most EST jC-gmf102220103b07d1

Seq. No. 29792

Contig ID 199531\_1.R1040

5'-most EST uC-gmflminsoy118d07b1

Method BLASTX NCBI GI g2459421 BLAST score 248



E value 5.0e-21 Match length 73 % identity 63

NCBI Description (AC002332) putative calcium-binding EF-hand protein

[Arabidopsis thaliana]

Seq. No. 29793

Contig ID 199533\_1.R1040 5'-most EST gsv701056160.h1

Seq. No. 29794

Contig ID 199535\_1.R1040

5'-most EST uC-gmrominsoy032b01b1

Method BLASTN
NCBI GI g22635
BLAST score 35
E value 5.0e-10
Match length 59
% identity 90

NCBI Description P.vulgaris mRNA for 70 kD heat shock protein

Seq. No. 29795

Contig ID 199670\_1.R1040 5'-most EST crh700850007.h1

Seq. No. 29796

Contig ID 199801\_1.R1040 5'-most EST dpv701100931.h1

Seq. No. 29797

Contig ID 199813\_1.R1040 5'-most EST awf700838065.h1

Seq. No. 29798

Contig ID 199813\_3.R1040 5'-most EST jex700905882.h1

Seq. No. 29799

Contig ID 199844\_1.R1040 5'-most EST awf700838110.h1

Seq. No. 29800

Contig ID 199921\_1.R1040 5'-most EST awf700838214.h1

Method BLASTX
NCBI GI g4417267
BLAST score 286
E value 2.0e-42
Match length 114
% identity 68

NCBI Description (AC007019) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29801

Contig ID 199925 1.R1040 5'-most EST zhf700953264.h1

Method BLASTX NCBI GI g1652942



```
BLAST score 145
E value 3.0e-09
Match length 118
% identity 31
NCBI Description (D90909
```

NCBI Description (D90909) extragenic suppressor [Synechocystis sp.]

Seq. No. 29802

Contig ID 200013 1.R1040 5'-most EST awf700838363.h1 Method BLASTN

NCBI GI g3413510 BLAST score 77 E value 2.0e-35 Match length 197 % identity 85

NCBI Description Spinacia oleracea mRNA (nuclear-encoded) for chloroplast

glucose-6-phosphate isomerase

 Seq. No.
 29803

 Contig ID
 200043\_1.R1040

 5'-most EST
 awf700838485.h1

 Method
 BLASTX

Method BLASTX
NCBI GI g3063693
BLAST score 301
E value 8.0e-28
Match length 78
% identity 64

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 29804

Contig ID 200080 1.R1040 5'-most EST crh700852040.h1

Method BLASTX
NCBI GI g135406
BLAST score 390
E value 4.0e-38
Match length 91
% identity 85

NCBI Description TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi 99768 pir A32712 tubulin

alpha-5 chain - Arabidopsis thaliana >gi\_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi\_166918 (M84698)

alpha-5 tubulin [Arabidopsis thaliana]

Seq. No. 29805

Contig ID 200088\_1.R1040 5'-most EST awf700838455.h1

Seq. No. 29806

Contig ID 200103\_1.R1040

5'-most EST jC-gmle01810008d10a1

Seq. No. 29807

Contig ID 200188\_1.R1040 5'-most EST awf700839224.h1

Seq. No. 29808

Contig ID 200237\_1.R1040



5'-most EST zhf700953591.h1
Method BLASTX
NCBI GI g4558673
BLAST score 188

E value 1.0e-13 Match length 148 % identity 34

NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29809

Contig ID 200317\_1.R1040 5'-most EST epx701108756.h1

Seq. No. 29810

Contig ID 200336\_1.R1040 5'-most EST fC-gmse700838355b1

Method BLASTN
NCBI GI g576508
BLAST score 171
E value 3.0e-91
Match length 474
% identity 84

NCBI Description Pisum sativum GTP-binding protein (IAP86) mRNA, complete

cds

Seq. No. 29811

Contig ID 200363\_1.R1040 5'-most EST awf700838891.h1

Seq. No. 29812

Contig ID 200388\_1.R1040 5'-most EST awf700838927.h1

Seq. No. 29813

Contig ID 200414\_1.R1040

5'-most EST g4396062
Method BLASTX
NCBI GI g3928086
BLAST score 577
E value 1.0e-59
Match length 160
% identity 71

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 29814

Contig ID 200443\_1.R1040 5'-most EST asn701137407.h1

Seq. No. 29815

Contig ID 200450\_1.R1040 5'-most EST awf700839014.h1

Method BLASTX
NCBI GI g3043529
BLAST score 322
E value 5.0e-30
Match length 109
% identity 57



NCBI Description (AJ002204) polyamine oxidase [Zea mays]

Seq. No.

29816

Contig ID 5'-most EST

200470 1.R1040 awf700839042.hl

Seq. No.

29817

Contig ID 5'-most EST 200473 1.R1040 epx701104690.h1

Seq. No.

29818

Contig ID 5'-most EST

200482 1.R1040 awf700839061.hl

Method NCBI GI BLASTX q2979498

BLAST score

181

E value Match length

2.0e-13 101

% identity

35

NCBI Description (AB012143) mRNA capping enzyme [Homo sapiens]

Seq. No.

29819

Contig ID

200503 1.R1040

5'-most EST

jC-gmle01810044c10a1

Seq. No.

29820

Contig ID

200568 1.R1040

5'-most EST

uC-gmropic063h11b1

Seq. No.

29821

Contig ID 5'-most EST 200590 1.R1040 asn701142174.h1

Method

BLASTX

NCBI GI

q2244806

BLAST score

325

E value

Match length

5.0e-30 123

% identity

59

NCBI Description (297336) hypothetical protein [Arabidopsis thaliana]

Seq. No.

29822

Contig ID

200617 1.R1040 awf700842228.h1

5'-most EST

Seq. No.

29823 200651 1.R1040

Contig ID 5'-most EST

awf700839338.h1

Seq. No.

29824

Contig ID

200662 1.R1040

5'-most EST

jC-gmf102220083g01a1

Seq. No.

29825

Contig ID

200725 1.R1040

5'-most EST

fC-gmse700841319f1

Method

BLASTX

NCBI GI

q4185136



BLAST score 343 E value 3.0e-32 Match length 93 % identity 69

NCBI Description (AC005724) putative trehalose-6-phosphate synthase

[Arabidopsis thaliana]

Seq. No. 29826

Contig ID 200736\_1.R1040 5'-most EST jex700906335.h1

Method BLASTX
NCBI GI 94557060
BLAST score 375
E value 2.0e-36
Match length 94
% identity 73

NCBI Description (AC007154) putative chromosome-associated polypeptide, 5'

partial [Arabidopsis thaliana]

Seq. No. 29827

Contig ID 200776\_1.R1040 5'-most EST awf700839527.h1

Seq. No. 29828

Contig ID 200778\_1.R1040 5'-most EST awf700839530.h1

Seq. No. 29829

Contig ID 200782\_1.R1040 5'-most EST awf700839602.h1

Seq. No. 29830

Contig ID 200875 1.R1040

5'-most EST jC-gmst02400065g06a2

Seq. No. 29831

Contig ID 200891\_1.R1040 5'-most EST awf700839780.h1

Seq. No. 29832

Contig ID 200942\_1.R1040 5'-most EST zhf700958504.h1

Seq. No. 29833

Contig ID 200951\_1.R1040 5'-most EST zhf700963648.h1

Seq. No. 29834

Contig ID 200953 1.R1040 5'-most EST kl1701212871.h1

Method BLASTX
NCBI GI g4490330
BLAST score 713
E value 1.0e-75
Match length 132
% identity 99

NCBI Description (AL035656) splicing factor-like protein [Arabidopsis



## thaliana]

Seq. No. 29835

Contig ID 200956\_1.R1040 5'-most EST fC-gmse700839826a5

Method BLASTX
NCBI GI g113595
BLAST score 696
E value 2.0e-73
Match length 194
% identity 64

NCBI Description ALDOSE REDUCTASE (AR) (ALDEHYDE REDUCTASE)

>gi 100562 pir S15024 aldose reductase-related protein -

barley >gi\_18891\_emb\_CAA40747\_ (X57526) aldose reductase-related protein [Hordeum vulgare]

Seq. No. 29836

Contig ID 201015\_1.R1040 5'-most EST awf700839928.h1

Seq. No. 29837

Contig ID 201019\_1.R1040 5'-most EST crh700853734.h1

Seq. No. 29838

Contig ID 201122\_1.R1040

5'-most EST uC-gmrominsoy028a09b1

Method BLASTX
NCBI GI g4206122
BLAST score 290
E value 5.0e-28
Match length 94
% identity 67

NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum

crystallinum]

Seq. No. 29839

Contig ID 201144\_1.R1040 5'-most EST awf700840151.h1

Seq. No. 29840

Contig ID 201146\_1.R1040 5'-most EST awf700840154.h1

Method BLASTX
NCBI GI g4091808
BLAST score 129
E value 8.0e-13
Match length 103
% identity 40

NCBI Description (AF053307) deacetylvindoline 4-0-acetyltransferase

[Catharanthus roseus]

Seq. No. 29841

Contig ID 201155\_1.R1040 5'-most EST kll701213171.h1

Method BLASTX NCBI GI 94539005



BLAST score 326 E value 2.0e-30 Match length 108 % identity 77

NCBI Description (AL049481) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 29842

Contig ID 201173\_1.R1040 5'-most EST awf700840201.h1

Seq. No. 29843

Contig ID 201250 1.R1040 5'-most EST dpv701100926.h1

Method BLASTX
NCBI GI g2506985
BLAST score 220
E value 5.0e-18
Match length 78

% identity 55 NCBI Description CDC4-LIKE PROTEIN >gi\_1580781 (M83822) beige-like protein

[Homo sapiens]

Seq. No. 29844

Contig ID 201258\_1.R1040 5'-most EST awf700840338.h1

Method BLASTX
NCBI GI g3402754
BLAST score 251
E value 9.0e-22
Match length 61
% identity 75

NCBI Description (AL031187) putative protein [Arabidopsis thaliana]

Seq. No. 29845

Contig ID 201314\_1.R1040 5'-most EST awf700840446.h1

Seq. No. 29846

Contig ID 201381\_1.R1040 5'-most EST zhf700964591.h1

Seq. No. 29847

Contig ID 201396 1.R1040

5'-most EST uC-gmflminsoy014c07b1

Method BLASTX
NCBI GI g2262113
BLAST score 716
E value 6.0e-76
Match length 165
% identity 76

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 29848

Contig ID 201410\_1.R1040 5'-most EST awf700840648.h1

Seq. No. 29849



148

201494 1.R1040 Contig ID awf700840829.h1 5'-most EST 29850 Seq. No. Contig ID 201523 1.R1040 fC-gmse700840889f1 5'-most EST BLASTX Method g2708745 NCBI GI BLAST score 694 2.0e-73 E value

90 % identity (AC003952) putative calcium-dependent ser/thr protein NCBI Description

kinase [Arabidopsis thaliana]

Seq. No. 29851

Match length

201596 1.R1040 Contig ID awf700841048.hl 5'-most EST

29852 Seq. No.

201650 1.R1040 Contig ID 5'-most EST q5607054 BLASTX Method

q4455358 NCBI GI 198 BLAST score 6.0e-15 E value Match length 75 52 % identity

(AL035524) putative protein [Arabidopsis thaliana] NCBI Description

29853 Seq. No.

201728 1.R1040 Contig ID awf700842888.h1 5'-most EST

Seq. No. 29854

201752 1.R1040 Contig ID al1700863237.hl 5'-most EST

BLASTX Method g2853087 NCBI GI 171 BLAST score 3.0e-12 E value Match length 105 % identity 41

(ALO21768) putative protein [Arabidopsis thaliana] NCBI Description

29855 Seq. No.

201813 1.R1040 Contig ID kl1701214532.hl 5'-most EST

BLASTX Method g4544422 NCBI GI 655 BLAST score 7.0e-69 E value 144 Match length 44 % identity

(AC006955) putative fimbrin [Arabidopsis thaliana] NCBI Description

29856 Seq. No.



201845 1.R1040 Contig ID bth700848401.hl 5'-most EST BLASTX Method

q4512685 NCBI GI BLAST score 301 E value 2.0e-27 117 Match length 49 % identity

(AC006931) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi\_4559325\_gb\_AAD22987.1\_AC007087\_6 (AC007087)

hypothetical protein [Arabidopsis thaliana]

29857 Seq. No.

201887 1.R1040 Contig ID 5'-most EST awf700842954.hl

Seq. No. 29858

Contig ID 201896 1.R1040 awf700841536.h1 5'-most EST

29859 Seq. No.

201899 1.R1040 Contig ID zsq701119244.hl 5'-most EST

BLASTX Method g1778376 NCBI GI 373 BLAST score E value 5.0e-36 104 Match length % identity 71

(U81288) PsRT17-1 [Pisum sativum] NCBI Description

29860 Seq. No.

202021 1.R1040 Contig ID pmv700890618.h1 5'-most EST

29861 Seq. No.

202037 1.R1040 Contig ID awf700841816.hl 5'-most EST

29862 Seq. No.

Contig ID 202045 1.R1040 all700863107.hl 5'-most EST

Method BLASTX q2462750 NCBI GI BLAST score 316 3.0e-29 E value 80 Match length 72 % identity

(AC002292) Highly similar to auxin-induced protein NCBI Description (aldo/keto reductase family) [Arabidopsis thaliana]

29863 Seq. No.

202071 1.R1040 Contig ID

jC-gmst02400073g02a1 5'-most EST

29864 Seq. No.

202174 1.R1040 Contig ID



```
uC-gmrominsoy102h10b1
5'-most EST
                  BLASTX
Method
                  g3461820
NCBI GI
BLAST score
                  252
                  8.0e-22
E value
                  113
Match length
% identity
                   (AC004138) unknown protein [Arabidopsis thaliana]
NCBI Description
                  29865
Seq. No.
                   202200 1.R1040
Contig ID
                   jC-gmf102220141h10a1
5'-most EST
                   BLASTN
Method
                   g416257
NCBI GI
BLAST score
                   75
E value
                   6.0e - 34
Match length
                   191
                   86
% identity
                   Rice mRNA for elongation factor G, partial sequence
NCBI Description
                   >gi_3107867_dbj_D42263_D42263 Rice callus cDNA, S155
Seq. No.
                   29866
                   202215 1.R1040
Contig ID
                   awf700842019.hl
5'-most EST
                   BLASTX
Method
                   g2829912
NCBI GI
BLAST score
                   285
                   3.0e-32
E value
Match length
                   131
% identity
                   54
                   (AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis
NCBI Description
                   thaliana]
                   29867
Seq. No.
                   202272_1.R1040
Contig ID
                   uC-gmrominsoy284a09b1
5'-most EST
                   BLASTN
Method
                   g2618602
NCBI GI
                   175
BLAST score
                   1.0e-93
E value
                   483
Match length
                   84
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSJ1, complete sequence [Arabidopsis thaliana]
                   29868
Seq. No.
                   202309 1.R1040
Contig ID
                   awf700842163.hl
5'-most EST
                   BLASTX
Method
                   g4415914
NCBI GI
BLAST score
                   382
E value
                   9.0e-37
                   170
Match length
                   44
 % identity
```

NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]

Seq. No. 29869



Contig ID 202317\_1.R1040 5'-most EST bth700849528.h1

Seq. No. 29870

Contig ID 202320\_1.R1040

5'-most EST g5605865

Seq. No. 29871

Contig ID 202334 1.R1040 5'-most EST awf700842202.h1

Seq. No. 29872

Contig ID 202342\_1.R1040 5'-most EST awf700842212.h1

Seq. No. 29873

Contig ID 202387\_1.R1040 5'-most EST awf700842274.h1

Seq. No. 29874

Contig ID 202404\_1.R1040 5'-most EST crh700852351.h1

Method BLASTX
NCBI GI g2911049
BLAST score 241
E value 1.0e-20
Match length 75
% identity 57

NCBI Description (AL021961) glucosyltransferase -like protein [Arabidopsis

thaliana]

Seq. No. 29875

Contig ID 202446\_1.R1040

5'-most EST g5676878
Method BLASTX
NCBI GI g3914212
BLAST score 594
E value 2.0e-61
Match length 181
% identity 62

NCBI Description 5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE)

(5-OPASE) >gi\_1732065 (U70825) 5-oxo-L-prolinase [Rattus

norvegicus]

Seq. No. 29876

Contig ID 202470\_1.R1040

5'-most EST q5126398

Seq. No. 29877

Contig ID 202481\_1.R1040

5'-most EST g4305630
Method BLASTX
NCBI GI g3150410
BLAST score 325
E value 5.0e-30
Match length 98
% identity 60





## NCBI Description (AC004165) unknown protein [Arabidopsis thaliana]

Seq. No. 29878

Contig ID 202489\_1.R1040

5'-most EST uC-gmrominsoy238e05b1

Seq. No. 29879

Contig ID 202531\_1.R1040 5'-most EST pxt700944238.h1

Seq. No. 29880

Contig ID 202661\_1.R1040 5'-most EST crh700856508.h1

Seq. No. 29881

Contig ID 202673\_1.R1040 5'-most EST dpv701097491.h1

Seq. No. 29882

Contig ID 202710 1.R1040

5'-most EST uC-gmflminsoy027b12b1

Seq. No. 29883

Contig ID 202762 1.R1040 5'-most EST awf700842852.h1

Method BLASTX
NCBI GI g2292907
BLAST score 176
E value 3.0e-13
Match length 77

% identity 48

NCBI Description (Y10099) P-glycoprotein homologue [Hordeum vulgare]

Seq. No. 29884

Contig ID 202789\_1.R1040 5'-most EST awf700842907.h1

Method BLASTX
NCBI GI g2190544
BLAST score 260
E value 2.0e-22
Match length 64
% identity 84

NCBI Description (AC001229) Similar to Saccharomyces hypothetical protein

P9642.2 (gb U40828). [Arabidopsis thaliana]

Seq. No. 29885

Contig ID 202806\_1.R1040 5'-most EST zhf700956048.h1

Seq. No. 29886

Contig ID 202857\_1.R1040 5'-most EST awf700843008.h1

Method BLASTX
NCBI GI g1619946
BLAST score 364
E value 3.0e-34
Match length 251



% identity NCBI Description

(U71300) snRNA activating protein complex 50kD subunit [Homo sapiens] >gi\_4097682 (U66413) proximal sequence element-binding transcription factor beta subunit [Homo sapiens] >gi\_4507105\_ref\_NP\_003075.1\_pSNAPC3\_ small nuclear

RNA activating complex, polypeptide 3, 50kD

Seq. No. 29887

Contig ID 202878\_1.R1040 5'-most EST leu701147877.h1

Seq. No. 29888

Contig ID 202962\_1.R1040

5'-most EST uC-gmrominsoy212g10b1

Method BLASTN
NCBI GI g18729
BLAST score 124
E value 3.0e-63
Match length 132
% identity 98

NCBI Description Soybean (Glycine max) 18S ribosomal RNA

Seq. No. 29889

Contig ID 202962\_2.R1040 5'-most EST asn701136722.h1

Method BLASTN
NCBI GI g18729
BLAST score 167
E value 7.0e-89
Match length 285
% identity 99

NCBI Description Soybean (Glycine max) 18S ribosomal RNA

Seq. No. 29890

Contig ID 202962\_3.R1040 5'-most EST rlr700896170.h1

Method BLASTN
NCBI GI g18729
BLAST score 235
E value 1.0e-129
Match length 251
% identity 99

NCBI Description Soybean (Glycine max) 18S ribosomal RNA

Seq. No. 29891

Contig ID 202962\_5.R1040

5'-most EST jC-gmle01810084g01d1

Seq. No. 29892

Contig ID 202971\_1.R1040 5'-most EST awf700843186.h1

Seq. No. 29893

Contig ID 203016\_1.R1040

5'-most EST g4291629 Method BLASTX NCBI GI g2224931

BLAST score 669 E value 2.0e-70 Match length 165 % identity 75

NCBI Description (AF004215) ethylene-insensitive3-like3 [Arabidopsis

thaliana]

Seq. No. 29894

Contig ID 203019\_1.R1040 5'-most EST awf700843274.h1

Seq. No. 29895

Contig ID 203056\_1.R1040 5'-most EST fC-gmse700843342f1

Method BLASTX
NCBI GI g3024425
BLAST score 417
E value 3.0e-41
Match length 101
% identity 80

NCBI Description PYRUVATE, PHOSPHATE DIKINASE PRECURSOR

(PYRUVATE, ORTHOPHOSPHATE DIKINASE) >gi\_1076700\_pir\_\_S53297 pyruvate, orthophosphate dikinase (EC 2.7.9.1) - Flaveria

pringlei >gi\_577776\_emb\_CAA53223\_ (X75516)

pyruvate, orthophosphate dikinase [Flaveria pringlei]

Seq. No. 29896

Contig ID 203103\_1.R1040 5'-most EST awf700843412.h1

Seq. No. 29897

Contig ID 203167\_1.R1040 5'-most EST yuv700862711.h1

Seq. No. 29898

Contig ID 203172\_1.R1040 5'-most EST uC-gmropic071e12b1

Method BLASTX
NCBI GI g2781351
BLAST score 376
E value 4.0e-36
Match length 99
% identity 82

NCBI Description (AC003113) F2401.7 [Arabidopsis thaliana]

Seq. No. 29899

Contig ID 203172\_2.R1040 5'-most EST yuv700862718.h1

Method BLASTX
NCBI GI g2781351
BLAST score 193
E value 7.0e-15
Match length 52
% identity 79

NCBI Description (AC003113) F2401.7 [Arabidopsis thaliana]

Seq. No. 29900

203263 1.R1040 Contig ID uC-gmrominsoy062b06b1 5'-most EST BLASTX Method g2262136 NCBI GI BLAST score 254 E value 9.0e-22 87 Match length 57 % identity (AC002330) predicted protein of unknown function NCBI Description [Arabidopsis thaliana] >gi\_4263520\_gb\_AAD15346\_ (AC004044) predicted protein of unknown function [Arabidopsis thaliana] 29901 Seq. No. 203306 1.R1040 Contig ID jC-gmro02910014h03d1 5'-most EST Seq. No. 29902 203318 1.R1040 Contig ID gsv701056554.hl 5'-most EST 29903 Seq. No. 203335 1.R1040 Contig ID zhf700955211.h1 5'-most EST 29904 Seq. No. Contig ID 203404 1.R1040 zvp700764256.hl 5'-most EST Seq. No. 29905 203430 1.R1040 Contig ID  $jC-gms\overline{t}02400024g05d1$ 5'-most EST Seq. No. 29906 203449 1.R1040 Contig ID fC-gmro7000764321f1 5'-most EST BLASTX Method g2062174 NCBI GI 148 BLAST score 4.0e-09

E value Match length 77 51 % identity

(AC001645) transcription factor (TINY) isolog [Arabidopsis NCBI Description

thaliana]

29907 Seq. No.

203499 1.R1040 Contig ID

uC-gmrominsoy111f11b1 5'-most EST

BLASTX Method g3540207 NCBI GI BLAST score 220 E value 7.0e-18 97 Match length 51 % identity

(AC004260) Putative protein kinase [Arabidopsis thaliana] NCBI Description

29908 Seq. No.



```
203501 1.R1040
Contig ID
                  bth700844066.h1
5'-most EST
                  29909
Seq. No.
                  203506_1.R1040
Contig ID
                  fC-gmro7000764393f1
5'-most EST
                  BLASTX
Method
                  q2924777
NCBI GI
                  610
BLAST score
                  3.0e-63
E value
Match length
                  214
                  10
% identity
                  (AC002334) putative receptor protein kinase [Arabidopsis
NCBI Description
                   29910
Seq. No.
                   203514 1.R1040
Contig ID
5'-most EST
                   fua701040193.hl
                   BLASTX
Method
                   q4314363
NCBI GI
                   394
BLAST score
                   2.0e-38
E value
                   111
Match length
                   64
% identity
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   29911
Seq. No.
                   203534 1.R1040
Contig ID
                   ary700764437.hl
5'-most EST
                   29912
Seq. No.
                   203552 1.R1040
Contig ID
5'-most EST
                   yz1700966943.h1
                   29913
Seq. No.
                   203564 1.R1040
Contig ID
5'-most EST
                   ary700764472.h1
Method
                   BLASTX
                   q1086601
NCBI GI
BLAST score
                   139
                   9.0e-09
E value
Match length
                   81
% identity
                   (U41008) Similar to reverse transcriptase [Caenorhabditis
NCBI Description
                   elegans]
                   29914
 Seq. No.
                   203592 1.R1040
Contig ID
                   bth700843507.h1
 5'-most EST
                   BLASTX
Method
                   g4559382
 NCBI GI
                   213
 BLAST score
```

2.0e-17 E value

62 Match length % identity

(AC006526) putative DNA binding protein [Arabidopsis NCBI Description

thaliana]



29915 Seq. No. 203595 1.R1040 Contig ID 5'-most EST leu701149186.hl Method BLASTX g2827552 NCBI GI 159 BLAST score 5.0e-11 E value Match length 40 % identity 70 (AL021635) predicted protein [Arabidopsis thaliana] NCBI Description 29916 Seq. No. 203607 1.R1040 Contig ID 5'-most EST dkc700968027.h1 29917 Seq. No. 203620 1.R1040 Contig ID bth700843540.h1 5'-most EST Seq. No. 29918 203623 1.R1040 Contig ID leu701156525.h1 5'-most EST 29919 Seq. No. Contig ID 203639 1.R1040 5'-most EST uC-gmrominsoy232a01b1 Method BLASTX NCBI GI q728868 BLAST score 169 1.0e-11 E value Match length 91 49 % identity ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) NCBI Description >gi\_99824\_pir\_\_S16748 proline-rich protein - rape (fragment) >gi\_22597\_emb\_CAA42924\_ (X60376) proline-rich protein [Brassica napus] 29920 Seq. No. 203656 1.R1040 Contig ID uC-gmrominsoy122a12b1 5'-most EST BLASTX Method g2275204 NCBI GI 523 BLAST score 6.0e-53 E value

202 Match length % identity

(AC002337) DNA binding protein isolog [Arabidopsis NCBI Description

thaliana]

29921

Seq. No. Contig ID

203656\_2.R1040

uC-gmrominsoy047b10b1 5'-most EST

BLASTX Method g2275204 NCBI GI BLAST score 172 7.0e-15 E value



Match length 69
% identity 70
NCBI Description (AC002337) DNA binding protein isolog [Arabidopsis thaliana]

Seq. No. 29922 Contig ID 203656\_3.R1040

5'-most EST dpv701102808.h1

Seq. No. 29923

Contig ID 203684\_1.R1040 5'-most EST bth700843616.h1

Seq. No. 29924

Contig ID 203687\_1.R1040 5'-most EST bth700843620.h1

Seq. No. 29925

Contig ID 203695 1.R1040 5'-most EST rlr700901381.h1

Seq. No. 29926

Contig ID 203700\_1.R1040 5'-most EST bth700843635.h1

Method BLASTX
NCBI GI g2245081
BLAST score 303
E value 9.0e-28
Match length 127
% identity 54

NCBI Description (Z97343) myosin II heavy chain homolog [Arabidopsis

thaliana]

Seq. No. 29927

Contig ID 203724\_1.R1040 5'-most EST bth700843661.h1

Method BLASTX
NCBI GI g4490309
BLAST score 418
E value 4.0e-41
Match length 134
% identity 63

NCBI Description (AL035678) peroxidase ATP17a-like protein [Arabidopsis

thaliana]

Seq. No. 29928

Contig ID 203728\_1.R1040 5'-most EST bth700843665.h1

Seq. No. 29929

Contig ID 203754\_1.R1040

5'-most EST jC-gmle01810094g10a1

Method BLASTX
NCBI GI g4006861
BLAST score 339
E value 8.0e-32
Match length 106



% identity 60
NCBI Description (Z99707) tubulin-like protein [Arabidopsis thaliana]

Seq. No. 29930

Contig ID 203784\_1.R1040 5'-most EST bth700843730.h1

Method BLASTX
NCBI GI g2499903
BLAST score 393
E value 2.0e-38
Match length 108
% identity 64

NCBI Description PUROMYCIN-SENSITIVE AMINOPEPTIDASE (PSA) >gi\_1184161

(U35646) aminopeptidase [Mus musculus]

>gi 1585925 prf 2202260A puromycin sensitive

aminopeptidase [Mus musculus]

Seq. No. 29931

Contig ID 203828\_1.R1040 5'-most EST bth700843779.h1

Method BLASTX
NCBI GI 94314387
BLAST score 705
E value 2.0e-74
Match length 152
% identity 87

NCBI Description (AC006232) putative beta-alanine synthetase [Arabidopsis

thaliana]

Seq. No. 29932

Contig ID 203847\_1.R1040

5'-most EST jC-gmro02910020b02a1

Seq. No. 29933

Contig ID 203870\_1.R1040 5'-most EST dpv701101957.h1

Method BLASTX
NCBI GI g4538981
BLAST score 261
E value 2.0e-22
Match length 73
% identity 63

NCBI Description (AL049487) putative protein [Arabidopsis thaliana]

Seq. No. 29934

Contig ID 203895\_1.R1040 5'-most EST bth700843863.h1

Method BLASTX
NCBI GI g1483150
BLAST score 356
E value 4.0e-34
Match length 92
% identity 75

NCBI Description (D84417) monodehydroascorbate reductase [Arabidopsis

thaliana]

Seq. No. 29935



```
203969 1.R1040
Contig ID
                  uC-gmrominsoy053g11b1
5'-most EST
                  29936
Seq. No.
Contig ID
                  203979 1.R1040
                  pmv700893093.h1
5'-most EST
                  BLASTX
Method
                  q3287695
NCBI GI
BLAST score
                  459
                  1.0e-45
E value
Match length
                  142
% identity
                  (AC003979) Similar to hypothetical protein C34B7.2
NCBI Description
                   gb 1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis
                  thaliana]
                   29937
Seq. No.
Contig ID
                   203981 1.R1040
                  bth700843977.hl
5'-most EST
                  BLASTX
Method
                   g3540207
NCBI GI
BLAST score
                   133
                   9.0e-16
E value
                   70
Match length
% identity
                  (AC004260) Putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   29938
Seq. No.
                   204023 1.R1040
Contig ID
                   fC-gmro700844046f1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4371296
BLAST score
                   269
E value
                   2.0e-23
                   107
Match length
                   53
% identity
                   (AC006260) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   29939
Seq. No.
                   204035 1.R1040
Contig ID
                   hrw701058057.h1
5'-most EST
Method
                   BLASTX
                   q4454468
NCBI GI
                   716
BLAST score
                   7.0e-76
E value
                   182
Match length
                   74
% identity
                   (AC006234) putative NADH dehydrogenase [Arabidopsis
NCBI Description
```

thaliana]

29940

Seq. No.

204104 1.R1040 Contig ID dpv701102894.h1 5'-most EST

29941 Seq. No.

204152 1.R1040 Contig ID



```
5'-most EST
                   a5687881
Method
                   BLASTX
-NCBI GI
                   q3047104
BLAST score
                   777
E value
                   5.0e-83
Match length
                  192
                   79
% identity
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
                  29942
Seq. No.
                  204169 1.R1040
Contig ID
5'-most EST
                  dpv701099601.h1
                  BLASTX
Method
                  g2160150
NCBI GI
BLAST score
                  514
E value
                   5.0e-52
Match length
                  184
                   54
% identity
NCBI Description (AC000375) EST gb T43829 comes from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                   29943
Contig ID
                   204207 1.R1040
5'-most EST
                   fC-qmro700844289f1
Method
                  BLASTX
NCBI GI
                  g3582021
BLAST score
                   443
E value
                   4.0e-44
Match length
                   131
% identity
                   61
NCBI Description (Y09423) cytochrome P450 [Nepeta racemosa]
                   29944
Seq. No.
                   204209 1.R1040
Contig ID
5'-most EST
                   dpv701101518.h1
Seq. No.
                   29945
                   204260 1.R1040
Contig ID
5'-most EST
                   fua701041238.hl
Seq. No.
                   29946
                   204282 1.R1040
Contig ID
5'-most EST
                   fC-gmro700844391a3
Method
                   BLASTX
NCBI GI
                   g129586
BLAST score
                   3132
E value
                   0.0e+00
Match length
                   699
% identity
                   88
                  PHENYLALANINE AMMONIA-LYASE CLASS III >qi 81878 pir S04128
NCBI Description
                   phenylalanine ammonia-lyase (EC 4.3.1.5) class III - kidney
```

Seq. No. 29947

Contig ID 204385 1.R1040

5'-most EST jC-gmro02910007c03d1

bean



```
29948
Seq. No.
                   204399 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910040h01a1
                   29949
Seq. No.
                   204409 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810073e01a1
Method
                  BLASTX
NCBI GI
                  q3549679
BLAST score
                   535
                   2.0e-54
E value
Match length
                  214
                   55
% identity
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
                   29950
Seq. No.
Contig ID
                   204433 1.R1040
5'-most EST
                   jC-gmro02910066d05a1
Method
                  BLASTX
NCBI GI
                   q3786008
BLAST score
                   173
                   4.0e-12
E value
Match length
                   186
                   30
% identity
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]
                  29951
Seq. No.
                   204467 1.R1040
Contig ID
5'-most EST
                  bth700845393.h1
Method
                   BLASTX
                   g4105794
NCBI GI
                   306
BLAST score
                   6.0e-28
E value
Match length
                   119
                   49
% identity
NCBI Description (AF049928) PGP224 [Petunia x hybrida]
Seq. No.
                   29952
                   204473 1.R1040
Contig ID
                   bth700844643.h1
5'-most EST
Seq. No.
                   29953
                   204531 1.R1040
Contig ID
                   fC-gmro700844719f1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1313907
BLAST score
                   469
E value
                   8.0e-47
Match length
                   122
```

% identity 72

NCBI Description (D84507) CDPK-related protein kinase [Zea mays]

Seq. No. 29954

204563 1.R1040 Contig ID

5'-most EST jC-gmro02910038d02d1

29955 Seq. No.

```
204600 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy257f01b1
                   BLASTX
Method
NCBI GI
                   g1616741
BLAST score
                   336
                   2.0e-31
E value
                   135
Match length
                   49
% identity
NCBI Description (U60276) hASNA-I [Homo sapiens]
                   29956
Seq. No.
                   204600 2.R1040
Contig ID
5'-most EST
                   q5606382
Method
                   BLASTX
NCBI GI
                   g267453
BLAST score
                   383
E value
                   5.0e-37
Match length
                   127
% identity
NCBI Description
```

HYPOTHETICAL 37.5 KD PROTEIN ZK637.5 IN CHROMOSOME III >qi 102496 pir S15791 arsenical pump-driving ATPase homolog - Caenorhabditis elegans >gi 3881667 emb CAA77452 (Z11115) predicted using Genefinder; ArsA homologue; cDNA EST EMBL: D73741 comes from this gene; cDNA EST EMBL: D71137 comes from this gene; cDNA EST EMBL: C08164 comes from this gene; cDNA EST EMBL: C09807 comes from this gene; cD

29957 Seq. No. Contig ID 204643 1.R1040 5'-most EST  $g56062\overline{3}9$ 

29958 Seq. No. Contig ID 204649 1.R1040 5'-most EST bth700844872.h1 Method BLASTX

NCBI GI q2494736 BLAST score 763 E value 1.0e-88 Match length 228 71 % identity

GLUCOSE INHIBITED DIVISION PROTEIN A NCBI Description

>gi\_1001595\_dbj\_BAA10223\_ (D64000) glucose inhibited

division protein A [Synechocystis sp.]

29959 Seq. No. 204668 1.R1040 Contig ID 5'-most EST fua701038236.h1 Method BLASTX

NCBI GI g3947735 BLAST score 147 2.0e-10 E value Match length 135 % identity 36

(AJ009720) NL27 [Solanum tuberosum] NCBI Description

29960 Seq. No. 204713 1.R1040 Contig ID

NCBI GI

E value

BLAST score

Match length

% identity

315

108

64

5.0e-30



```
jC-gmle01810012d08a1
5'-most EST
                  29961
Seq. No.
                  204716 1.R1040
Contig ID
                  uC-gmrominsoy176b11b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4415924
                   403
BLAST score
                   2.0e-48
E value
                   174
Match length
                   57
% identity
                   (AC006282) putative glucosyl transferase [Arabidopsis
NCBI Description
                   thaliana]
                   29962
Seq. No.
                   204718 1.R1040
Contig ID
                   leu701155225.hl
5'-most EST
                   BLASTX
Method
                   g3367522
NCBI GI
                   284
BLAST score
                   2.0e-25
E value
                   102
Match length
                   52
% identity
                   (AC004392) EST gb T04691 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
                   29963
Seq. No.
                   204731 1.R1040
Contig ID
                   uC-gmflminsoy016b12b1
5'-most EST
                   BLASTX
Method
                   q2191136
NCBI GI
                   289
BLAST score
                   5.0e-26
E value
                   131
Match length
% identity
                   (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                   coded for by A. thaliana cDNA T46230; coded for by A.
                   thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
                   29964
Seq. No.
                   204764 1.R1040
Contig ID
 5'-most EST
                   dpv701101540.h1
                    29965
 Seq. No.
                    204773 1.R1040
 Contig ID
                    leu701156438.h1
 5'-most EST
                    29966
 Seq. No.
                    204791 1.R1040
 Contig ID
                    k11701\overline{2}07611.h1
 5'-most EST
                    BLASTX
 Method
                    g2459441
```



(AC002332) putative SWI/SNF complex subunit BAF170 NCBI Description · [Arabidopsis thaliana]

29967 Seq. No.

204791 2.R1040 Contig ID fua701037770.h1 5'-most EST

29968 Seq. No.

204793 1.R1040 Contig ID

5'-most EST g5126294

29969 Seq. No.

204811 1.R1040 Contig ID

g4286952 5'-most EST

29970 Seq. No.

204818 1.R1040 Contig ID zsg701118888.hl 5'-most EST

29971 Seq. No.

204852 1.R1040 Contig ID bth700846660.hl 5'-most EST

BLASTX Method g4467156 NCBI GI 170 BLAST score 2.0e-12 E value 56 Match length

62 % identity

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

29972 Seq. No.

204862 1.R1040 Contig ID bth700848868.h1 5'-most EST

BLASTN Method q3005575 NCBI GI BLAST score 169 1.0e-89 E value Match length 397 % identity

NCBI Description Glycine max putative high affinity nitrate transporter

(NRT2) mRNA, complete cds

Seq. No. 29973

Contig ID 204866 1.R1040 jC-gmr002910008f11a1 5'-most EST

BLASTX Method g2746086 NCBI GI BLAST score 504 4.0e-51 E value 159 Match length % identity 65

(AF025292) putative high-affinity potassium transporter NCBI Description

[Hordeum vulgare]

29974 Seq. No.

204870 1.R1040 Contig ID bth700845152.h1 5'-most EST



Method BLASTX
NCBI GI g4056506
BLAST score 544
E value 1.0e-55
Match length 228
% identity 46

NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 29975

Contig ID 204922\_1.R1040

5'-most EST jC-gmst02400025a10d1

Seq. No. 29976

Contig ID 204933\_1.R1040 5'-most EST gsv701048851.h1

Method BLASTX
NCBI GI g1169421
BLAST score 504
E value 3.0e-51
Match length 125
% identity 74

NCBI Description DEVELOPMENTALLY REGULATED GTP-BINDING PROTEIN DRG (XDRG)

>gi\_2120159\_pir\_\_I51426 GTP-binding protein DRG - African clawed frog >gi\_433422 dbj\_BAA02978 (D13865) GTP-binding

protein DRG [Xenopus laevis]

Seq. No. 29977

Contig ID 204937\_1.R1040 5'-most EST kl1701203446.h1

Seq. No. 29978

Contig ID 204938 1.R1040 5'-most EST epx701110347.h1

Method BLASTX
NCBI GI g2342682
BLAST score 390
E value 5.0e-38
Match length 102
% identity 73

NCBI Description (AC000106) Contains similarity to Rattus AMP-activated

protein kinase (gb X95577). [Arabidopsis thaliana]

Seq. No. 29979

Contig ID 204941\_1.R1040 5'-most EST jC-gmle01810051e07a1

Method BLASTX
NCBI GI 94467096
BLAST score 241
E value 1.0e-25
Match length 87
% identity 67

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 29980

Contig ID 204956\_1.R1040 5'-most EST uC-gmropic068e03b1



Seq. No. 29981 204970 1.R1040 Contig ID 5'-most EST bth700845277.hl Method BLASTX NCBI GI g3152576 BLAST score 295 E value 1.0e-26 Match length 155 39 % identity NCBI Description (AC002986) Similar to liver-specific transport protein gb L27651 from Rattus norviegicus. [Arabidopsis thaliana] 29982 Seq. No. 204995 1.R1040 Contig ID

5'-most EST jC-gmst02400026c11d1

Seq. No. 29983

Contig ID 205005 1.R1040 5'-most EST gsv701052539.h1

Seq. No. 29984

Contig ID 205088 1.R1040

5'-most EST uC-gmflminsoy046e06b1

Method BLASTX
NCBI GI g3953475
BLAST score 216
E value 2.0e-17
Match length 68
% identity 65

NCBI Description (AC002328) F2202.20 [Arabidopsis thaliana]

Seq. No. 29985

Contig ID 205090 1.R1040

5'-most EST  $g42926\overline{5}1$ 

Seq. No. 29986

Contig ID 205118\_1.R1040 5'-most EST asn701135365.h1

Seq. No. 29987

Contig ID 205121 1.R1040 5'-most EST bth700845459.h1

Method BLASTX
NCBI GI g2262113
BLAST score 527
E value 1.0e-53
Match length 142
% identity 70

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 29988

Contig ID 205136\_1.R1040 5'-most EST uC-gmropic056e02b1

Method BLASTX NCBI GI g3184082 BLAST score 288 E value 1.0e-25



Match length 145 % identity 39

NCBI Description (AL023781) N-terminal acetyltransferase 1

[Schizosaccharomyces pombe]

Seq. No. 29989

Contig ID 205179\_1.R1040 5'-most EST bth700845537.h1

Seq. No. 29990

Contig ID 205198\_1.R1040 5'-most EST bth700845558.h1

Method BLASTX
NCBI GI g3510251
BLAST score 280
E value 5.0e-25
Match length 118
% identity 46

NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 29991

Contig ID 205215\_1.R1040 5'-most EST jex700905993.h1

Seq. No. 29992

Contig ID 205244\_1.R1040 5'-most EST bth700845626.h1

Method BLASTX
NCBI GI g3250676
BLAST score 284
E value 9.0e-26
Match length 85
% identity 61

NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 29993

Contig ID 205294\_1.R1040 5'-most EST dpv701099773.h1

Seq. No. 29994

Contig ID 205295\_1.R1040 5'-most EST bth700845691.h1

Method BLASTX
NCBI GI g3643088
BLAST score 128
E value 5.0e-09
Match length 55
% identity 62

NCBI Description (AF075581) protein phosphatase-2C; PP2C [Mesembryanthemum

crystallinum]

Seq. No. 29995

Contig ID 205333 1.R1040 5'-most EST fC-gmf1700863043f1

Method BLASTX
NCBI GI g2459435
BLAST score 153



E value 4.0e-10 Match length 34 82

NCBI Description (AC002332) putative serine carboxypeptidase [Arabidopsis

thaliana]

Seq. No. 29996

Contig ID 205413\_1.R1040 5'-most EST bth700845840.h1

Seq. No. 29997

Contig ID 205432\_1.R1040 5'-most EST zhf700954646.h1

Seq. No. 29998

Contig ID 205488 1.R1040 5'-most EST kl1701203633.h2

Seq. No. 29999

Contig ID 205494\_1.R1040

5'-most EST g5175573

Method BLASTX

NCBI GI g4006864

BLAST score 447

E value 4.0e-45

Match length 227

% identity 52

NCBI Description (Z99707) nucleoporin-like protein [Arabidopsis thaliana]

Seq. No. 30000

Contig ID 205502\_1.R1040

NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis

thaliana]

Seq. No. 30001

Contig ID 205526\_1.R1040

5'-most EST uC-gmrominsoy187f10b1

Method BLASTX
NCBI GI g3122957
BLAST score 222
E value 6.0e-18
Match length 149
% identity 30

NCBI Description TYPE II DNA TOPOISOMERASE VI SUBUNIT B >gi\_2649967

(AE001060) DNA topoisomerase VI, subunit B (top6B)

[Archaeoglobus fulgidus]

Seq. No. 30002

Contig ID 205551\_1.R1040 5'-most EST bth700846004.h1



```
30003
Seq. No.
                  205573 1.R1040
Contig ID
                  zhf700953977.hl
5'-most EST
                  30004
Seq. No.
                  205588 1.R1040
Contig ID
                  fC-gmro700847605a1
5'-most EST
                  BLASTX
Method
                  g1161167
NCBI GI
                   331
BLAST score
                   7.0e-31
E value
                  120
Match length
                   53
% identity
                  (L42466) ethylene-forming enzyme [Picea glauca]
NCBI Description
                   30005
Seq. No.
                   205645 1.R1040
Contig ID
                   g4296319
5'-most EST
                   30006
Seq. No.
                   205683 1.R1040
Contig ID
                   fC-gmro700748726d3
5'-most EST
                   30007
Seq. No.
                   205683 2.R1040
Contig ID
                   zhf700957022.h1
5'-most EST
                   30008
Seq. No.
                   205697 1.R1040
Contig ID
                   bth700846175.hl
5'-most EST
                   BLASTN
Method
                   g4200043
NCBI GI
BLAST score
                   44
                   1.0e-15
E value
                   84
Match length
                   88
% identity
                   Glycyrrhiza echinata CYP Ge-31 mRNA for cytochrome P450,
NCBI Description
                   complete cds
                   30009
Seq. No.
                   205698 1.R1040
Contig ID
 5'-most EST
                   jex700908673.hl
Seq. No.
                    30010
                   205706 1.R1040
Contig ID
                   asn701139026.h1
 5'-most EST
                   BLASTX
Method
NCBI GI
                   g544184
                    340
```

Method BLASTX
NCBI GI g544184
BLAST score 340
E value 7.0e-32
Match length 81
% identity 70
NCBI Description 4-ALPHA-

4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE)

(DISPROPORTIONATING ENZYME) (D-ENZYME)

>gi\_322785\_pir\_\_A45049 4-alpha-glucanotransferase (EC
2.4.1.25) - potato >gi\_296692\_emb\_CAA48630\_ (X68664)



## 4-alpha-glucanotransferase [Solanum tuberosum]

30011 Seq. No. Contig ID 205768 1.R1040 bth700846263.h1 5'-most EST Method BLASTX NCBI GI q4262224 BLAST score 288 E value 6.0e-26 Match length 126 % identity 45 (AC006200) putative amino acid or GABA permease NCBI Description [Arabidopsis thaliana] 30012 Seq. No. 205797 1.R1040 Contig ID bth700846303.h1 5'-most EST

Seq. No. 30013

Contig ID 205871\_1.R1040 5'-most EST bth700846401.h1

Seq. No. 30014

Contig ID 205875\_1.R1040 5'-most EST bth700846406.h1

Seq. No. 30015

Contig ID 205884\_1.R1040 5'-most EST bth700846417.h1

Seq. No. 30016

Contig ID 205923 1.R1040 5'-most EST kl1701214749.h1

Seq. No. 30017

Contig ID 205927\_1.R1040 5'-most EST bth700846470.h1

Method BLASTX
NCBI GI g2827556
BLAST score 213
E value 6.0e-17
Match length 83
% identity 51

NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

Seq. No. 30018

Contig ID 206044\_1.R1040 5'-most EST bth700846633.h1

Method BLASTX
NCBI GI 94467156
BLAST score 291
E value 5.0e-47
Match length 122
% identity 75

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 30019

4611

NCBI Description

thaliana]



```
Contig ID
                  206060 1.R1040
5'-most EST
                  jC-qmst02400077e12a1
                  30020
Seq. No.
                  206088 1.R1040
Contig ID
5'-most EST
                  bth700846687.h1
Method
                  BLASTX
NCBI GI
                  g3157932
BLAST score
                  309
E value
                  1.0e-28
                  78
Match length
                  72
% identity
NCBI Description (AC002131) Similar to hypothetical protein HYP1 gb_Z97338
                  from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                  30021
                  206095 1.R1040
Contig ID
5'-most EST
                  gsv701046866.hl
Method
                  BLASTX
NCBI GI
                  q4220517
BLAST score
                  219
E value
                  7.0e-18
Match length
                  52
% identity
                  77
NCBI Description (AL035356) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  30022
Contig ID
                  206102 1.R1040
5'-most EST
                  bth700846712.h1
                  30023
Seq. No.
                  206109 1.R1040
Contig ID
                  bth700846768.h1
5'-most EST
Seq. No.
                  30024
Contig ID
                  206113 1.R1040
5'-most EST
                  jC-gmf102220093b10a1
                  30025
Seq. No.
Contig ID
                  206130 1.R1040
5'-most EST
                  zsg701122592.hl
                   30026
Seq. No.
                   206165 1.R1040
Contig ID
5'-most EST
                  bth700846993.hl
Seq. No.
                   30027
                  206181_1.R1040
Contig ID
                  uC-gmflminsoy030d08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4512701
BLAST score
                  395
                  2.0e-38
E value
Match length
                  88
% identity
```

(AC006569) putative tyrosine decarboxylase [Arabidopsis



Contig ID 206185\_1.R1040 5'-most EST bth700846826.h1

Seq. No. 30029

Contig ID 206227\_1.R1040 5'-most EST pmv700890991.h1

Seq. No. 30030

Contig ID 206230 1.R1040

5'-most EST jC-gmro02910068h01a1

Seq. No. 30031

Contig ID 206233\_1.R1040 5'-most EST pxt700942737.h1

Method BLASTX
NCBI GI g2947063
BLAST score 429
E value 5.0e-42
Match length 176
% identity 51

NCBI Description (AC002521) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 30032

Contig ID 206300\_1.R1040 5'-most EST fua701039394.h1

Method BLASTX
NCBI GI g4263818
BLAST score 295
E value 2.0e-26
Match length 184
% identity 38

NCBI Description (AC006067) unknown protein [Arabidopsis thaliana]

Seq. No. 30033

Contig ID 206355\_1.R1040 5'-most EST jC-gmro02800030g03a1

Method BLASTX
NCBI GI g4063742
BLAST score 306
E value 1.0e-27
Match length 116
% identity 56

NCBI Description (AC005851) putative phaseolin G-box binding protein

[Arabidopsis thaliana]

Seq. No. 30034

Contig ID 206370\_1.R1040 5'-most EST jC-gmle01810042c10a1

Seq. No. 30035

Contig ID 206426\_1.R1040 5'-most EST bth700847167.h1

Method BLASTX NCBI GI g3341694



BLAST score 6.0e-09 E value 77 Match length 44 % identity

(AC003672) PREG-like protein [Arabidopsis thaliana] NCBI Description

Seq. No. Contig ID 5'-most EST 30036 206440 1.R1040 zsq701120332.h1

Seq. No. Contig ID 5'-most EST 30037 206468 1.R1040 fC-gmro700848531a1

Seq. No. Contig ID 5'-most EST 30038 206469 1.R1040 bth700848245.h1

Seq. No. Contig ID 5'-most EST 30039 206470 1.R1040 rlr700901269.hl

Seq. No. Contig ID 5'-most EST 30040 206494 1.R1040

g4284646

Seq. No. Contig ID 30041 206497 1.R1040

uC-qmrominsoy081g09b1 5'-most EST BLASTX

Method q4468812 NCBI GI BLAST score 277 1.0e-24 E value 75 Match length % identity

(AL035601) putative protein [Arabidopsis thaliana] NCBI Description

٠. 5

Seq. No. Contig ID

30042 206513 1.R1040 bth700847267.h1

5'-most EST

30043

Seq. No. 206551 1.R1040 Contig ID

jC-gmle01810088b07d1 5'-most EST

30044

Seq. No.

206551 2.R1040 Contig ID uC-gmropic027a09b1 5'-most EST

Seq. No. Contig ID 5'-most EST

30045 206585 1.R1040 bth700847358.h1

BLASTX Method g4325338 NCBI GI 564 BLAST score 2.0e-58 E value Match length 120

4614



```
% identity
                  (AF128392) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  30046
                  206591 1.R1040
Contig ID
                  bth700847364.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4335745
BLAST score
                  223
E value
                   4.0e-18
                   98
Match length
% identity
                   43
                   (AC006284) putative hydrolase (contains an
NCBI Description
                   esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
                   30047
Seq. No.
                   206653 1.R1040
Contig ID
5'-most EST
                   jex700907913.hl
                   30048
Seq. No.
Contig ID
                  206675 1.R1040
                  jC-qmle01810077e06d1
5'-most EST
                   30049
Seq. No.
Contig ID
                   206691 1.R1040
5'-most EST
                  pmv700893634.h1
Method
                   BLASTX
NCBI GI
                   g2827630
                   295
BLAST score
E value
                   7.0e-39
Match length
                   109
% identity
                   72
NCBI Description
                  (AL021636) putative protein [Arabidopsis thaliana]
Seq. No.
                   30050
                   206700 1.R1040
Contig ID
5'-most EST
                   fua701040870.hl
Method
                   BLASTX
                   g2829887
NCBI GI
BLAST score
                   282
                   2.0e-25
E value
Match length
                   87
% identity
                   61
NCBI Description
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   30051
Contig ID
                   206726 1.R1040
5'-most EST
                   uC-gmrominsoy193g08b1
Method
                   BLASTX
NCBI GI
                   g3335060
BLAST score
                   293
E value
                   2.0e-28
                   97
Match length
```

(AF025842) plasma membrane-type calcium ATPase [Arabidopsis

thaliana] >gi 4468989 emb CAB38303 (AL035605) plasma

74

% identity

NCBI Description



membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

Seq. No. 30052

Contig ID 206750\_1.R1040 5'-most EST bth700848082.h1

Seq. No. 30053

Contig ID 206768\_1.R1040 5'-most EST pmv700889038.h1

Seq. No. 30054

Contig ID 206773\_1.R1040 5'-most EST bth700847609.h1

Method BLASTX
NCBI GI g3510259
BLAST score 268
E value 7.0e-24
Match length 66
% identity 82

NCBI Description (AC005310) putative inorganic pyrophosphatase [Arabidopsis

thaliana] >gi\_3522960 (AC004411) putative inorganic

pyrophosphatase [Arabidopsis thaliana]

Seq. No. 30055

Contig ID 206774\_1.R1040 5'-most EST asn701142575.h1

Method BLASTX
NCBI GI g2501494
BLAST score 162
E value 3.0e-11
Match length 85
% identity 44

NCBI Description FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5 (UDP-GLUCOSE FLAVONOID

3-O-GLUCOSYLTRANSFERASE 5) >gi\_542015\_pir\_\_S41951

UTP-glucose glucosyltransferase - cassava >gi\_453249\_emb\_CAA54612\_ (X77462) UTP-glucose

glucosyltransferase [Manihot esculenta]

Seq. No. 30056

Contig ID 206798\_1.R1040 5'-most EST zhf700953387.h1

Seq. No. 30057

Contig ID 206804 1.R1040 5'-most EST bth700847649.h1

Seq. No. 30058

Contig ID 206824 1.R1040 5'-most EST gsv701051171.h1

Seq. No. 30059

Contig ID 206829\_1.R1040 5'-most EST fC-gmle700870704a2

Method BLASTX
NCBI GI g3912917
BLAST score 1703
E value 0.0e+00



426 Match length 78 % identity

(AF001308) putative NAK-like ser/thr protein kinase NCBI Description

[Arabidopsis thaliana]

30060 Seq. No.

206844 1.R1040 Contig ID zsq701118010.h2 5'-most EST

BLASTX Method g2225877 NCBI GI 484 BLAST score 1.0e-48 E value 119 Match length % identity 77

(AB002406) TIP49 [Rattus norvegicus] >gi\_4106528 (AF100694) NCBI Description

Pontin52 [Mus musculus] >gi\_4521276\_dbj\_BAA76313.1\_

(AB001581) DNA helicase p50 [Rattus norvegicus]

30061 Seq. No.

206847 1.R1040 Contig ID fC-qmst700892002d3 5'-most EST

30062 Seq. No.

206847 2.R1040 Contig ID  $zsg701\overline{1}23575.h1$ 5'-most EST

30063 Seq. No.

206874 1.R1040 Contig ID jC-gmst02400028f01a1 5'-most EST

BLASTX Method g2781345 NCBI GI 587 BLAST score 1.0e-60 E value 233 Match length 51 % identity

(AC003113) F2401.2 [Arabidopsis thaliana] NCBI Description

30064 Seq. No.

206876 1.R1040 Contig ID

g4397509 5'-most EST

30065 Seq. No.

206885 1.R1040 Contig ID leu701154624.h1 5'-most EST

BLASTX Method q1809257 NCBI GI 98 BLAST score 2.0e-09 E value 89 Match length 46 % identity

(U59316) serine/threonine protein kinase Pto [Lycopersicon NCBI Description

esculentum]

30066 Seq. No.

206885 2.R1040 Contig ID jC-gmle01810021g05a1 5'-most EST

BLASTX Method

BLAST score

Match length

E value

384

95

2.0e-37



```
NCBI GI
                   g1644291
BLAST score
                   213
E value
                   6.0e-17
Match length
                  109
% identity
                   45
NCBI Description (Z73295) receptor-like protein kinase [Catharanthus roseus]
Seq. No.
                  30067
                  206885 3.R1040
Contig ID
5'-most EST
                  jsh701068122.h1
                  30068
Seq. No.
                  206919 1.R1040
Contig ID
5'-most EST
                  pmv700893156.h1
Method
                  BLASTX
NCBI GI
                  g3228668
BLAST score
                  430
E value
                  2.0e-42
Match length
                  153
% identity
                  52
NCBI Description (AF069988) nitrilase 1 [Mus musculus]
                  30069
Seg. No.
Contig ID
                  206958 1.R1040
5'-most EST
                  jC-gmro02910062a12a1
Method
                  BLASTX
                  g4314357
NCBI GI
BLAST score
                  138
                   4.0e-12
E value
Match length
                  162
% identity
                  41
NCBI Description (AC006340) putative nucleic acid binding protein
                   [Arabidopsis thaliana]
                   30070
Seq. No.
                   207003 1.R1040
Contig ID
5'-most EST
                  bth700847903.h1
Method
                  BLASTX
NCBI GI
                  g1621461
BLAST score
                  165
                  1.0e-11
E value
                  114
Match length
                  39
% identity
NCBI Description (U73103) laccase [Liriodendron tulipifera]
Seq. No.
                  30071
Contig ID
                  207011 1.R1040
5'-most EST
                  bth700847911.h1
Seq. No.
                   30072
Contig ID
                  207016 1.R1040
5'-most EST
                   epx701104603.h1
Method
                  BLASTX
NCBI GI
                  q3096947
```



% identity (Y16327) putative cyclic nucleotide-regulated ion channel NCBI Description [Arabidopsis thaliana] 30073 Seq. No. Contig ID 207054 1.R1040 iC-qmf102220054d02a1 5'-most EST BLASTX Method q539079 NCBI GI BLAST score 463 E value 4.0e-46 202 Match length 45 % identity NCBI Description peroxisomal assembly protein 5 - yeast (Pichia pastoris) Seq. No. Contig ID 207072 1.R1040 5'-most EST bth700847992.hl 30075 Seq. No. 207093 1.R1040 Contig ID 5'-most EST asn701141385.hl 30076 Seq. No. 207110 1.R1040 Contig ID uC-gmrominsoy035c07b1 5'-most EST 30077 Seq. No. 207154 1.R1040 Contig ID uC-gmflminsoy075e07b1 5'-most EST 30078 Seq. No. 207158 1.R1040 Contig ID bth700848109.h1 5'-most EST 30079 Seq. No. Contig ID 207161 1.R1040 pxt700943435.hl 5'-most EST Method BLASTX q4544432 NCBI GI BLAST score 369 3.0e-35 E value Match length 77 91 % identity (AC006955) putative mannose-1-phosphate guanyltransferase NCBI Description [Arabidopsis thaliana] 30080 Seq. No. 207162 1.R1040 Contig ID

jC-gmle01810021c05d1 5'-most EST

30081 Seq. No.

207163 1.R1040 Contig ID

jC-gmro02910056f02a1 5'-most EST

BLASTX Method q1304227 NCBI GI BLAST score 448



E value 2.0e-44
Match length 154
% identity 51

NCBI Description (D63781) Epoxide hydrolase [Glycine max]

>gi 2764804\_emb\_CAA55293\_ (X78547) epoxide hydrolase

[Glycine max]

Seq. No. 30082

Contig ID 207197\_1.R1040 5'-most EST zhf700958167.h1

Seq. No. 30083

Contig ID 207215\_1.R1040 5'-most EST bth700848183.h1

Method BLASTX
NCBI GI 94567283
BLAST score 222
E value 1.0e-18
Match length 62
% identity 73

NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.

Contig ID 207226 1.R1040

30084

5'-most EST g5510282
Method BLASTX
NCBI GI g3482918
BLAST score 308
E value 4.0e-28
Match length 79
% identity 75

NCBI Description (AC003970) Similar to ATP-citrate-lyase [Arabidopsis

thaliana]

Seq. No. 30085

Contig ID 207238\_1.R1040 5'-most EST bth700848214.h1

Seq. No. 30086

Contig ID 207244\_1.R1040 5'-most EST bth700848221.h1

Seq. No. 30087

Contig ID 207257\_1.R1040 5'-most EST zhf700956222.h1

Seq. No. 30088

Contig ID 207331\_1.R1040 5'-most EST fC-gmro700846765a1

Method BLASTX
NCBI GI g3334661
BLAST score 440
E value 1.0e-43
Match length 123
% identity 63

NCBI Description (Y10490) putative cytochrome P450 [Glycine max]



Contig ID 207346\_1.R1040 5'-most EST dpv701101241.h1

Method BLASTX
NCBI GI g3912919
BLAST score 368
E value 4.0e-35
Match length 118
% identity 59

NCBI Description (AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30090

Contig ID 207362\_1.R1040 5'-most EST bth700848369.h1

Method BLASTX
NCBI GI g2688828
BLAST score 158
E value 1.0e-17
Match length 84
% identity 52

NCBI Description (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus

armeniaca]

Seq. No. 30091

Contig ID 207421\_1.R1040 5'-most EST bth700848443.h1

Method BLASTX
NCBI GI g3402685
BLAST score 167
E value 5.0e-15
Match length 60
% identity 75

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 30092

Contig ID 207431\_1.R1040 5'-most EST bth700848453.h1

Method BLASTX
NCBI GI g4539301
BLAST score 216
E value 1.0e-17
Match length 99
% identity 49

NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis

thaliana]

Seq. No. 30093

Contig ID 207455\_1.R1040 5'-most EST zhf700959259.h1

Seq. No. 30094

Contig ID 207461 1.R1040

5'-most EST uC-gmflminsoy082e11b1

Seq. No. 30095

Contig ID 207532\_1.R1040 5'-most EST fua701039758.h1



Contig ID 207546\_1.R1040 5'-most EST jC-gmst02400067d12d1

Seq. No. 30097

Contig ID 207574\_1.R1040 5'-most EST uC-gmropic050g01b1

Seq. No. 30098

Contig ID 207592\_1.R1040 5'-most EST dpv701102879.h1

Method BLASTN
NCBI GI g170029
BLAST score 56
E value 7.0e-23
Match length 95
% identity 91

NCBI Description Glycine max cv. Dare nodulin 26 gene fragment

Seq. No. 30099

Contig ID 207615\_1.R1040 5'-most EST fC-gmro700848694a1

Method BLASTX
NCBI GI g3292831
BLAST score 286
E value 7.0e-50
Match length 131
% identity 77

NCBI Description (AL031018) putative serine/threonine kinase [Arabidopsis

thaliana]

Seq. No. 30100

Contig ID 207620\_1.R1040 5'-most EST bth700848707.h1

Method BLASTN
NCBI GI g3292807
BLAST score 55
E value 4.0e-22
Match length 153

% identity 85 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19

(ESSAII project)

Seq. No. 30101

Contig ID 207663\_1.R1040 5'-most EST uC-gmropic090d03b1

Method BLASTX
NCBI GI g2191145
BLAST score 227
E value 1.0e-18
Match length 146

% identity 41
NCBI Description (AF007269) A\_IG002N01.4 gene product [Arabidopsis thaliana]

Seq. No. 30102

Contig ID 207727\_1.R1040

4622



5'-most EST hrw701063119.h1

Seq. No. 30103

Contig ID 207746\_1.R1040 5'-most EST bth700848864.h1

Seq. No. 30104

Contig ID 207753\_1.R1040 5'-most EST uC-gmropic023a06b1

Method BLASTX
NCBI GI g3096947
BLAST score 184
E value 2.0e-13
Match length 103
% identity 45

NCBI Description (Y16327) putative cyclic nucleotide-regulated ion channel

[Arabidopsis thaliana]

Seq. No. 30105

Contig ID 207769\_1.R1040 5'-most EST bth700848894.h1

Seq. No. 30106

Contig ID 207784\_1.R1040 5'-most EST bth700848917.h1

Method BLASTX
NCBI GI g4559380
BLAST score 205
E value 2.0e-18
Match length 61

% identity 79

NCBI Description (AC006526) putative auxin-responsive GH3 protein

[Arabidopsis thaliana]

Seq. No. 30107

Contig ID 207795\_1.R1040 5'-most EST kl1701207346.h1

Seq. No. 30108

Contig ID 207796\_1.R1040 5'-most EST uC-gmropic004a12b1

Method BLASTX
NCBI GI g3559816
BLAST score 286
E value 6.0e-39
Match length 132
% identity 63

NCBI Description (Y15782) transketolase 2 [Capsicum annuum]

Seq. No. 30109

Contig ID 207803\_1.R1040 5'-most EST fua701037395.h1

Seq. No. 30110

Contig ID 207866\_1.R1040 5'-most EST bth700849032.h1



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Seq. No.
                  207883 1.R1040
Contig ID
                  bth700849050.h1
5'-most EST
                  30112
Seq. No.
                  207891 1.R1040
Contig ID
5'-most EST
                  uC-gmropic054f11b1
                  BLASTX
Method
                  g4539383
NCBI GI
                  317
BLAST score
                  5.0e-29
E value
                  119
Match length
                  48
% identity
                   (AL035526) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                  30113
Seq. No.
                  207892 1.R1040
Contig ID
                  bth700849061.h1
5'-most EST
                   30114
Seq. No.
                   207903 1.R1040
Contig ID
                   jC-gmst02400001f09a1
5'-most EST
Seq. No.
                   30115
                   207905 1.R1040
Contig ID
                   uC-gmropic054c04b1
5'-most EST
                   {\tt BLASTX}
Method
                   g2493895
NCBI GI
                   601
BLAST score
                   3.0e-62
E value
                   170
Match length
                   68
% identity
                   CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)
NCBI Description
                   (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                   >gi 1071911 pir S46438 cysteine synthase (EC 4.2.99.8) -
                   watermelon >gi 540497 dbj BAA05965 (D28777) cysteine
                   synthase [Citrullus lanatus]
                   30116
Seq. No.
                   207905 2.R1040
Contig ID
                   jC-gmle01810030e09d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3127890
                   181
BLAST score
                   4.0e-13
E value
```

73 Match length

% identity

(AJ006024) cysteine synthase, O-acetyl-L-serine NCBI Description

(thiol)-lyase [Cicer arietinum]

30117 Seq. No.

207905 3.R1040 Contig ID 5'-most EST jsh701064170.h1

Seq. No. 30118

207907 1.R1040 Contig ID



```
5'-most EST
                  bth700849086.h1
                  30119
Seq. No.
                  207909 1.R1040
Contig ID
5'-most EST
                  bth700849090.h1
Method
                  BLASTX
NCBI GI
                  g520570
                  246
BLAST score
                   4.0e-21
E value
                   69
Match length
% identity
                  (U12315) peroxidase [Cenchrus ciliaris]
NCBI Description
                   30120
Seq. No.
                   207919 1.R1040
Contig ID
                   uC-gmflminsoy017e02b1
5'-most EST
                  BLASTX
Method
                   g4191786
NCBI GI
BLAST score
                   592
                   2.0e-61
E value
                   163
Match length
                   71
% identity
NCBI Description (AC005917) unknown protein [Arabidopsis thaliana]
Seq. No.
                   30121
                   207968 1.R1040
Contig ID
5'-most EST
                   fua701040728.h1
                   BLASTX
Method
                   q2829864
NCBI GI
BLAST score
                   154
                   2.0e-10
E value
                   45
Match length
% identity
                   (AC002396) similar to zinc metalloproteinases [Arabidopsis
NCBI Description
                   thaliana]
                   30122
Seq. No.
                   207983 1.R1040
Contig ID
                   uC-gmropic043g07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3668087
BLAST score
                   518
                   1.0e-52
E value
Match length
                   161
% identity
                  (AC004667) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30123
                   208017 1.R1040
Contig ID
                   bth700849224.h1
5'-most EST
                   30124
Seq. No.
                   208024 1.R1040
Contig ID
                   bth700849231.h1
5'-most EST
```

4625

BLASTX

173

g2252847

Method

NCBI GI

BLAST score



3.0e-12 E value Match length 35 % identity

(AF013293) No definition line found [Arabidopsis thaliana] NCBI Description

30125 Seq. No.

208030 1.R1040 Contig ID jC-qmro02910011c09a1 5'-most EST

BLASTX Method q3335375 NCBI GI 908 BLAST score 2.0e-98 E value 191 Match length 88 % identity

(AC003028) putative amidase [Arabidopsis thaliana] NCBI Description

30126 Seq. No.

208066 1.R1040 Contig ID bth700849280.h1 5'-most EST

BLASTX Method g4567305 NCBI GI 195 BLAST score 7.0e-15 E value 81 Match length % identity

(AC005956) hypothetical protein [Arabidopsis thaliana] NCBI Description

30127 Seq. No.

208109 1.R1040 Contig ID uC-gmropic009e01b1 5'-most EST

30128 Seq. No.

208111 1.R1040 Contig ID gsv701050584.hl 5'-most EST

30129 Seq. No.

208176 1.R1040 Contig ID

5'-most EST g4313893

30130 Seq. No.

208183 1.R1040 Contig ID 5'-most EST zhf700955854.hl

BLASTX Method NCBI GI q3212539 657 BLAST score 9.0e-69 E value Match length 200 % identity 63

Chain A, Structure Of Human Isovaleryl-Coa Dehydrogenase At NCBI Description 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity >gi\_3212540\_pdb\_1IVH\_B Chain B, Structure Of

Human Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity >qi 3212541 pdb 1IVH C Chain C, Structure Of Human

Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms Resolution:

Structural Basis For Substrate Specificity

>gi\_3212542\_pdb\_1IVH\_D Chain D, Structure Of Human



Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity

Seq. No. 30131

Contig ID 208226\_1.R1040

5'-most EST  $g56770\overline{3}8$ 

Seq. No. 30132

Contig ID 208260\_1.R1040 5'-most EST bth700849533.h1

Seq. No. 30133

Contig ID 208280 1.R1040 5'-most EST bth700849556.h1

Method BLASTN
NCBI GI g4220631
BLAST score 49
E value 1.0e-18
Match length 204
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K5J14, complete sequence [Arabidopsis thaliana]

Seq. No. 30134

Contig ID 208289 1.R1040

5'-most EST uC-gmflminsoy061b05b1

Method BLASTX
NCBI GI g2583122
BLAST score 223
E value 3.0e-18
Match length 105
% identity 48

NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30135

Contig ID 208305\_1.R1040 5'-most EST zsg701128405.h1

Seq. No. 30136

Contig ID 208333\_1.R1040 5'-most EST uC-gmropic038h11b1

Method BLASTX
NCBI GI g1172584
BLAST score 215
E value 3.0e-17
Match length 89
% identity 49

NCBI Description POLYPHENOL OXIDASE PRECURSOR (PPO) (CATECHOL OXIDASE)

>gi\_1076478\_pir\_\_S52984 catechol oxidase (EC 1.10.3.1)
precursor - apple tree >gi\_507280 (L29450) polyphenol

oxidase [Malus domestica]

Seq. No. 30137

Contig ID 208349 1.R1040

5'-most EST jC-gmle01810032g11d1

Seq. No. 30138



Contig ID 208398\_1.R1040 5'-most EST bth700849701.h1

Method BLASTX
NCBI GI g559713
BLAST score 115
E value 1.0e-10
Match length 57
% identity 63

NCBI Description (D38552) The ha1539 protein is related to cyclophilin.

[Homo sapiens]

Seq. No. 30139

Contig ID 208405\_1.R1040 5'-most EST bth700849710.h1

Method BLASTX
NCBI GI 94006829
BLAST score 208
E value 1.0e-16
Match length 93
% identity 54

NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.

Contig ID 208408\_1.R1040 5'-most EST bth700849713.h1

30140

Seq. No. 30141

Contig ID 208451\_1.R1040 5'-most EST bth700849769.h1

Seq. No. 30142

Contig ID 208501 1.R1040

5'-most EST jC-gmle01810016f08d1

Seq. No. 30143

Contig ID 208550 1.R1040 5'-most EST bnh700764501.h1

Method BLASTX
NCBI GI 94204257
BLAST score 167
E value 1.0e-20
Match length 71
% identity 73

NCBI Description (AC005223) 5493 [Arabidopsis thaliana]

Seq. No. 30144

Contig ID 208583\_1.R1040 5'-most EST bnh700764543.h1

Seq. No. 30145

Contig ID 208665\_1.R1040 5'-most EST dpv701099937.h1

Seq. No. 30146

Contig ID 208687\_1.R1040 5'-most EST jex700902966.h1

Method BLASTX



```
q3776025
NCBI GI
                   254
BLAST score
                   7.0e-24
E value
                   79
Match length
% identity
                  (AJ010474) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   30147
Seq. No.
                   208688 2.R1040
Contig ID
                   zhf700953167.h1
5'-most EST
                   30148
Seq. No.
                   208691 1.R1040
Contig ID
                   jex700\overline{9}02980.h1
5'-most EST
                   BLASTX
Method
                   g2194125
NCBI GI
                   509
BLAST score
                   1.0e-51
E value
                   115
Match length
                   77
% identity
                   (AC002062) ESTs gb_R30459,gb_N38441 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                   30149
Seq. No.
                   208694 1.R1040
Contig ID
                   jex700904478.hl
5'-most EST
                   30150
Seq. No.
                   208715 1.R1040
Contig ID
                   jC-gmf102220073a05a1
5'-most EST
                   30151
Seq. No.
                   208744 1.R1040
Contig ID
                   jex700903170.hl
5'-most EST
                   BLASTX
Method
                   q624943
NCBI GI
                   157
BLAST score
                    9.0e-11
E value
                    81
Match length
 % identity
                   (X79432) unnamed protein product [Brassica oleracea]
NCBI Description
 Seq. No.
                    30152
 Contig ID
                    208751 1.R1040
                    jex700903527.hl
 5'-most EST
                    BLASTX
Method
```

q3334665 NCBI GI 386 BLAST score E value 2.0e-37 132 Match length % identity

NCBI Description (Y10492) putative cytochrome P450 [Glycine max]

30153 Seq. No.

208754 1.R1040 Contig ID jex700904555.h1 5'-most EST



Contig ID 208756\_1.R1040 5'-most EST jC-gmle01810010h12a1

Seq. No. 30155

Contig ID 208814 1.R1040 5'-most EST zhf700955093.h1

Method BLASTX
NCBI GI g125889
BLAST score 414
E value 1.0e-40
Match length 124
% identity 63

NCBI Description PROBABLE PECTATE LYASE P59 PRECURSOR >gi\_280400\_pir\_\_S27098

pectate lyase (EC 4.2.2.2) LAT59 - tomato

>gi\_19271\_emb\_CAA33523\_ (X15499) P59 protein [Lycopersicon

esculentum]

Seq. No. 30156

Contig ID 208817\_1.R1040 5'-most EST zhf700953936.h1

Method BLASTX
NCBI GI g2088651
BLAST score 162
E value 5.0e-11
Match length 83
% identity 55

NCBI Description (AF002109) hypersensitivity-related gene 201 isolog

[Arabidopsis thaliana]

Seq. No. 30157

Contig ID 208828\_1.R1040 5'-most EST uC-gmropic027c09b1

Method BLASTX
NCBI GI g4220529
BLAST score 637
E value 1.0e-66
Match length 160
% identity 76

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 30158

Contig ID 208848\_1.R1040

5'-most EST jC-gmfl02220103d01a1

Method BLASTX
NCBI GI g529353
BLAST score 414
E value 1.0e-40
Match length 121
% identity 55

NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No. 30159

Contig ID 208850\_1.R1040 5'-most EST zsg701119787.h1

Method BLASTN NCBI GI g2465528



```
BLAST score
                   4.0e-40
E value
                   169
Match length
                   88
% identity
                  Medicago truncatula phosphate transporter (MtPT2) mRNA,
NCBI Description
                   complete cds
                   30160
Seq. No.
                   208859 1.R1040
Contig ID
                   q5058240
5'-most EST
                   BLASTX
Method
                   q4038036
NCBI GI
                   155
BLAST score
                   3.0e-17
E value
                   185
Match length
                   43
% identity
NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]
                   30161
Seq. No.
                   208891 1.R1040
Contig ID
                   zhf700964182.h1
5'-most EST
                   BLASTX
Method
                   q4218120
NCBI GI
                   509
BLAST score
                   1.0e-51
E value
                   139
Match length
% identity
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   30162
Seq. No.
                   208892 1.R1040
Contig ID
                   leu701151880.h1
5'-most EST
                   BLASTX
Method
                   g1669341
NCBI GI
BLAST score
                   290
                   3.0e-26
E value
Match length
                   108
                   56
% identity
                   (D45066) AOBP (ascorbate oxidase promoter-binding protein)
NCBI Description
                    [Cucurbita maxima]
Seq. No.
                   30163
                   208911 1.R1040
Contig ID
                   jex700903566.h1
5'-most EST
                    30164
Seq. No.
                    208926 1.R1040
Contig ID
                    jex700\overline{9}03603.h1
 5'-most EST
                    BLASTX
Method
                    g2088651
NCBI GI
                    323
```

Method BLASTX
NCBI GI g2088651
BLAST score 323
E value 8.0e-30
Match length 145
% identity 48

NCBI Description (AF002109) hypersensitivity-related gene 201 isolog

[Arabidopsis thaliana]



Contig ID 208930\_1.R1040 5'-most EST jex700903610.h1

Seq. No. 30166

Contig ID 208955\_1.R1040 5'-most EST jex700903642.h1

Method BLASTX
NCBI GI 94455246
BLAST score 188
E value 5.0e-14
Match length 94
% identity 50

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 30167

Contig ID 208969\_1.R1040 5'-most EST jex700903674.h1

Seq. No. 30168

Contig ID 208971\_1.R1040 5'-most EST zsg701123853.h1

Method BLASTX
NCBI GI g1711618
BLAST score 444
E value 4.0e-44
Match length 126
% identity 69

NCBI Description LOW AFFINITY SULPHATE TRANSPORTER 3 >gi\_1085993\_pir\_\_S51765

low affinity sulphate transporter - Stylosanthes hamata >gi 607188 emb\_CAA57831\_ (X82454) low affinity sulphate

transporter [Stylosanthes hamata]

Seq. No. 30169

Contig ID 208991\_1.R1040 5'-most EST fC-gmf1700904235a1

Method BLASTX
NCBI GI g3047095
BLAST score 272
E value 7.0e-24
Match length 109
% identity 30

NCBI Description (AF058826) similar to eukaryotic protein kinase domains (Pfam: pkinase.hmm, score: 72.39) [Arabidopsis thaliana]

Seq. No. 30170

Contig ID 209019\_1.R1040 5'-most EST fC-gmfl700903761f4

Method BLASTX
NCBI GI g1150406
BLAST score 293
E value 3.0e-26
Match length 142
% identity 43

NCBI Description (Z46868) exo-1,3-beta-glucanase/1,3-beta-D-glucan

glucanohydrolase [Pichia angusta]



Contig ID 209026\_1.R1040 5'-most EST leu701149594.h1

Seq. No. 30172

Contig ID 209044\_1.R1040 5'-most EST jex700906355.h1

Seq. No. 30173

Contig ID 209057\_1.R1040 5'-most EST jex700903826.h1

Seq. No. 30174

Contig ID 209062\_1.R1040 5'-most EST jC-gmro02910004g06a1

Seq. No. 30175

Contig ID 209078\_1.R1040 5'-most EST jex700903873.h1

Seq. No. 30176

Contig ID 209094\_1.R1040 5'-most EST jex700903894.h1

Seq. No. 30177

Contig ID 209127\_1.R1040 5'-most EST uC-gmropic010c06b1

Method BLASTX
NCBI GI g1297187
BLAST score 654
E value 2.0e-68
Match length 212
% identity 60

NCBI Description (U53501) similar to protein encoded by GenBank Accession

Number U41815, nucleoporin 98 [Arabidopsis thaliana]

Seq. No. 30178

Contig ID 209142 1.R1040 5'-most EST jex700904010.h1

Seq. No. 30179

Contig ID 209146\_1.R1040 5'-most EST jex700904018.h1

Seq. No. 30180

Contig ID 209173 1.R1040

5'-most EST uC-gmflminsoy012g11b1

Method BLASTX
NCBI GI g2576361
BLAST score 568
E value 1.0e-58
Match length 138
% identity 74

NCBI Description (U39782) lysine and histidine specific transporter

[Arabidopsis thaliana]



Contig ID 209186\_1.R1040 5'-most EST jex700904081.h1

Seq. No. 30182

Contig ID 209246\_1.R1040 5'-most EST crh700852687.h1

Seq. No. 30183

Contig ID 209247\_1.R1040 5'-most EST leu701154524.h1

Seq. No. 30184

Contig ID 209293\_1.R1040 5'-most EST uC-gmropic028a03b1

Method BLASTX
NCBI GI g2388971
BLAST score 277
E value 3.0e-24
Match length 122
% identity 48

NCBI Description (298979) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 30185

Contig ID 209298\_1.R1040 5'-most EST rlr700895783.h1

Method BLASTX
NCBI GI g452593
BLAST score 252
E value 6.0e-22
Match length 91
% identity 49

NCBI Description (D21814) ORF [Lilium longiflorum]

Seq. No. 30186

Contig ID 209330\_1.R1040 5'-most EST uC-gmropic109h07b1

Method BLASTN
NCBI GI g1165321
BLAST score 58
E value 7.0e-24
Match length 193
% identity 20

NCBI Description Glycine max extensin (SbHRGP3) gene, complete cds

Seq. No. 30187

Contig ID 209374\_1.R1040

5'-most EST jC-gmro02800038c01d1

Seq. No. 30188

Contig ID 209436\_1.R1040 5'-most EST fC-gmf1700902268a1

Method BLASTX
NCBI GI g3641252
BLAST score 280
E value 5.0e-25
Match length 127



% identity 7
NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No. 30189

Contig ID 209469\_1.R1040

5'-most EST uC-gmflminsoy005b09b1

Seq. No. 30190

Contig ID 209471\_1.R1040 5'-most EST leu701149690.h1

Seq. No. 30191

Contig ID 209485\_1.R1040 5'-most EST fC-gmf1700904490f4

Method BLASTX
NCBI GI g1352075
BLAST score 619
E value 8.0e-67
Match length 178
% identity 61

NCBI Description BETA-GALACTOSIDASE PRECURSOR (LACTASE)

>gi\_1076460\_pir\_\_S52393 beta-galactosidase (EC 3.2.1.23) -

wild cabbage  $>gi_669059$ \_emb\_CAA59162\_ (X84684)

beta-galactosidase [Brassica oleracea]

Seq. No. 30192

Contig ID 209487\_1.R1040 5'-most EST fC-gmfl700904492f4

Method BLASTX
NCBI GI g3721856
BLAST score 422
E value 2.0e-41
Match length 109
% identity 69

NCBI Description (AB014057) beta-Amyrin Synthase [Panax ginseng]

Seq. No. 30193

Contig ID 209503 1.R1040 5'-most EST leu701145795.h1

Method BLASTX
NCBI GI g1653033
BLAST score 163
E value 3.0e-11
Match length 36
% identity 86

NCBI Description (D90910) hypothetical protein [Synechocystis sp.]

Seq. No. 30194

Contig ID 209545\_1.R1040 5'-most EST jex700905108.h1

Seq. No. 30195

Contig ID 209549\_1.R1040 5'-most EST jex700904589.h1

Seq. No. 30196



Contig ID 209566\_1.R1040 5'-most EST uC-gmropic022a02b1

Seq. No. 30197

Contig ID 209574\_1.R1040 5'-most EST zhf700958011.h1

Method BLASTX
NCBI GI g99808
BLAST score 570
E value 9.0e-59
Match length 171
% identity 63

NCBI Description gene Bp10 protein - rape >gi\_17797\_emb\_CAA47178\_ (X66609)

Bplo [Brassica napus]

Seq. No. 30198

Contig ID 209577\_1.R1040 5'-most EST jC-qmf102220142h02a1

Seq. No. 30199

Contig ID 209616\_1.R1040

5'-most EST  $jC-gmf\overline{1}02220100e08a1$ 

Method BLASTX
NCBI GI g1708972
BLAST score 217
E value 3.0e-17
Match length 101
% identity 50

NCBI Description (R)-MANDELONITRILE LYASE ISOFORM 3 PRECURSOR

(HYDROXYNITRILE LYASE 3) ((R)-OXYNITRILASE 3) >gi\_1262279

(U51562) (R)-(+)-mandelonitrile lyase isoform MDL $\overline{3}$  precursor [Prunus serotina] >gi\_2343181 (AF013161)

(R)-(+)-mandelonitrile lyase isoform MDL3 precursor [Prunus

serotina]

Seq. No. 30200

Contig ID 209640 1.R1040 5'-most EST kl1701205153.h1

Seq. No. 30201

Contig ID 209667\_1.R1040 5'-most EST jex700904771.h1

Method BLASTX
NCBI GI g4455171
BLAST score 751
E value 6.0e-80
Match length 196
% identity 66

NCBI Description (AL035521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30202

Contig ID 209683 1.R1040 5'-most EST leu701149039.h1

Seq. No. 30203

Contig ID 209717\_1.R1040 5'-most EST leu701153716.h1



BLASTX Method q2842496 NCBI GI 448 BLAST score 2.0e-44E value 121 Match length % identity 73

(ALO21749) NAM / CUC2 -like protein [Arabidopsis thaliana] NCBI Description

30204 Seq. No.

209723 1.R1040 Contig ID 5'-most EST jex700904868.hl

BLASTX Method q4415912 NCBI GI 148 BLAST score 8.0e-10 E value 85 Match length % identity

(AC006282) putative protease [Arabidopsis thaliana] NCBI Description

30205 Seq. No.

209745 1.R1040 Contig ID 5'-most EST gsv701051266.hl

BLASTX Method q4559320 NCBI GI 278 BLAST score 8.0e-25 E value 100 Match length 52 % identity

(AC007087) putative 50S ribosomal protein L1 [Arabidopsis NCBI Description

thaliana]

Seq. No. 30206

209767 1.R1040 Contig ID jex700904935.h1 5'-most EST

BLASTX Method g2114104 NCBI GI BLAST score 341 1.0e-64 E value 178 Match length 71 % identity

(AB003590) sulfate transporter [Arabidopsis thaliana] NCBI Description

>gi 2114106 dbj\_BAA20085\_ (AB003591) sulfate transporter

[Arabidopsis thaliana]

30207 Seq. No.

209780 1.R1040 Contig ID jex700905528.h1 5'-most EST

30208 Seq. No.

209808 1.R1040 Contig ID  $jex700\overline{9}04983.h1$ 5'-most EST

BLASTX Method g4008008 NCBI GI 251 BLAST score 2.0e-21 E value 93 Match length % identity 56



NCBI Description (AF084035) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 30209

Contig ID 209826\_1.R1040 5'-most EST jC-gmro02910010e04a1

Seq. No. 30210

Contig ID 209832\_1.R1040 5'-most EST jC-gmst02400044b04a1

Method BLASTX
NCBI GI g3885344
BLAST score 172
E value 4.0e-12
Match length 126
% identity 34

NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

>gi 4557057 gb\_AAD22497.1\_AC007154\_1 (AC007154) unknown

protein [Arabidopsis thaliana]

Seq. No. 30211

Contig ID 209864\_1.R1040 5'-most EST jex700905078.h1

Seq. No. 30212

Contig ID 209902\_1.R1040

5'-most EST jC-gmf102220099h10d1

Seq. No. 30213

Contig ID 209926\_1.R1040 5'-most EST fC-gmfl700906103a1

Seq. No. 30214

Contig ID 209939\_1.R1040

5'-most EST jC-gmro02910047b05a1

Method BLASTX
NCBI GI 94539335
BLAST score 375
E value 1.0e-35
Match length 249
% identity 35

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 30215

Contig ID 209939\_2.R1040

5'-most EST uC-gmrominsoy302e03b1

Method BLASTX
NCBI GI 94539335
BLAST score 243
E value 1.0e-20
Match length 137
% identity 39

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 30216

Contig ID 209949\_1.R1040 5'-most EST zhf700955913.h1

Match length

NCBI Description

% identity

108

thaliana]

61



```
BLASTX
Method
                   q3335359
NCBI GI
                   434
BLAST score
                   8.0e-43
E value
                   129
Match length
% identity
                   66
                  (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
                   30217
Seq. No.
                   209973 1.R1040
Contig ID
5'-most EST
                   jex700905225.hl
                   BLASTX
Method
                   g4454012
NCBI GI
                   481
BLAST score
                   3.0e-48
E value
                   142
Match length
                   63
% identity
                   (AL035396) Pollen-specific protein precursor like
NCBI Description
                   [Arabidopsis thaliana]
                   30218
Seq. No.
                   209997 1.R1040
Contig ID
                   jex700905268.h1
5'-most EST
                   BLASTX
Method
                   g3006088
NCBI GI
                   183
BLAST score
                   6.0e-14
E value
Match length
                   70
                   49
% identity
                   (AJ222724) SGT protein [Rattus norvegicus]
NCBI Description
                   30219
Seq. No.
                   210012 1.R1040
Contig ID
                   jex700905275.h1
5'-most EST
                    30220
Seq. No.
                    210014 1.R1040
Contig ID
                   uC-gmf\overline{l}minsoy012g09b1
5'-most EST
                    BLASTX
Method
                    g3402694
NCBI GI
BLAST score
                   566
E value
                    4.0e-58
Match length
                    218
 % identity
                    55
                   (AC004697) putative Mlo-hi protein [Arabidopsis thaliana]
NCBI Description
                    30221
 Seq. No.
                    210020 1.R1040
 Contig ID
                    fC-gmf1700903761a1
 5'-most EST
                    BLASTX
 Method
                    q4263791
 NCBI GI
                    306
 BLAST score
 E value
                    4.0e-30
```

4639

(AC006068) putative receptor protein kinase [Arabidopsis



```
30222
Seq. No.
                   210040 1.R1040
Contig ID
                   zhf700961857.hl
5'-most EST
                   BLASTX
Method
                   q3810593
NCBI GI
                   285
BLAST score
                   9.0e-26
E value
                   59
Match length
% identity
                   (AC005398) putative sucrose-proton symporter [Arabidopsis
NCBI Description
                   thaliana]
                   30223
Seq. No.
                   210095 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}05408.h1
                   30224
Seq. No.
                   210107 1.R1040
Contig ID
                   leu701144948.hl
5'-most EST
                   30225
Seq. No.
                   210163 1.R1040
Contig ID
                   jC-gmst02400041d08a1
5'-most EST
                   BLASTX
Method
                   g2864618
NCBI GI
                   424
BLAST score
                   9.0e-42
E value
                   123
Match length
% identity
                   (AL021811) putative protein [Arabidopsis thaliana]
NCBI Description
                   30226
Seq. No.
                   210169 1.R1040
Contig ID
                   jC-qmf102220108c12a1
5'-most EST
                    30227
Seq. No.
Contig ID
                    210206 1.R1040
                    jex700905582.hl
5'-most EST
                    BLASTX
Method
                    q4218122
NCBI GI
BLAST score
                    384
E value
                    7.0e-37
Match length
                    195
% identity
                   (AL035353) putative protein [Arabidopsis thaliana]
NCBI Description
                    30228
Seq. No.
                    210210 1.R1040
Contig ID
                    jex700\overline{9}05587.h1
 5'-most EST
                    BLASTX
Method
                    q4455171
NCBI GI
BLAST score
                    441
                    4.0e-44
E value
```

(AL035521) hypothetical protein [Arabidopsis thaliana]

96

77

Match length

NCBI Description

% identity



Contig ID 210222\_1.R1040

5'-most EST jC-gmfl02220140h03d1

Method BLASTX
NCBI GI g4510348
BLAST score 289
E value 7.0e-26
Match length 72
% identity 67

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 30230

Contig ID 210228\_1.R1040 5'-most EST jex700905613.h1

Seq. No. 30231

Contig ID 210245\_1.R1040 5'-most EST jex700905630.h1

Method BLASTX
NCBI GI g2367431
BLAST score 224
E value 1.0e-18
Match length 55
% identity 76

NCBI Description (AF000403) putative cytochrome P450 [Lotus japonicus]

Seq. No. 30232

Contig ID 210269\_1.R1040 5'-most EST fua701037858.h1

Seq. No. 30233

Contig ID 210283\_1.R1040 5'-most EST leu701147850.h1

Seq. No. 30234

Contig ID 210287\_1.R1040 5'-most EST jex700905693.h1

Method BLASTX
NCBI GI g927025
BLAST score 262
E value 2.0e-22
Match length 74
% identity 32

NCBI Description (L44134) SPF1-like DNA-binding protein [Cucumis sativus]

Seq. No. 30235

Contig ID 210327 1.R1040 5'-most EST kll701210291.h1

Seq. No. 30236

Contig ID 210398\_1.R1040 5'-most EST zhf700952832.h1

Seq. No. 30237

Contig ID 210432 1.R1040 5'-most EST pmv700888230.h1



Method BLASTN
NCBI GI g2924653
BLAST score 35
E value 2.0e-10
Match length 107
% identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDA7, complete sequence [Arabidopsis thaliana]

Seq. No. 30238

Contig ID 210537 1.R1040

5'-most EST uC-gmflminsoy061f12b1

Method BLASTX
NCBI GI g4467153
BLAST score 232
E value 3.0e-19
Match length 118
% identity 45

NCBI Description (AL035540) putative thaumatin-like protein [Arabidopsis

thaliana]

Seq. No. 30239

Contig ID 210570\_1.R1040 5'-most EST jex700906075.h1

Seq. No. 30240

Contig ID 210578\_1.R1040 5'-most EST epx701105248.h1

Method BLASTX
NCBI GI g1848214
BLAST score 298
E value 5.0e-27
Match length 66
% identity 80

NCBI Description (Y11210) uracil phosphoribosyltransferase [Nicotiana

tabacum]

Seq. No. 30241

Contig ID 210582\_1.R1040 5'-most EST jex700906094.h1

Seq. No. 30242

Contig ID 210636 1.R1040

5'-most EST g50578<del>6</del>9

Seq. No. 30243

Contig ID 210663 1.R1040 5'-most EST kl1701212062.h1

Seq. No. 30244

Contig ID 210678 1.R1040 5'-most EST jex700906255.h1

Seq. No. 30245

Contig ID 210697\_1.R1040 5'-most EST fC-gmro700564904d3

Method BLASTN



NCBI GI g1935018 BLAST score 150 E value 1.0e-78 Match length 408 % identity 88

NCBI Description V.faba mRNA for sucrose transporter

Seq. No. 30246

Contig ID 210710\_1.R1040 5'-most EST jC-gmst02400025d03a1

Method BLASTX
NCBI GI g2244840
BLAST score 253
E value 1.0e-21
Match length 116
% identity 47

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30247

Contig ID 210747\_1.R1040 5'-most EST jex700906370.h1

Seq. No. 30248

Contig ID 210764\_1.R1040 5'-most EST uC-gmronoir076f12b1

Method BLASTX
NCBI GI g2160144
BLAST score 252
E value 1.0e-21
Match length 128
% identity 42

NCBI Description (AC000375) Strong similarity to Arabidopsis oligopeptide

transporter (gb X77503). [Arabidopsis thaliana]

Seq. No. 30249

Contig ID 210765\_1.R1040 5'-most EST rlr700895313.h1

Method BLASTX
NCBI GI g2462931
BLAST score 359
E value 2.0e-34
Match length 89
% identity 71

NCBI Description (Z83833) UDP-glucose: sterol glucosyltransferase

[Arabidopsis thaliana]

Seq. No. 30250

Contig ID 210776\_1.R1040 5'-most EST jex700906414.h1

Seq. No. 30251

Contig ID 210786\_1.R1040 5'-most EST epx701108547.h1

Method BLASTX
NCBI GI g3114713
BLAST score 148
E value 1.0e-09



Match length 73 % identity 48

(AF061346) Edp1 protein [Mus musculus] NCBI Description

Seq. No. Contig ID

5'-most EST

30252 210813 1.R1040 leu701153394.h1

Seq. No.

30253

Contig ID 5'-most EST 210841 1.R1040 jex700906520.hl

Seq. No.

30254

210857 1.R1040 Contig ID 5'-most EST  $jex700\overline{9}06549.h1$ 

Seq. No. Contig ID 30255 210921 1.R1040 jex700906708.h1

5'-most EST Method BLASTX NCBI GI q3128477 BLAST score 270 3.0e-24E value Match length 81 % identity

NCBI Description

(AF062640) metalloproteinase [Arabidopsis thaliana]

Seq. No. 30256

210932 1.R1040 Contig ID

g5605826 5'-most EST

30257 Seq. No.

210933 1.R1040 Contig ID fC-gmf1700905073a1 5'-most EST

BLASTX Method g3641836 NCBI GI 405 BLAST score 2.0e-43 E value Match length 141 % identity 64

(AL023094) putative serine/threonine protein kinase NCBI Description

[Arabidopsis thaliana]

30258 Seq. No.

210943 1.R1040 Contig ID 5'-most EST uC-gmropic009e05b1

. 30259 Seq. No.

210949 1.R1040 Contig ID  $zhf700\overline{9}64978.h1$ 5'-most EST

Seq. No. 30260

Contig ID 210956 1.R1040  $jex700\overline{9}06761.h1$ 5'-most EST

Seq. No. 30261

210998\_1.R1040 Contig ID



```
leu701154452.h1
5'-most EST
Seq. No.
                   30262
Contig ID
                   211029 1.R1040
                   hrw701063013.h1
5'-most EST
                   30263
Seq. No.
                   211048 1.R1040
Contig ID
                   k11701\overline{2}08991.h1
5'-most EST
Method
                   BLASTX
                   g4455340
NCBI GI
BLAST score
                   249
                   1.0e-21
E value
Match length
                   94
% identity
                   (AL035522) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30264
                   211055 1.R1040
Contig ID
                   fC-qmf1700906939a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3915022
BLAST score
                   411
E value
                   3.0e-40
Match length
                   128
                   64
% identity
                   SUCROSE-PHOSPHATE SYNTHASE 2
NCBI Description
                   (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 2)
                   >gi 2190350_emb CAA72491 (Y11795) sucrose-phosphate
                   synthase [Craterostigma plantagineum]
Seq. No.
                   30265
                   211082 1.R1040
Contia ID
                   jex700907578.hl
5'-most EST
                   30266
Seq. No.
Contig ID
                   211091 1.R1040
                   dpv701\overline{1}01879.h1
5'-most EST
                   BLASTX
Method
                   g2245012
NCBI GI
                   304
BLAST score
                   8.0e-28
E value
Match length
                   75
                   76
% identity
                   (Z97341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   30267
Seq. No.
                   211094 1.R1040
Contig ID
                   jex700\overline{9}07013.h1
5'-most EST
                   BLASTX
Method
                   g3386611
NCBI GI
BLAST score
                   294
                   6.0e-27
E value
                   75
Match length
```

(AC004665) unknown protein [Arabidopsis thaliana]

63

% identity

NCBI Description



Contig ID 211141\_1.R1040 5'-most EST jex700907089.h1

Seq. No. 30269

Contig ID 211145\_1.R1040 5'-most EST jC-gmf102220081f09d1

Method BLASTX
NCBI GI g3335372
BLAST score 522
E value 6.0e-53
Match length 186
% identity 51

NCBI Description (AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No. 30270

Contig ID 211215\_1.R1040 5'-most EST fC-gmle700788247g2

Method BLASTX
NCBI GI g2651300
BLAST score 392
E value 1.0e-37
Match length 170
% identity 49

NCBI Description (AC002336) putative initiator tRNA

phosphoribosyl-transferase [Arabidopsis thaliana]

Seq. No. 30271

Contig ID 211237\_1.R1040 5'-most EST jex700907301.h1

Method BLASTX
NCBI GI g2244866
BLAST score 304
E value 5.0e-28
Match length 91
% identity 60

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30272

Contig ID 211278\_1.R1040 5'-most EST jex700907361.h1

Seq. No. 30273

Contig ID 211281 1.R1040 5'-most EST jex700907666.h1

Seq. No. 30274

Contig ID 211282\_1.R1040 5'-most EST jex700907564.h1

Seq. No. 30275

Contig ID 211319\_1.R1040 5'-most EST asn701141526.h1

Seq. No. 30276

Contig ID 211326\_1.R1040 5'-most EST epx701109165.h1



Method BLASTX

NCBI GI g2126113

BLAST score 169

E value 1.0e-11

Match length 116
% identity 36

NCBI Description prolyl aminopeptidase (EC 3.4.11.5) - Hafnia alvei

prolyl aminopeptidase (EC 3.4.11.5) - Hafnia alvei

prolyl aminopeptidase (EC 3.4.11.5) - Hafnia alvei

>gi\_1754489\_dbj\_BAA09605\_ (D61383) prolyl aminopeptidase [Hafnia alvei] >gi\_1588323\_prf\_\_2208340A Pro aminopeptidase [Hafnia alvei]

Seq. No. 30277

Contig ID 211346\_1.R1040 5'-most EST leu701148125.h1

Seq. No. 30278

Contig ID 211382\_1.R1040 5'-most EST kl1701209577.h1

Method BLASTX
NCBI GI 94006915
BLAST score 332
E value 3.0e-31
Match length 107
% identity 61

NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30279

Contig ID 211394\_1.R1040 5'-most EST jex700907530.h1

Method BLASTX
NCBI GI g2781433
BLAST score 246
E value 7.0e-21
Match length 131
% identity 40

NCBI Description (AF030052) RSW1-like cellulose synthase catalytic subunit

[Oryza sativa subsp. japonica]

Seq. No. 30280

Contig ID 211399 1.R1040

5'-most EST jC-gmst02400076g02a1

Method BLASTX
NCBI GI g4115379
BLAST score 277
E value 2.0e-24
Match length 123
% identity 54

NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis

thaliana]

30281

Seq. No.

Contig ID 211442 1.R1040 5'-most EST zsg701118392.h1

Method BLASTX
NCBI GI g2911067
BLAST score 585
E value 1.0e-60



```
Match length
                    137
% identity
                    81
                    (AL021960) UV-damaged DNA-binding protein- like
NCBI Description
                    [Arabidopsis thaliana]
                    30282
Seq. No.
                    211471 1.R1040
Contig ID
                    leu701\overline{1}52212.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g1931652
BLAST score
                    221
                    9.0e-18
E value
```

18 % identity (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog NCBI Description [Arabidopsis thaliana]

Seq. No. 30283 211583 1.R1040 Contig ID 5'-most EST epx701106685.hl

188

Seq. No. 30284 Contig ID 211591 1.R1040 leu701145967.h1 5'-most EST

Method BLASTX NCBI GI g2642157 BLAST score 201 3.0e-19E value Match length 69 % identity 70

Match length

(AC003000) ankyrin-like protein [Arabidopsis thaliana] NCBI Description

30285 Seq. No. 211626 1.R1040 Contig ID fC-gmro700876145d1 5'-most EST BLASTN Method g1089903 NCBI GI 56 BLAST score

1.0e-22 E value Match length 128 86 % identity

P.sativum mRNA for carboxypeptidase NCBI Description

30286 Seq. No.

211644 1.R1040 Contig ID 5'-most EST zhf700963153.h1

Method BLASTX g2655008 NCBI GI 600 BLAST score E value 3.0e-62 Match length 186 % identity 55

(AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon NCBI Description

esculentum]

Seq. No. 30287

211656\_1.R1040 Contig ID



NCBI Description Vigna radiata auxin-regulated mRNA

Seq. No. 30288

Contig ID 211715\_1.R1040 5'-most EST jex700908106.h1

Seq. No. 30289

Contig ID 211732\_1.R1040 5'-most EST leu701149360.h1

Method BLASTX
NCBI GI g4559368
BLAST score 213
E value 2.0e-17
Match length 58
% identity 72

NCBI Description (AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30290

Contig ID 211817\_1.R1040 5'-most EST asn701133909.h2

Method BLASTN
NCBI GI g2351065
BLAST score 34
E value 2.0e-09
Match length 82
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MHF15, complete sequence [Arabidopsis thaliana]

Seq. No. 30291

Contig ID 211924\_1.R1040 5'-most EST leu701150702.h1

Method BLASTX
NCBI GI g4218120
BLAST score 167
E value 6.0e-12
Match length 43
% identity 77

NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis

thaliana]

Seq. No. 30292

Contig ID 211929\_1.R1040 5'-most EST gsv701044336.h1

Method BLASTX
NCBI GI g3877205
BLAST score 286
E value 2.0e-25
Match length 112
% identity 45

4649



```
(270780) similar to lipase [Caenorhabditis elegans]
NCBI Description
                   30293
Seq. No.
                   211941 1.R1040
Contig ID
                   jex700908407.h1
5'-most EST
                   BLASTX
Method
                   g2642450
NCBI GI
BLAST score
                   608
                   2.0e-63
E value
                   140
Match length
                   81
% identity
                   (AC002391) putative metal ion transporter (Nramp)
NCBI Description
                   [Arabidopsis thaliana] >gi_3169188 (AC004401) putative
                   metal ion transporter (Nramp) [Arabidopsis thaliana]
                   30294
Seq. No.
                   211956 1.R1040
Contig ID
                   zhf700\overline{9}54347.h1
5'-most EST
                   30295
Seq. No.
                   211976 1.R1040
Contig ID
                   fC-gmf1700909836a1
5'-most EST
                   BLASTX
Method
                   g3024387
NCBI GI
BLAST score
                   544
                   8.0e-56
E value
                   148
Match length
% identity
                   67
                   POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi 668998
NCBI Description
                   (U20431) polygalacturonase [Medicago sativa]
                   30296
Seq. No.
                   211990 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}08496.h1
                   30297
Seq. No.
                   211994_1.R1040
Contig ID
                   jC-gmle01810035f10d1
5'-most EST
                   30298
Seq. No.
                   212002 1.R1040
Contig ID
                   jex700\overline{9}08480.h1
5'-most EST
                   30299
Seq. No.
Contig ID
                   212045 1.R1040
                   jex700\overline{9}08548.h1
5'-most EST
Method
                   BLASTX
                   q4512263
NCBI GI
BLAST score
                    191
                    1.0e-21
E value
Match length
                    74
                   78
% identity
```

Contig ID 212057 1.R1040

5'-most EST uC-gmflminsoy017h03b1

NCBI Description (AB018526) H+/Ca2+ exchanger 2 [Ipomoea nil]



Method BLASTX
NCBI GI 94093155
BLAST score 165
E value 1.0e-11
Match length 103
% identity 36

NCBI Description (AF088281) phytochrome-associated protein 1 [Arabidopsis

thaliana]

Seq. No. 30301

Contig ID 212062\_1.R1040 5'-most EST pmv700892882.h1

Method BLASTX
NCBI GI g477430
BLAST score 438
E value 1.0e-43
Match length 103
% identity 82

NCBI Description nucleolar protein p120 - mouse (fragment)

Seq. No. 30302

Contig ID 212068\_1.R1040 5'-most EST gsv701056516.h1

Seq. No.

Contig ID 212077\_1.R1040 5'-most EST gsv701046554.h1

30303

Method BLASTX
NCBI GI g3335347
BLAST score 613
E value 1.0e-63
Match length 214
% identity 55

NCBI Description (AC004512) Contains similarity to ARI, RING finger protein

gb\_X98309 from Drosophila melanogaster. ESTs gb\_T44383, gb\_W43120, gb\_N65868, gb\_H36013, gb\_AA042241, gb\_T76869 and gb\_AA042359 come from this gene. [Arabidopsis thaliana]

Seq. No. 30304

Contig ID 212083 1.R1040 5'-most EST epx701109802.h1

Method BLASTX
NCBI GI g3298502
BLAST score 414
E value 2.0e-40
Match length 157
% identity 53

NCBI Description (AB015046) xylulokinase [Homo sapiens]

Seq. No. 30305

Contig ID 212094\_1.R1040 5'-most EST crh700855625.h1

Seq. No. 30306

Contig ID 212096\_1.R1040 5'-most EST jex700908622.h1

Method BLASTX



```
NCBI GI g1345643
BLAST score 419
E value 5.0e-49
Match length 138
% identity 74
```

NCBI Description FLAVONOID 3',5'-HYDROXYLASE 2 (F3'5'H) (CYTOCHROME P450

75A3) (CYPLXXVA3) >gi\_629709\_pir\_\_S38984 flavonoid 3',5'-hydroxylase Hf2 - garden petunia >gi\_311654\_emb\_CAA80265\_ (Z22544) flavonoid

3',5'-hydroxylase [Petunia x hybrida] >gi 738771 prf 2001426A flavonoid 3',5'-hydroxylase

[Petunia x hybrida]

 Seq. No.
 30307

 Contig ID
 212108\_1.R1040

 5'-most EST
 pxt700944644.h1

 Method
 BLASTX

 NCBI GI
 g1871193

 BLAST score
 424

BLAST score 424 E value 1.0e-42 Match length 163 % identity 52

NCBI Description (U90439) receptor-like protein kinase isolog [Arabidopsis

thaliana] >gi\_2335090 (AC002339) putative receptor-like

protein kinase [Arabidopsis thaliana]

Seq. No. 30308

Contig ID 212118\_1.R1040 5'-most EST jex700908656.h1

Seq. No. 30309

Contig ID 212134 1.R1040 5'-most EST zhf700954902.h1

Seq. No.

Contig ID 212181\_1.R1040 5'-most EST jex700909274.h1

30310

Method BLASTX
NCBI GI g3687230
BLAST score 637
E value 1.0e-66
Match length 163
% identity 70

NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30311

Contig ID 212187\_1.R1040

5'-most EST g5510128
Method BLASTX
NCBI GI g4530126
BLAST score 227
E value 1.0e-18
Match length 90
% identity 51

NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1

[Phaseolus vulgaris]



Seq. No. 30312 Contig ID 21219

Contig ID 212193\_1.R1040 5'-most EST jex700908757.h1

Seq. No. 30313

Contig ID 212197\_1.R1040 5'-most EST dpv701098985.h1

Seq. No. 30314

Contig ID 212218\_1.R1040

5'-most EST uC-gmflminsoy061b07b1

Method BLASTX
NCBI GI g4567279
BLAST score 194
E value 6.0e-15
Match length 95
% identity 45

NCBI Description (AC006841) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 30315

Contig ID 212225\_1.R1040 5'-most EST uC-gmronoir011a01b1

Seq. No. 30316

Contig ID 212250\_1.R1040 5'-most EST jex700908836.h1

Seq. No. 30317

Contig ID 212251\_1.R1040 5'-most EST jex700908845.h1

Seq. No.

Contig ID 212253\_1.R1040 5'-most EST jex700908848.h1

30318

Method BLASTX
NCBI GI g2738248
BLAST score 405
E value 6.0e-40
Match length 89
% identity 88

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 30319

Contig ID 212285\_1.R1040 5'-most EST uC-gmropic016d09b1

Seq. No. 30320

Contig ID 212311\_1.R1040 5'-most EST jex700908934.h1

Method BLASTX
NCBI GI g3377517
BLAST score 201
E value 2.0e-15
Match length 52
% identity 62

4653



NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No. 30321

Contig ID 212315 1.R1040

5'-most EST uC-gmrominsoy220g05b1

Seq. No. 30322

Contig ID 212323\_1.R1040 5'-most EST jex700908953.h1

Method BLASTX
NCBI GI g4105698
BLAST score 171
E value 2.0e-12
Match length 66
% identity 52

NCBI Description (AF049870) small hydrophobic protein [Arabidopsis thaliana]

Seq. No. 30323

Contig ID 212331\_1.R1040 5'-most EST kl1701214360.h1

Method BLASTX
NCBI GI g4522012
BLAST score 546
E value 8.0e-56
Match length 185
% identity 57

NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30324

Contig ID 212379\_1.R1040

5'-most EST uC-gmrominsoy158a10b1

Seq. No. 30325

Contig ID 212408\_1.R1040 5'-most EST fC-gmse700755370a2

Seq. No. 30326

Contig ID 212416\_1.R1040 5'-most EST jC-gmro02910013e12a1

Method BLASTX
NCBI GI g2252472
BLAST score 813
E value 3.0e-87
Match length 182
% identity 85

NCBI Description (Z97558) argininosuccinate lyase [Arabidopsis thaliana]

Seq. No. 30327

Contig ID 212437\_1.R1040 5'-most EST gsv701056350.h1

Method BLASTX
NCBI GI g1076580
BLAST score 223
E value 3.0e-18
Match length 75
% identity 56

NCBI Description alcohol dehydrogenase homolog ADH3b - tomato



>gi\_913446\_bbs\_160508 (S75487) alcohol dehydrogenase ADH
{EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red
cherry, Peptide, 390 aa] [Lycopersicon esculentum]

Seq. No. 30328 Contig ID 212442\_1.R1040 5'-most EST jex700909113.h1

Method BLASTX
NCBI GI g464900
BLAST score 497
E value 4.0e-50
Match length 127
% identity 73

NCBI Description PUTATIVE KINASE-LIKE PROTEIN TMKL1 PRECURSOR

>gi\_539008\_pir\_\_S39476 kinase-like transmembrane protein

TMKL1 precursor - Arabidopsis thaliana

>gi\_313190\_emb\_CAA51385\_ (X72863) TMKL1 [Arabidopsis

thaliana]

Seq. No. 30329

Contig ID 212458\_1.R1040 5'-most EST leu701145458.h1

Method BLASTN
NCBI GI 9429107
BLAST score 126
E value 2.0e-64
Match length 326
% identity 85

NCBI Description L.esculentum S-adenosyl-L-methionine synthetase mRNA,

complete CDS

Seq. No. 30330

Contig ID 212460\_1.R1040 5'-most EST zhf700960731.h1

Seq. No. 30331

Contig ID 212461\_1.R1040

5'-most EST g5607028

Seq. No. 30332

Contig ID 212464\_1.R1040 5'-most EST zsg701126409.h1

Method BLASTX
NCBI GI g4530126
BLAST score 153
E value 8.0e-10
Match length 155
% identity 28

NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1

[Phaseolus vulgaris]

Seq. No. 30333

Contig ID 212530\_1.R1040 5'-most EST zhf700963094.h1

Method BLASTX
NCBI GI g2739370
BLAST score 334



E value 2.0e-31 Match length 112 % identity 56

NCBI Description (AC002505) putative pectinesterase [Arabidopsis thaliana]

Seq. No. 30334

Contig ID 212541\_1.R1040 5'-most EST zhf700958684.h1

Seq. No. 30335

Contig ID 212544\_1.R1040 5'-most EST zsg701125485.h1

Seq. No. 30336

Contig ID 212555\_1.R1040 5'-most EST jex700909294.h1

Method BLASTN
NCBI GI g2656030
BLAST score 33
E value 4.0e-09
Match length 65
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUL8

Seq. No. 30337

Contig ID 212564\_1.R1040 5'-most EST gsv701056257.h1

Seq. No. 30338

Contig ID 212567\_1.R1040 5'-most EST jex700909318.h1

Seq. No. 30339

Contig ID 212569\_1.R1040 5'-most EST jex700909321.h1

Method BLASTN
NCBI GI g2293111
BLAST score 207
E value 1.0e-113
Match length 378
% identity 89

NCBI Description V.faba mRNA for potassium channel

Seq. No. 30340

Contig ID 212575\_1.R1040 5'-most EST jex700909329.h1

Seq. No. 30341

Contig ID 212585\_1.R1040 5'-most EST fC-gmfl700909057a1

Method BLASTX
NCBI GI g2829204
BLAST score 208
E value 3.0e-16
Match length 81
% identity 47

4656



NCBI Description (AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No. 30342

Contig ID 212592\_1.R1040 5'-most EST jex700909349.h1

Method BLASTX
NCBI GI g3193298
BLAST score 178
E value 7.0e-13
Match length 113
% identity 33

NCBI Description (AF069298) T14P8.17 gene product [Arabidopsis thaliana]

Seq. No. 30343

Contig ID 212605\_1.R1040 5'-most EST epx701108145.h1

Seq. No. 30344

Contig ID 212636\_1.R1040 5'-most EST jex700909421.h1

Method BLASTX
NCBI GI g4455316
BLAST score 278
E value 1.0e-24
Match length 76
% identity 70

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 30345

Contig ID 212657\_1.R1040 5'-most EST jex700909449.h1

Seq. No. 30346

Contig ID 212685\_1.R1040 5'-most EST hrw701057006.h2

Method BLASTX
NCBI GI g3643604
BLAST score 211
E value 5.0e-17
Match length 102
% identity 43

NCBI Description (AC005395) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 30347

Contig ID 212711\_1.R1040 5'-most EST jex700909530.h1

Method BLASTN
NCBI GI 9460088
BLAST score 52
E value 2.0e-20
Match length 72
% identity 93

NCBI Description Arabidopsis thaliana Columbia ecotype gl-tubulin (TUBG1)

gene, complete cds



Contig ID 212719\_1.R1040 5'-most EST jex700909543.h1

Method BLASTX
NCBI GI g3249065
BLAST score 396
E value 2.0e-44
Match length 181
% identity 63

NCBI Description (AC004473) Similar to HAK1 gb\_U22945 high affinity

potassium transporter from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 30349

Contig ID 212733\_1.R1040 5'-most EST jC-gmf102220141g10a1

Seq. No. 30350

Contig ID 212734\_1.R1040 5'-most EST kl1701213345.h1

Method BLASTX
NCBI GI g3212867
BLAST score 272
E value 4.0e-24
Match length 110
% identity 50

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 30351

Contig ID 212749\_1.R1040 5'-most EST jex700909579.h1

Seq. No. 30352

Contig ID 212766\_1.R1040 5'-most EST zhf700955870.h1

Seq. No. 30353

Contig ID 212838\_1.R1040 5'-most EST fC-gmfl700906093h1

Method BLASTX
NCBI GI g2388565
BLAST score 163
E value 6.0e-11
Match length 71
% identity 42

NCBI Description (AC000098) Similar to Prunus pectinesterase (gb\_X95991).

[Arabidopsis thaliana]

Seq. No. 30354

Contig ID 212845 1.R1040 5'-most EST zhf700963860.h1

Method BLASTN
NCBI GI g3702728
BLAST score 46
E value 2.0e-16
Match length 289
% identity 84



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]

Seq. No. 30355

212859 1.R1040 Contig ID fC-gmf1700910054a1 5'-most EST

30356 Seq. No.

212879 1.R1040 Contig ID zhf700955947.hl 5'-most EST

BLASTX Method g3608134 NCBI GI BLAST score 243 8.0e-21 E value Match length 88 % identity 57

(AC005314) dnaJ-like protein [Arabidopsis thaliana] NCBI Description

30357 Seq. No.

212882 1.R1040 Contig ID  $jex700\overline{9}09781.h1$ 5'-most EST

Method BLASTN g18680 NCBI GI BLAST score 130 4.0e-67 E value Match length 247 % identity 88

NCBI Description G.max mRNA for mitotic cyclin (S13-7)

30358 Seq. No.

212893 1.R1040 Contig ID jC-qmf102220065f08a1 5'-most EST

BLASTX Method g1495802 NCBI GI BLAST score 638 1.0e-66 E value 199 Match length % identity 61

(X96405) 13-lipoxygenase [Solanum tuberosum] NCBI Description

Seq. No.

30359 212893 2.R1040 Contig ID  $jex700\overline{9}09795.h1$ 5'-most EST

BLASTX Method g1495802 NCBI GI BLAST score 511 6.0e-52 E value 129 Match length 71 % identity

(X96405) 13-lipoxygenase [Solanum tuberosum] NCBI Description

Seq. No. 30360

212932 1.R1040 Contig ID jC-gmf102220065f12d1 5'-most EST

BLASTX Method NCBI GI g2827548

BLAST score 403



E value 3.0e-39
Match length 112
% identity 65

NCBI Description (AL021635) cytochrome P450 - like protein [Arabidopsis

thaliana]

Seq. No. 30361

Contig ID 212943 1.R1040 5'-most EST jex700909885.h1

Seq. No. 30362

Contig ID 212989\_1.R1040 5'-most EST epx701105703.h1

Seq. No. 30363

Contig ID 213002 1.R1040 5'-most EST jex700909975.h1

Seq. No. 30364

Contig ID 213016\_1.R1040 5'-most EST jex700910001.h1

Seq. No. 30365

Contig ID 213020\_1.R1040 5'-most EST fC-qmf1700907612a1

Method BLASTX
NCBI GI g3928519
BLAST score 239
E value 5.0e-23
Match length 119
% identity 49

NCBI Description (AB011670) wpk4 protein kinase [Triticum aestivum]

Seq. No. 30366

Contig ID 213029\_1.R1040 5'-most EST hrw701059588.h1

Method BLASTN
NCBI GI g4567193
BLAST score 98
E value 1.0e-47
Match length 434
% identity 81

NCBI Description Arabidopsis thaliana chromosome II BAC T26C19 genomic

sequence, complete sequence

Seq. No. 30367

Contig ID 213043\_1.R1040 5'-most EST zhf700952854.h1

Method BLASTX
NCBI GI g2598575
BLAST score 436
E value 3.0e-43
Match length 106
% identity 81

NCBI Description (Y15293) MtN21 [Medicago truncatula]

Seq. No. 30368



Contig ID 213051\_1.R1040 5'-most EST jex700910053.h1

Method BLASTX
NCBI GI g3367576
BLAST score 246
E value 2.0e-22
Match length 122
% identity 43

NCBI Description (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No. 30369

Contig ID 213072 1.R1040 5'-most EST kl1701209063.h1

Seq. No. 30370

Contig ID 213081\_1.R1040 5'-most EST gsv701054104.h1

Method BLASTX
NCBI GI g3157945
BLAST score 280
E value 7.0e-25
Match length 111
% identity 41

NCBI Description (AC002131) Contains similarity to axi 1 gene gb\_X80301 from

Nicotiana tabacum. [Arabidopsis thaliana]

Seq. No. 30371

Contig ID 213082\_1.R1040 5'-most EST fC-gmfl700907613a1

Method BLASTX
NCBI GI g1351945
BLAST score 691
E value 9.0e-73
Match length 186
% identity 56

NCBI Description FLORAL HOMEOTIC PROTEIN APETALA2 >gi\_533709 (U12546)

APETALA2 protein [Arabidopsis thaliana]

>gi 2464888 emb CAB16765 (Z99707) APETALA2 protein

[Arabidopsis thaliana]

Seq. No. 30372

Contig ID 213091\_1.R1040 5'-most EST zhf700962041.h1

Method BLASTX
NCBI GI g1237086
BLAST score 299
E value 2.0e-27
Match length 109
% identity 59

NCBI Description (X96766) ADP-glucose pyrophosphorylase [Pisum sativum]

Seq. No. 30373

Contig ID 213147\_1.R1040

5'-most EST jC-gmfl02220056c12a1

Seq. No. 30374

Contig ID 213150 1.R1040



5'-most EST zhf700951787.h1

Method BLASTX
NCBI GI g2246458
BLAST score 165
E value 2.0e-11
Match length 41
% identity 76

NCBI Description (U81313) S-adenosyl-methionine-sterol-C- methyltransferase

[Ricinus communis]

Seq. No. 30375

Contig ID 213150\_2.R1040 5'-most EST jC-gmle01810004e10a1

Method BLASTN
NCBI GI g1399379
BLAST score 108
E value 1.0e-53
Match length 268
% identity 85

NCBI Description Glycine max S-adenosyl-L-methionine:delta24-sterol-C-

methyltransferase mRNA, complete cds

Seq. No. 30376

Contig ID 213155\_1.R1040 5'-most EST zhf700951794.h1

Seq. No. 30377

Contig ID 213203\_1.R1040 5'-most EST zhf700962818.h1

Seq. No. 30378

Contig ID 213233 1.R1040 5'-most EST zhf700951901.h1

Method BLASTX
NCBI GI g3335350
BLAST score 122
E value 3.0e-14
Match length 84
% identity 51

NCBI Description (AC004512) Similar to gb\_Z84386 anthranilate

N-hydroxycinnamoyl/benzoyltransferase from Dianthus

caryophyllus. [Arabidopsis thaliana]

Seq. No. 30379

Contig ID 213290\_1.R1040 5'-most EST leu701154862.h1

Seq. No. 30380

Contig ID 213302\_1.R1040

5'-most EST jC-gmro02910016b06a1

Seq. No. 30381

Contig ID 213338\_1.R1040 5'-most EST zhf700952049.h1

Seq. No. 30382

Contig ID 213339\_1.R1040



5'-most EST zhf700952050.h1

Seq. No. 30383

Contig ID 213345\_1.R1040 5'-most EST zhf700952057.h1

Method BLASTX
NCBI GI g2583128
BLAST score 142
E value 9.0e-09
Match length 75
% identity 40

NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30384

Contig ID 213412\_1.R1040 5'-most EST zhf700952138.h1

Method BLASTX
NCBI GI g2384675
BLAST score 168
E value 7.0e-12
Match length 65
% identity 54

NCBI Description (AF012659) putative potassium transporter AtKT4p

[Arabidopsis thaliana]

Seq. No. 30385

Contig ID 213419\_1.R1040

5'-most EST jC-gmf102220115c03a1

Seq. No. 30386

Contig ID 213439 1.R1040 5'-most EST fua701042188.h1

Seq. No. 30387

Contig ID 213476\_1.R1040 5'-most EST pxt700944312.h1

Method BLASTX
NCBI GI g3121917
BLAST score 193
E value 6.0e-15
Match length 99
% identity 27

NCBI Description COCKAYNE SYNDROME WD-REPEAT PROTEIN CSA

>gi 1362773 pir A57090 CSA protein - human >gi\_975302

(U28413) CSA protein [Homo sapiens]

>gi\_4557467\_ref\_NP\_000073.1\_pCKN1\_ Cockayne syndrome 1

protein

Seq. No. 30388

Contig ID 213503\_1.R1040 5'-most EST zhf700962122.h1

Seq. No. 30389

Contig ID 213505 1.R1040 5'-most EST zhf700952252.h1

Seq. No. 30390



Contig ID 213519\_1.R1040 5'-most EST zhf700952272.h1

Method BLASTX
NCBI GI g2623248
BLAST score 264
E value 3.0e-25
Match length 93
% identity 68

NCBI Description (AF030882) SU1 isoamylase [Zea mays]

Seq. No. 30391

Contig ID 213533 1.R1040

5'-most EST uC-gmflminsoy058f04b1

Seq. No. 30392

Contig ID 213537\_1.R1040 5'-most EST zhf700952301.h1

Method BLASTX
NCBI GI g1351945
BLAST score 177
E value 3.0e-22
Match length 107
% identity 59

NCBI Description FLORAL HOMEOTIC PROTEIN APETALA2 >gi\_533709 (U12546)

APETALA2 protein [Arabidopsis thaliana]

>gi\_2464888\_emb\_CAB16765\_ (Z99707) APETALA2 protein

[Arabidopsis thaliana]

Seq. No. 30393

Contig ID 213598\_1.R1040 5'-most EST zhf700952364.h1

Method BLASTN
NCBI GI g2330650
BLAST score 49
E value 2.0e-18
Match length 205
% identity 90

NCBI Description Pisum sativum mRNA for topoisomerase II

Seq. No. 30394

Contig ID 213627\_1.R1040 5'-most EST zhf700952402.h1

Seq. No. 30395

Contig ID 213640\_1.R1040

5'-most EST g4313837
Method BLASTX
NCBI GI g3738297
BLAST score 487
E value 2.0e-49
Match length 111
% identity 31

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 30396

Contig ID 213655\_1.R1040 5'-most EST fua701037671.h1



Seq. No. 30397 Contig ID 213661\_1.R1040

5'-most EST g5606683

Seq. No. 30398

Contig ID 213669\_1.R1040

5'-most EST uC-gmflminsoy120h06b1

Seq. No. 30399

Contig ID 213679\_1.R1040 5'-most EST gsv701043845.h1

Seq. No. 30400

Contig ID 213700\_1.R1040 5'-most EST gsv701053917.h1

Seq. No. 30401

Contig ID 213709 1.R1040

5'-most EST uC-gmflminsoy023f05b1

Seq. No. 30402

Contig ID 213721 1.R1040 5'-most EST zhf700952524.h1

Method BLASTX
NCBI GI g2443881
BLAST score 243
E value 2.0e-20
Match length 181
% identity 41

NCBI Description (AC002294) contains beta-transducin motif [Arabidopsis

thaliana]

Seq. No. 30403

Contig ID 213724\_1.R1040 5'-most EST uC-gmropic011c08b1

Seq. No. 30404

Contig ID 213734\_1.R1040 5'-most EST zhf700952545.h1

Seq. No. 30405

Contig ID 213770\_1.R1040 5'-most EST leu701154568.h1

Method BLASTX
NCBI GI g3413322
BLAST score 501
E value 1.0e-50
Match length 161
% identity 61

NCBI Description (Y11118) polygalacturonase [Medicago sativa]

Seq. No. 30406

Contig ID 213789 1.R1040 5'-most EST dpv701097122.h1

Method BLASTX NCBI GI g4468813



BLAST score 358
E value 3.0e-34
Match length 81
% identity 73

NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 30407

Contig ID 213790\_1.R1040 5'-most EST zhf700952630.h1

Seq. No. 30408

Contig ID 213814\_1.R1040 5'-most EST zhf700952674.h1

Method BLASTX
NCBI GI g2281330
BLAST score 333
E value 3.0e-31
Match length 108
% identity 57

NCBI Description (U85646) putative pectate lyase Nt59 [Nicotiana tabacum]

Seq. No. 30409

Contig ID 213850\_1.R1040

5'-most EST jC-gmf102220061a06a1

Seq. No. 30410

Contig ID 213873\_1.R1040 5'-most EST zhf700952757.h1

Seq. No. 30411

Contig ID 213958\_1.R1040 5'-most EST uC-gmropic098d04b1

Method BLASTX
NCBI GI g4138137
BLAST score 452
E value 6.0e-45
Match length 108
% identity 78

NCBI Description (AJ012796) ss-galactosidase [Lycopersicon esculentum]

Seq. No. 30412

Contig ID 213963\_1.R1040

5'-most EST jC-gmf102220081h02d1

Seq. No. 30413

Contig ID 213977\_1.R1040

5'-most EST jC-gmf102220138g05d1

Seq. No. 30414

Contig ID 213988 1.R1040 5'-most EST dpv701099482.h1

Seq. No. 30415

Contig ID 214016\_1.R1040

5'-most EST uC-gmrominsoy053b01b1

Method BLASTX NCBI GI g3928097

4666



BLAST score 211 E value 1.0e-22 Match length 140 % identity 43

NCBI Description (AC005770) unknown protein, 5' partial [Arabidopsis

thaliana]

Seq. No. 30416

Contig ID 214017\_1.R1040 5'-most EST zhf700963236.h1

Seq. No. 30417

Contig ID 214022\_1.R1040 5'-most EST gsv701055630.h1

Seq. No. 30418

Contig ID 214035\_1.R1040

5'-most EST uC-gmflminsoy017f01b1

Seq. No. 30419

Contig ID 214057\_1.R1040 5'-most EST zhf700953006.h1

Method BLASTX
NCBI GI g2245070
BLAST score 150
E value 2.0e-09
Match length 167
% identity 28

NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30420

Contig ID 214099 1.R1040 5'-most EST zhf700953069.h1

Method BLASTX
NCBI GI g3075382
BLAST score 320
E value 6.0e-30
Match length 82
% identity 77

NCBI Description (AC002505) putative peroxisome assembly protein PER8 [Arabidopsis thaliana] >gi\_3075384 (AC004484) putative

peroxisome assembly protein PER8 [Arabidopsis thaliana]

Seq. No. 30421

Contig ID 214157\_1.R1040 5'-most EST uC-gmronoir009al1b1

Seq. No. 30422

Contig ID 214160\_1.R1040 5'-most EST zhf700964709.h1

Method BLASTX
NCBI GI g3415115
BLAST score 542
E value 1.0e-55
Match length 131
% identity 39

NCBI Description (AF081202) villin 2 [Arabidopsis thaliana]



Contig ID 214172\_1.R1040 5'-most EST uC-gmronoir071g02b1

Method BLASTX
NCBI GI g2911058
BLAST score 317
E value 8.0e-29
Match length 145
% identity 42

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 30424

Contig ID 214210\_1.R1040 5'-most EST epx701103943.h1

Method BLASTX
NCBI GI g3980401
BLAST score 189
E value 1.0e-20
Match length 78
% identity 55

NCBI Description (AC004561) putative tropinone reductase [Arabidopsis

thaliana]

Seq. No. 30425

Contig ID 214227\_1.R1040 5'-most EST uC-gmropic042a01b1

Seq. No. 30426

Contig ID 214227\_2.R1040 5'-most EST kl1701206481.h1

Seq. No. 30427

Contig ID 214229\_1.R1040 5'-most EST zhf700953234.h1

Seq. No. 30428

Contig ID 214259 1.R1040

5'-most EST jC-gmst02400076e02a1

Method BLASTX
NCBI GI g3201624
BLAST score 220
E value 1.0e-17
Match length 124
% identity 56

NCBI Description (AC004669) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30429

Contig ID 214261 1.R1040

5'-most EST uC-gmflminsoy020b01b1

Seq. No. 30430

Contig ID 214263 1.R1040 5'-most EST zhf700953279.h1

Seq. No. 30431

Contig ID 214278\_1.R1040

4668



```
zhf700953302.h1
5'-most EST
Seq. No.
                  30432
Contig ID
                   214281 1.R1040
                   jC-gmle01810015g10d1
5'-most EST
Method
                  BLASTX
                   q4432846
NCBI GI
BLAST score
                   201
                   1.0e-15
E value
Match length
                   70
% identity
                   57
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   30433
Seq. No.
                   214299 1.R1040
Contig ID
5'-most EST
                   crh700852282.hl
Method
                   BLASTX
NCBI GI
                   g2982431
BLAST score
                   176
                   8.0e-13
E value
                   81
Match length
% identity
                   47
                   (AL022224) leucine rich repeat-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   30434
Seq. No.
                   214336 1.R1040
Contig ID
5'-most EST
                   zhf700953372.h1
                   30435
Seq. No.
                   214346 1.R1040
Contig ID
                   zhf700953382.h1
5'-most EST
                   30436
Seq. No.
                   214359 1.R1040
Contig ID
                   jC-gmf\overline{1}02220058e01a1
5'-most EST
                   30437
Seq. No.
                   214364 1.R1040
Contig ID
5'-most EST
                   g5753099
                   BLASTX
Method
                   g3193293
NCBI GI
                   386
BLAST score
                   3.0e-37
E value
                   150
Match length
                   56
% identity
                   (AF069298) contains a short region of similarity to another
NCBI Description
                   Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)
                   [Arabidopsis thaliana]
                   30438
Seq. No.
                   214388 1.R1040
Contig ID
                   jC-gmle01810082f04a1
5'-most EST
                   BLASTX
Method
```

Method BLASTX
NCBI GI g4325282
BLAST score 386
E value 2.0e-37



Match length 119 % identity 66

NCBI Description (AF123310) NAC domain protein NAM [Arabidopsis thaliana]

>gi\_4325286\_gb\_AAD17314\_ (AF123311) NAC domain protein NAM

[Arabidopsis thaliana]

Seq. No. 30439

Contig ID 214437\_1.R1040

5'-most EST jC-gmfl02220082f01d1

Seq. No. 30440

Contig ID 214437\_2.R1040

5'-most EST jC-gmf102220082g02a1

Seq. No. 30441

Contig ID 214453\_1.R1040 5'-most EST zhf700953514.h1

Seq. No. 30442

Contig ID 214455\_1.R1040 5'-most EST zhf700953516.h1

Method BLASTX
NCBI GI g960289
BLAST score 476
E value 4.0e-48
Match length 101

% identity 89

MCBI Description (L34343) anthranilate synthase alpha subunit [Ruta

graveolens]

Seq. No. 30443

Contig ID 214469\_1.R1040

5'-most EST jC-gmf102220054b08a1

Seq. No. 30444

Contig ID 214489\_1.R1040

5! most EST uC-gmflminsoy046a06b1

Method BLASTX
NCBI GI g3367520
BLAST score 537
E value 7.0e-55
Match length 179
% identity 57

NCBI Description (AC004392) Similar to protein kinase APK1A,

tyrosine-serine-threonine kinase gb\_D12522 from A.

thaliana. [Arabidopsis thaliana]

Seq. No. 30445

Contig ID 214496\_1.R1040 5'-most EST kl1701205657.h1

Seq. No. 30446

Contig ID 214500\_1.R1040 5'-most EST zhf700954982.h1

Seq. No. 30447

Contig ID 214500\_2.R1040



```
uC-gmropic101h09b1
5'-most EST
                  30448
Seq. No.
                  214507 1.R1040
Contig ID
                  zhf700953580.h1
5'-most EST
                  BLASTX
Method
                  g3298550
NCBI GI
                  419
BLAST score
                  4.0e-41
E value
                  162
Match length
                  52
% identity
                   (AC004681) putative cellulose synthase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  30449
                  214526 1.R1040
Contig ID
                   jC-gmf102220136h02d1
5'-most EST
                   30450
Seq. No.
                   214566 1.R1040
Contig ID
                   zhf700960157.hl
5'-most EST
                   30451
Seq. No.
                   214623 1.R1040
Contig ID
                   k11701\overline{2}10714.h1
5'-most EST
Method
                   BLASTX
                   q3953475
NCBI GI
                   275
BLAST score
                   2.0e-24
E value
                   93
Match length
                   54
% identity
                  (AC002328) F2202.20 [Arabidopsis thaliana]
NCBI Description
                   30452
Seq. No.
                   214627 1.R1040
Contig ID
                   zhf700953726.h1
5'-most EST
                   30453
Seq. No.
                   214691_1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy126e11b1
                   BLASTN
Method
                   q3869069
NCBI GI
BLAST score
                   53
                   1.0e-20
E value
                   230
Match length
% identity
                   83
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MEB5, complete sequence [Arabidopsis thaliana]
                   30454
Seq. No.
                   214720 1.R1040
Contig ID
                   jC-qmf102220143a07a1
5'-most EST
```

Contig ID 214744\_1.R1040 5'-most EST zhf700953878.h1

Method BLASTX



NCBI GI g4038042 BLAST score 477 E value 4.0e-48 Match length 117 % identity 79

NCBI Description (AC005936) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 30456

Contig ID 214749\_1.R1040 5'-most EST zhf700953884.h1

Method BLASTX
NCBI GI g4469024
BLAST score 500
E value 7.0e-51
Match length 110
% identity 79

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 30457

Contig ID 214768\_1.R1040 5'-most EST zhf700953912.h1

Seq. No. 30458

Contig ID 214814\_1.R1040

5'-most EST uC-gmrominsoy208g09b1

Seq. No. 30459

Contig ID 214848\_1.R1040 5'-most EST gsv701045630.h1

Seq. No. 30460

Contig ID 214859\_1.R1040 5'-most EST kl1701207659.h1

Method BLASTX
NCBI GI g2655098
BLAST score 209
E value 9.0e-17
Match length 54
% identity 67

NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

Seq. No. 30461

Contig ID 214860\_1.R1040 5'-most EST zhf700954023.h1

Seq. No. 30462

Contig ID 214873\_1.R1040 5'-most EST hrw701063257.h1

Seq. No. 30463

Contig ID 214894 1.R1040 5'-most EST zhf700954062.h1

Seq. No. 30464

Contig ID 214901\_1.R1040 5'-most EST zhf700954070.h1



Method BLASTX
NCBI GI g3928079
BLAST score 224
E value 3.0e-18
Match length 144
% identity 40
NCBI Description (AC00577

NCBI Description (AC005770) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30465

Contig ID 214922\_1.R1040 5'-most EST zhf700954102.h1

Method BLASTX
NCBI GI g3168884
BLAST score 171
E value 2.0e-12
Match length 65
% identity 48

NCBI Description (AF068716) similar to E. coli thermoresistant gluconokinase

(GB:U18997) [Caenorhabditis elegans]

Seq. No. 30466

Contig ID 214925\_1.R1040 5'-most EST zhf700954105.h1

Method BLASTX
NCBI GI 94249409
BLAST score 148
E value 1.0e-09
Match length 59
% identity 58

NCBI Description (AC006072) putative sugar transporter [Arabidopsis

thaliana]

Seq. No. 30467

Contig ID 214933\_1.R1040

5'-most EST uC-gmflminsoy042b07b1

Method BLASTX
NCBI GI g3643598
BLAST score 738
E value 2.0e-78
Match length 162
% identity 85

NCBI Description (AC005395) putative poly(A) polymerase [Arabidopsis

thaliana]

Seq. No. 30468

Contig ID 214940\_1.R1040 5'-most EST zhf700954122.h1

Seq. No. 30469

Contig ID 214942 1.R1040 5'-most EST zhf700955311.h1

Method BLASTX
NCBI GI g1491615
BLAST score 205
E value 2.0e-16
Match length 66
% identity 64



NCBI Description (X99923) male sterility 2-like protein [Arabidopsis thaliana]

Seq. No. 30470

Contig ID 214943 1.R1040 5'-most EST zhf700954126.h1

Seq. No. 30471

Contig ID 215022\_1.R1040

5'-most EST jC-gmle01810036e05d1

Method BLASTX
NCBI GI g2664210
BLAST score 334
E value 3.0e-31
Match length 69
% identity 87

NCBI Description (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis

thaliana]

Seq. No. 30472

Contig ID 215044\_1.R1040 5'-most EST uC-gmropic101g08b1

Seq. No. 30473

Contig ID 215132\_1.R1040 5'-most EST zhf700954354.h1

Seq. No. 30474

Contig ID 215173\_1.R1040 5'-most EST zhf700954408.h1

Seq. No. 30475

Contig ID 215221\_1.R1040 5'-most EST zhf700954476.h1

Seq. No. 30476

Contig ID 215223 1.R1040

5'-most EST uC-gmrominsoy126g08b1

Seq. No. 30477

Contig ID 215249\_1.R1040 5'-most EST fua701040622.h1

Seq. No. 30478

Contig ID 215268\_1.R1040 5'-most EST jC-gmle01810078f07a1

Method BLASTX
NCBI GI g3850588
BLAST score 525
E value 2.0e-53
Match length 152
% identity 69

NCBI Description (AC005278) Contains similarity to gb\_AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding

domain C2 PF\_00168. ESTs gb\_AA585988 and gb\_T04384 come

from this gene. [Arabidopsis thaliana]



Contig ID 215276\_1.R1040 5'-most EST leu701145160.h1

Seq. No. 30480

Contig ID 215309\_1.R1040 5'-most EST zhf700954581.h1

Seq. No. 30481

Contig ID 215324 1.R1040 5'-most EST kl1701213457.h1

Seq. No. 30482

Contig ID 215327 1.R1040

5'-most EST uC-gmflminsoy044c05b1

Method BLASTX
NCBI GI g4204315
BLAST score 234
E value 3.0e-19
Match length 195
% identity 30

NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No. 30483

Contig ID 215341\_1.R1040 5'-most EST zsg701117642.h1

Seq. No. 30484

Contig ID 215353\_1.R1040

5'-most EST jC-gmle01810016g02a1

Method BLASTX
NCBI GI g1175016
BLAST score 143
E value 1.0e-08
Match length 134
% identity 32

NCBI Description WHITE PROTEIN HOMOLOG >gi\_1160186\_emb\_CAA62631\_ (X91249)

white [Homo sapiens]

Seq. No. 30485

Contig ID 215369 1.R1040 5'-most EST zhf700954654.h1

Seq. No. 30486

Contig ID 215377\_1.R1040

5'-most EST g4313727
Method BLASTX
NCBI GI g3258570
BLAST score 172
E value 3.0e-12
Match length 45
% identity 73

NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]

Seq. No. 30487

Contig ID 215396\_1.R1040 5'-most EST jC-gmst02400029f12a1

4675



215433 1.R1040 Contig ID 5'-most EST zhf700954735.hl

Method BLASTX q4263722 NCBI GI 289 BLAST score 1.0e-43 E value 101 Match length % identity 88

(AC006223) putative glucan synthase [Arabidopsis thaliana] NCBI Description

30489 Seq. No.

215441 1.R1040 Contig ID 5'-most EST kl1701212167.h1

Method BLASTX q2507229 NCBI GI 329 BLAST score 1.0e-30 E value Match length 93 69 % identity

40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) NCBI Description

(ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED

PROTEIN) (ESTROGEN RECEPTOR BINDING CYCLOPHILIN) >gi 423247 pir A46579 estrogen receptor-binding

cyclophilin - bovine >gi\_393300\_dbj\_BAA03159\_ (D14074)

cyclophilin [Bos taurus]

Seq. No. 30490

215446 1.R1040 Contig ID fC-gmle7000743383r1 5'-most EST

30491 Seq. No.

215485 1.R1040 Contig ID  $zhf700\overline{9}54794.h1$ 5'-most EST

30492 Seq. No.

215492 1.R1040 Contig ID

jC-gmf102220097f08a1 5'-most EST

BLASTX Method q3982577 NCBI GI 295 BLAST score 4.0e-32 E value 102 Match length 67

% identity

(AF023141) histidinol dehydrogenase [Thlaspi goesingense] NCBI Description

30493 Seq. No.

215497\_1.R1040 Contig ID 5'-most EST uC-gmropic112d12b1

Method BLASTX q4508076 NCBI GI 190 BLAST score 2.0e-14 E value 96 Match length % identity 38

NCBI Description (AC005882) 55659 [Arabidopsis thaliana]



Contig ID 215509\_1.R1040 5'-most EST zsg701120956.h1

Seq. No. 30495

Contig ID 215538\_1.R1040 5'-most EST zhf700954859.h1

Method BLASTX
NCBI GI g2499535
BLAST score 553
E value 4.0e-57
Match length 114
% identity 89

NCBI Description 2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi\_595681

(U13238) 2-oxoglutarate/malate translocator [Spinacia

oleracea]

Seq. No. 30496

Contig ID 215547 1.R1040 5'-most EST asn701137057.h1

Method BLASTX
NCBI GI g3776581
BLAST score 144
E value 3.0e-09
Match length 35
% identity 71

NCBI Description (AC005388) Similar to Beta integral membrane protein

homolog gb\_U43629 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 30497

Contig ID 215559\_1.R1040 5'-most EST leu701153154.h1

Method BLASTX
NCBI GI g1771162
BLAST score 365
E value 5.0e-35
Match length 109
% identity 66

NCBI Description (X98930) SBT2 [Lycopersicon esculentum]

>gi\_3687307\_emb\_CAA07000\_ (AJ006379) subtilisin-like

protease [Lycopersicon esculentum]

Seq. No. 30498

Contig ID 215566\_1.R1040 5'-most EST epx701108914.h1

Method BLASTX
NCBI GI g2462826
BLAST score 602
E value 1.0e-62
Match length 182
% identity 42

NCBI Description (AF000657) unknown protein [Arabidopsis thaliana]

Seq. No. 30499

Contig ID 215578\_1.R1040 5'-most EST epx701109091.h1



```
30500
Seq. No.
                   215622 1.R1040
Contig ID
                   zhf700954991.h1
5'-most EST
                   BLASTX
Method
                   g2160190
NCBI GI
BLAST score
                   277
                   2.0e-48
E value
                   146
Match length
                   68
% identity
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   30501
Seq. No.
Contig ID
                   215673 1.R1040
                   \verb|jC-gmf\overline{1}02220115b09d1|
5'-most EST
                   BLASTX
Method
                   g2760543
NCBI GI
                   399
BLAST score
                   1.0e-38
E value
                   83
Match length
                   89
% identity
                   (Z97060) L-galactono-1,4-lactone dehydrogenase [Brassica
NCBI Description
                   oleracea]
Seq. No.
                   30502
                   215679 1.R1040
Contig ID
                   r1r700897214.h1
5'-most EST
Method
                   BLASTX
                   q4512698
NCBI GI
BLAST score
                   347
                   6.0e-33
E value
                   104
Match length
                   66
% identity
                   (AC006569) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   30503
Seq. No.
Contig ID
                   215828 1.R1040
                   uC-gmflminsoy035b01b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2829910
                   224
BLAST score
                   8.0e-22
E value
                   104
Match length
                   55
% identity
                   (AC002291) Unknown protein, contains regulator of
NCBI Description
                   chromosome condensation motifs [Arabidopsis thaliana]
                   30504
Seq. No.
                   215834 1.R1040
Contig ID
                   qsv701048383.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   q1122324
BLAST score
                   235
                   1.0e-129
E value
Match length
                   367
```

4678

91

NCBI Description P.sativum mRNA for SecA protein

% identity



```
30505
Seq. No.
                   215857 1.R1040
Contig ID
                   zhf700\overline{9}55308.h1
5'-most EST
                   30506
Seq. No.
                   215886 1.R1040
Contig ID
                   jC-gmf102220071f04a1
5'-most EST
                   BLASTX
Method
                   g3426037
NCBI GI
                   871
BLAST score
                   2.0e-99
E value
                   250
Match length
                   53
% identity
                   (AC005168) putative ABC transporter protein [Arabidopsis
NCBI Description
                   thaliana]
                   30507
Seq. No.
                   215897 1.R1040
Contig ID
                   zhf700955355.hl
5'-most EST
                   30508
Seq. No.
                   215952 1.R1040
Contig ID
                   zhf700964741.h1
5'-most EST
                   BLASTX
Method
                   g2129953
NCBI GI
                   155
BLAST score
E value
                   1.0e-10
Match length
                   43
                   63
% identity
                   laccase (EC 1.10.3.2) - common tobacco >gi 1685087 (U43542)
NCBI Description
                   diphenol oxidase [Nicotiana tabacum]
                   30509
Seq. No.
                   215967 1.R1040
Contig ID
                   q55088<u>9</u>8
5'-most EST
                   BLASTX
Method
                   g2252827
NCBI GI
BLAST score
                   299
                   5.0e-40
E value
                   99
Match length
                   78
% identity
                   (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30510
Contig ID
                   215980 1.R1040
                   uC-gmropic0001g10b1
5'-most EST
                   30511
Seq. No.
Contig ID
                   215994 1.R1040
5'-most EST
                   uC-qmropic059h04b1
                   BLASTX
Method
                   q4544446
NCBI GI
```

4679

288

109

58

9.0e-26

BLAST score

% identity

E value Match length



NCBI Description (AC006592) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30512

Contig ID 215997\_1.R1040 5'-most EST leu701145993.h1

Method BLASTX
NCBI GI g2342685
BLAST score 336
E value 2.0e-31
Match length 126
% identity 52

NCBI Description (AC000106) Contains similarity to Rhodococcus amidase

(gb\_D16207). ESTs gb\_T20504,gb\_H36650,gb\_N97423,gb\_H36595

come from this gene. [Arabidopsis thaliana]

Seq. No. 30513

Contig ID 215997\_2.R1040

5'-most EST jC-gmfl02220061a09a1

Method BLASTX
NCBI GI g2342685
BLAST score 231
E value 4.0e-19
Match length 147
% identity 37

NCBI Description (AC000106) Contains similarity to Rhodococcus amidase

(gb\_D16207). ESTs gb\_T20504, gb H36650, gb N97423, gb H36595

come from this gene. [Arabidopsis thaliana]

Seq. No. 30514

Contig ID 216033\_1.R1040

5'-most EST jC-gmro02910072e02a1

Method BLASTX
NCBI GI g3776559
BLAST score 671
E value 1.0e-70
Match length 151
% identity 81

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi\_3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb AC003970. ESTs gb\_Z35332 and gb\_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 30515

Contig ID 216037\_1.R1040 5'-most EST zhf700955536.h1

Seq. No. 30516

Contig ID 216060 1.R1040

5'-most EST uC-qmflminsoy017a05b1

Seq. No. 30517

Contig ID 216101\_1.R1040 5'-most EST uC-gmropic065c05b1

Seq. No. 30518

Contig ID 216111 1.R1040 5'-most EST zhf700955632.h1

```
BLASTX
Method
NCBI GI
                  q3135254
                  704
BLAST score
                  3.0e-74
E value
                   278
Match length
                   50
% identity
NCBI Description (AC003058) hypothetical protein [Arabidopsis thaliana]
                   30519
Seq. No.
                   216112 1.R1040
Contig ID
                   pxt700944059.hl
5'-most EST
                   BLASTX
```

Method BLASTX
NCBI GI g2760839
BLAST score 417
E value 1.0e-40
Match length 175
% identity 47

NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 30520

Contig ID 216131\_1.R1040

5'-most EST uC-gmrominsoy112e02b1

Method BLASTX
NCBI GI g2252843
BLAST score 482
E value 1.0e-48
Match length 147
% identity 62

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 30521

Contig ID 216137\_1.R1040 5'-most EST zhf700955669.h1 Method BLASTN

Method BLASTN
NCBI GI g1239962
BLAST score 38
E value 4.0e-12
Match length 62
% identity 90

NCBI Description A.majus mRNA for MADS-box protein (DEFH72)

Seq. No. 30522

Contig ID 216144\_1.R1040 5'-most EST zhf700955668.h1

Seq. No. 30523

Contig ID 216209\_1.R1040 5'-most EST zsg701119566.h1

Method BLASTX
NCBI GI g3256848
BLAST score 175
E value 8.0e-13
Match length 100
% identity 40

NCBI Description (AP000002) 219aa long hypothetical protein [Pyrococcus

horikoshii]



Seq. No. 3052

Contig ID 216211\_1.R1040 5'-most EST zhf700955970.h1

Seq. No. 30525

Contig ID 216228\_1.R1040 5'-most EST crh700850117.h1

Seq. No. 30526

Contig ID 216245\_1.R1040 5'-most EST kl1701208209.h1

Method BLASTX
NCBI GI g3386604
BLAST score 264
E value 8.0e-23
Match length 147
% identity 36

NCBI Description (AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No. 30527

Contig ID 216279\_1.R1040

5'-most EST jC-gmle01810089e12a1

Seq. No. 30528

Contig ID 216288\_1.R1040 5'-most EST zhf700955848.h1

Method BLASTX
NCBI GI g2914703
BLAST score 355
E value 1.0e-33
Match length 142
% identity 52

NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]

Seq. No. 30529

Contig ID 216315\_1.R1040 5'-most EST zhf700955880.h1

Seq. No. 30530

Contig ID 216321 1.R1040 5'-most EST zhf700955887.h1

Seq. No. 30531

Contig ID 216322\_1.R1040

5'-most EST jC-gmle01810060h09a1

Seq. No. 30532

Contig ID 216441\_1.R1040 5'-most EST zhf700956027.h1

Method BLASTX
NCBI GI g4558556
BLAST score 390
E value 5.0e-38
Match length 110
% identity 66

NCBI Description (AC007138) predicted protein of unknown function

[Arabidopsis thaliana]



Seq. No. 30533 216450 1.R1040 Contig ID zhf700956039.hl 5'-most EST

30534 Seq. No.

216483 1.R1040 Contig ID zhf700956079.h1 5'-most EST

30535 Seq. No.

216492 1.R1040 Contig ID

jC-gmf102220102c08a1 5'-most EST

Method BLASTX q4006913 NCBI GI 450 BLAST score 1.0e-44 E value 127 Match length 72 % identity

(Z99708) hypothetical protein [Arabidopsis thaliana] NCBI Description

30536 Seq. No.

216529 1.R1040 Contig ID 5'-most EST zhf700956142.h1

Method BLASTX q1708971 NCBI GI 226 BLAST score 8.0e-19 E value 98 Match length 49 % identity

(R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR NCBI Description

(HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)

>gi\_421871\_pir\_\_S32156 mandelonitrile lyase (EC 4.1.2.10) black cherry >gi\_288116\_emb\_CAA51194\_ (X72617)

mandelonitrile lyase [Prunus serotina] >gi\_1730332 (U78814) (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus serotina] >gi\_1090776\_prf\_\_2019441A mandelonitrile lyase

[Prunus serotina]

30537 Seq. No.

216530 1.R1040 Contig ID

uC-qmflminsoy024h03b1 5'-most EST

Method BLASTX NCBI GI g3337361 BLAST score 414 8.0e-41 E value Match length 106 % identity

(AC004481) ankyrin-like protein [Arabidopsis thaliana] NCBI Description

Seq. No. 30538

216546 1.R1040 Contig ID 5'-most EST zhf700956164.h1

30539 Seq. No.

216559 1.R1040 Contig ID zhf700956452.h1 5'-most EST

Method BLASTX



```
q431154
NCBI GI
                  201
BLAST score
                   5.0e-16
E value
                   68
Match length
                   59
% identity
NCBI Description (D21813) ORF [Lilium longiflorum]
                   30540
Seq. No.
                   216563 1.R1040
Contig ID
                   fua701038569.hl
5'-most EST
                   30541
Seq. No.
                   216632 1.R1040
Contig ID
5'-most EST
                   zhf700958851.h1
                  BLASTX
Method
                   g1408473
NCBI GI
```

224 BLAST score 9.0e-19 E value 55 Match length 73 % identity

(U48939) actin depolymerizing factor 2 [Arabidopsis NCBI Description

thaliana]

30542 Seq. No.

216634 1.R1040 Contig ID kl1701203845.hl 5'-most EST

30543 Seq. No.

216679 1.R1040 Contig ID 5'-most EST leu701146301.h1

BLASTX Method g3395585 NCBI GI 156 BLAST score 1.0e-10 E value Match length 67 42 % identity

NCBI Description (AL031179) hypothetical protein [Schizosaccharomyces pombe]

30544 Seq. No.

216690 1.R1040 Contig ID  $k11701\overline{2}04502.h2$ 5'-most EST

BLASTX Method q2245077 NCBI GI 327 BLAST score E value 9.0e-31 92 Match length 72 % identity

(Z97343) glucanase homolog [Arabidopsis thaliana] NCBI Description

30545 Seq. No.

216777 1.R1040 Contig ID zhf700956512.h1 5'-most EST

30546 Seq. No.

216780 1.R1040 Contig ID jC-gmf102220144e02a1 5'-most EST

BLASTX Method



```
g4337196
NCBI GI
                  595
BLAST score
                  1.0e-61
E value
Match length
                  171
% identity
                  71
                   (AC006403) putative serine/threonine receptor kinase
NCBI Description
                   [Arabidopsis thaliana]
                  30547
Seq. No.
                  216783 1.R1040
Contig ID
                  zhf700956558.hl
5'-most EST
                  BLASTX
Method
                  g2944178
NCBI GI
BLAST score
                  147
E value
                   3.0e-17
Match length
                   82
% identity
                   63
                   (AF007778) trehalose-6-phosphate phosphatase [Arabidopsis
NCBI Description
                   thaliana]
                   30548
Seq. No.
                   216801 1.R1040
Contig ID
                   jC-gmle01810026d03a1
5'-most EST
                   BLASTX
Method
                   g4567095
NCBI GI
BLAST score
                   691
                   6.0e-73
E value
Match length
                   160
% identity
                   80
                  (AF129516) fertilization-independent endosperm protein
NCBI Description
                   [Arabidopsis thaliana]
                   30549
Seq. No.
                   216810 1.R1040
Contig ID
                   zhf700956567.h1
5'-most EST
                   BLASTX
Method
                   g3337352
NCBI GI
                   156
BLAST score
                   2.0e-17
E value
                   86
Match length
                   57
% identity
                  (AC004481) putative chromatin structural protein Supt5hp
NCBI Description
                   [Arabidopsis thaliana]
                   30550
Seq. No.
                   216830 1.R1040
Contig ID
                   zhf700956605.h1
5'-most EST
                   BLASTX
Method
                   q1209756
NCBI GI
BLAST score
                   1039
E value
                   1.0e-113
                   279
```

Match length % identity

NCBI Description (U43629) integral membrane protein [Beta vulgaris]

Seq. No. 30551

216888 1.R1040 Contig ID



5'-most EST zhf700956689.h1

Seq. No. 30552

Contig ID 216910\_1.R1040 5'-most EST epx701107525.h1

Seq. No. 30553

Contig ID 216952\_1.R1040 5'-most EST zhf700956793.h1

Seq. No. 30554

Contig ID 216958\_1.R1040

5'-most EST uC-gmflminsoy016d12b1

Method BLASTX
NCBI GI g4336426
BLAST score 548
E value 2.0e-56
Match length 127
% identity 77

NCBI Description (AF090835) Ca2+-dependent protein kinase [Mesembryanthemum

crystallinum]

Seq. No. 30555

Contig ID 216970\_1.R1040 5'-most EST jC-gmro02910037f12a1

Seq. No. 30556

Contig ID 216970\_2.R1040

5'-most EST g5606159

Seq. No. 30557

Contig ID 217019\_1.R1040 5'-most EST zhf700956924.h1

Seq. No. 30558

Contig ID 217035\_1.R1040

5'-most EST jC-gmle01810028e12d1

Method BLASTX
NCBI GI g2262116
BLAST score 196
E value 4.0e-15
Match length 117
% identity 37

NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No. 30559

Contig ID 217045\_1.R1040 5'-most EST zhf700956981.h1

Seq. No. 30560

Contig ID 217052\_1.R1040 5'-most EST zhf700956992.h1

Seq. No. 30561

Contig ID 217082\_1.R1040 5'-most EST zhf700957045.h1

Method BLASTX

4686



NCBI GI g4415933 BLAST score 462 E value 3.0e-46 Match length 123 % identity 68

NCBI Description (AC006418) putative cellular apoptosis susceptibility

protein [Arabidopsis thaliana]

>gi\_4559390\_gb\_AAD23050.1\_AC006526\_15 (AC006526) putative cellular apoptosis susceptibility protein [Arabidopsis

thaliana]

Seq. No. 30562

Contig ID 217104\_1.R1040 5'-most EST zhf700957082.h1

Seq. No. 30563

Contig ID 217118 1.R1040

5'-most EST uC-gmflminsoy055c12b1

Method BLASTX
NCBI GI g2494116
BLAST score 865
E value 3.0e-93
Match length 215
% identity 78

NCBI Description (AC002376) Similar to Synechocystis hypothetical protein

(qb D90915). [Arabidopsis thaliana]

Seq. No. 30564

Contig ID 217126\_1.R1040 5'-most EST zhf700957121.h1

Method BLASTX
NCBI GI g2213624
BLAST score 481
E value 4.0e-48
Match length 252
% identity 44

NCBI Description (AC000103) F21J9.16 [Arabidopsis thaliana]

Seq. No. 30565

Contig ID 217128 1.R1040 5'-most EST gsv701055604.h1

Seq. No. 30566

Contig ID 217129\_1.R1040 5'-most EST zhf700958162.h1

Method BLASTX
NCBI GI g2245108
BLAST score 143
E value 4.0e-09
Match length 28
% identity 89

NCBI Description (Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No. 30567

Contig ID 217149\_1.R1040 5'-most EST zhf700957171.h1

30568 Seq. No. 217170 1.R1040 Contig ID jC-gmr002800027c07a1 5'-most EST BLASTX Method g4567197 NCBI GI 225 BLAST score 2.0e-18 E value 91 Match length 56 % identity (AC007168) unknown protein [Arabidopsis thaliana] NCBI Description 30569 Seq. No. 217188 1.R1040 Contig ID fua701040949.h1 5'-most EST BLASTX Method

Method BLASTX
NCBI GI g3396079
BLAST score 198
E value 1.0e-15
Match length 83
% identity 47

% identity 47
NCBI Description (AF080173) inositol 1,3,4-trisphosphate 5/6-kinase

[Arabidopsis thaliana]

Seq. No. 30570

Contig ID 217189\_1.R1040 5'-most EST leu701151606.h1

Method BLASTX
NCBI GI g4006924
BLAST score 684
E value 3.0e-72
Match length 155
% identity 75

NCBI Description (Z99708) beta-galactosidase like protein [Arabidopsis

thaliana]

Seq. No. 30571

Contig ID 217191\_1.R1040 5'-most EST zsg701120810.h1

Seq. No. 30572

Contig ID 217192\_1.R1040 5'-most EST uC-gmropic055a03b1

Seq. No. 30573

Contig ID 217240\_1.R1040

5'-most EST uC-gmflminsoy047b05b1

Method BLASTX
NCBI GI g2213590
BLAST score 477
E value 9.0e-48
Match length 188
% identity 49

NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No. 30574

Contig ID 217284\_1.R1040 5'-most EST gsv701056235.h1



```
Seq. No.
                  30575
                  217306 1.R1040
Contig ID
                  zhf700957456.h1
5'-most EST
                  BLASTX
Method
                  g2911075
NCBI GI
                   336
BLAST score
                  1.0e-31
E value
                  81
Match length
                  83
% identity
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                   30576
Seq. No.
Contig ID
                   217348 1.R1040
                   jC-gmst02400026a08d1
5'-most EST
                   30577
Seq. No.
                   217438 1.R1040
Contig ID
                   uC-gmrominsoy169h05b1
5'-most EST
                   BLASTX
Method
                   g3378491
NCBI GI
BLAST score
                   159
                   1.0e-10
E value
                   48
Match length
                   58
% identity
                   (AJ007578) pRIB5 protein [Ribes nigrum]
NCBI Description
                   30578
Seq. No.
                   217441 1.R1040
Contig ID
5'-most EST
                   uC-gmropic090c04b1
                   30579
Seq. No.
                   217452 1.R1040
Contig ID
                   uC-gmropic070c10b1
5'-most EST
                   BLASTX
Method
                   q3337361
NCBI GI
BLAST score
                   661
                   2.0e-69
E value
                   179
Match length
                   65
% identity
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
                   30580
Seq. No.
                   217459 1.R1040
Contig ID
5'-most EST
                   zhf700957744.h1
                   BLASTX
Method
                   q544006
NCBI GI
BLAST score
                   181
E value
                   1.0e-13
                   59
Match length
```

% identity

ACIDIC ENDOCHITINASE PRECURSOR >gi\_322686\_pir\_\_S31763 NCBI Description chitinase (EC 3.2.1.14) - chickpea >gi\_17942 emb\_CAA49998\_

(X70660) chitinase [Cicer arietinum]

30581 Seq. No.

217476 1.R1040 Contig ID

58



5'-most EST zhf700957764.h1

Method BLASTX
NCBI GI 94454035
BLAST score 278
E value 2.0e-24
Match length 94
% identity 56

NCBI Description (AL035394) polyprenyltransferase like protein [Arabidopsis

thaliana]

Seq. No. 30582

Contig ID 217498\_1.R1040 5'-most EST zhf700957796.h1

Seq. No. 30583

Contig ID 217536\_1.R1040 5'-most EST zhf700957857.h1

Method BLASTN
NCBI GI g2623245
BLAST score 111
E value 1.0e-55
Match length 206
% identity 89

NCBI Description Pisum sativum poly(A) polymerase mRNA, nuclear gene

encoding chloroplast protein, complete cds

Seq. No. 30584

Contig ID 217545\_1.R1040

5'-most EST uC-gmflminsoy083e05b1

Method BLASTX
NCBI GI g2623299
BLAST score 89
E value 1.0e-09
Match length 80
% identity 51

NCBI Description (AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30585

Contig ID 217571\_1.R1040

5'-most EST uC-gmflminsoy054f09b1

Seq. No. 30586

Contig ID 217579\_1.R1040 5'-most EST zhf700957923.h1

Seq. No. 30587

Contig ID 217591\_1.R1040 5'-most EST zhf700957939.h1

Seq. No. 30588

Contig ID 217607 1.R1040

5'-most EST uC-gmrominsoy059b01b1

Seq. No. 30589

Contig ID 217633\_1.R1040 5'-most EST pxt700945371.h1

```
30590
Seq. No.
                   217641 1.R1040
Contig ID
                   zhf700958020.h1
5'-most EST
                   BLASTX
Method
                   g4539435
NCBI GI
                   496
BLAST score
                   2.0e-50
E value
                   103
Match length
% identity
                   83
                  (AL049523) putative protein [Arabidopsis thaliana]
NCBI Description
                   30591
Seq. No.
                   217718 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy063h05b1
                   30592
Seq. No.
                   217723 1.R1040
Contig ID
                   zhf700\overline{9}58142.h1
5'-most EST
```

30593 Seq. No.

217726 1.R1040 Contig ID asn701142016.h1 5'-most EST

30594 Seq. No.

217787 1.R1040 Contig ID 5'-most EST uC-gmropic042d12b1

30595 Seq. No.

217791 1.R1040 Contig ID

g4260307 5'-most EST BLASTX Method q4006864 NCBI GI 241 BLAST score E value 1.0e-20 101 Match length 54 % identity

(Z99707) nucleoporin-like protein [Arabidopsis thaliana] NCBI Description

30596 Seq. No.

217865 1.R1040 Contig ID

5'-most EST jC-qmf102220143h08a1

BLASTX Method q728868 NCBI GI BLAST score 223 E value 3.0e-18 75 Match length 59 % identity

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) NCBI Description

>gi\_99824\_pir\_\_S16748 proline-rich protein - rape
(fragment) >gi\_22597\_emb\_CAA42924\_ (X60376) proline-rich

protein [Brassica napus]

30597 Seq. No.

217866 1.R1040 Contig ID

5'-most EST g4260349

Seq. No. 30598



```
217895 1.R1040
Contig ID
                  jC-gmf102220068c05d1
5'-most EST
                  30599
Seq. No.
Contig ID
                  217957 1.R1040
                  jC-gmro02910011g08a1
5'-most EST
                   30600
Seq. No.
                   217969 1.R1040
Contig ID
                   leu701151263.hl
5'-most EST
Seq. No.
                   30601
                   217977 1.R1040
Contig ID
                   zsq701126152.h1
5'-most EST
                   30602
Seq. No.
                   217984 1.R1040
Contig ID
                   zhf700958486.h1
5'-most EST
                   30603
Seq. No.
                   218000 1.R1040
Contig ID
                   pxt700945957.h1
5'-most EST
                   BLASTX
Method
                   g2262105
NCBI GI
                   638
BLAST score
                   1.0e-66
E value
                   180
Match length
% identity
                   60
                   (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30604
                   218014 1.R1040
Contig ID
                   zhf700961801.h1
5'-most EST
                   30605
Seq. No.
                   218021 1.R1040
Contig ID
                   zhf700958541.h1
5'-most EST
                   BLASTX
Method
                   g4191789
NCBI GI
                   218
BLAST score
                   9.0e-18
E value
                   83
Match length
                   58
% identity
                   (AC005917) putative transmembrane transport protein
NCBI Description
                    [Arabidopsis thaliana]
                    30606
Seq. No.
                    218022 1.R1040
Contig ID
                    jC-gms\u00aa\u00d100068g07d1
```

5'-most EST BLASTN Method NCBI GI g4519194

50 BLAST score 5.0e-19 E value 118 Match length 86 % identity NCBI Description

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MHM17, complete sequence



Seq. No.	3
Contig ID	2
5'-most EST	f

0607 18067 1.R1040 Tua701042740.hl

Seq. No. Contig ID 5'-most EST 30608 218077 1.R1040  $zhf700\overline{9}58626.h1$ 

Seq. No. Contig ID 5'-most EST 30609 218084 1.R1040  $zhf700\overline{9}58634.h1$ 

Seq. No. Contig ID 5'-most EST 30610 218112 1.R1040 zhf700959017.hl

Seq. No.

Seq. No.

30611 218118 1.R1040 zhf700958705.h1

Contig ID 5'-most EST

30612

Contig ID 5'-most EST 218163 1.R1040 jC-gmf102220114g03d1

Seq. No. Contig ID 30613 218232 1.R1040 zhf700958874.hl

5'-most EST

30614

Seq. No. Contig ID 5'-most EST

218272 1.R1040 zhf700958932.hl

Method NCBI GI BLAST score BLASTX g4371293 162

E value Match length % identity

4.0e-11 132 34

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. Contig ID 5'-most EST 30615

218304 1.R1040  $gsv701\overline{0}55031.h1$ 

Seq. No. Contig ID 5'-most EST 30616

218350 1.R1040 zhf700959050.h1

Seq. No. Contig ID 5'-most EST 30617

218384 1.R1040 asn701138736.hl

Seq. No. Contig ID 5'-most EST 30618

218391 1.R1040  $k11701\overline{2}08301.h1$ 

Method NCBI GI BLASTX g4098647

```
BLAST score
                   3.0e-47
E value
                   90
Match length
                   92
% identity
                   (U80668) homogentisate 1,2-dioxygenase [Arabidopsis
NCBI Description
                   thaliana]
                   30619
Seq. No.
                   218446 1.R1040
Contig ID
                   kl1701208553.h1
5'-most EST
                   BLASTX
Method
                   g3176714
NCBI GI
                   389
BLAST score
                   7.0e-46
E value
                   121
Match length
                   74
% identity
                   (AC002392) putative tRNA-splicing endonuclease positive
NCBI Description
                   effector [Arabidopsis thaliana]
                  ູ30620
Seq. No.
                   218459 1.R1040
Contig ID
                   k11701\overline{2}07149.h1
5'-most EST
                   BLASTX
Method
                   g2245378
NCBI GI
BLAST score
                   407
                   1.0e-39
E value
                   204
Match length
                   50
% identity
                   (U83245) auxin response factor 1 [Arabidopsis thaliana]
NCBI Description
                   30621
Seq. No.
                   218467 1.R1040
Contig ID
                   zhf700959231.h1
5'-most EST
                   BLASTX
Method
                   q2894567
NCBI GI
BLAST score
                   370
E value
                   2.0e-35
                   150
Match length
% identity
                   (AL021890) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   30622
Seq. No.
                   218497 1.R1040
Contig ID
```

 $k11701\overline{2}04387.h2$ 5'-most EST

30623 Seq. No.

218504 1.R1040 Contig ID 5'-most EST zhf700959281.h1

30624 Seq. No.

218524 1.R1040 Contig ID zhf700959307.hl 5'-most EST

30625 Seq. No.

218549 1.R1040 Contig ID zhf700959333.h1 5'-most EST BLASTX Method



```
q4454467
NCBI GI
BLAST score
                   240
                   1.0e-20
E value
                   87
Match length
% identity
                   (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   30626
Seq. No.
                   218558 1.R1040
Contig ID
                   epx701109743.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4128133
BLAST score
                   254
                   6.0e-22
E value
                   87
Match length
                   55
% identity
NCBI Description (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]
                   30627
Seq. No.
                   218583 1.R1040
Contig ID
                   pxt700946231.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4455338
BLAST score
                   289
                   6.0e-26
E value
Match length
                   144
                   47
% identity
                   (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
                   30628
Seq. No.
                   218591 1.R1040
Contig ID
                   q5175438
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1665817
BLAST score
                   152
E value
                   1.0e-09
Match length
                   108
                   35
% identity
                   (D87466) Similar to S.cerevisiae hypothetical protein L3111
NCBI Description
                   (S59316) [Homo sapiens]
                   30629
Seq. No.
                   218682 1.R1040
Contig ID
                   zhf700\overline{9}59510.h1
5'-most EST
                   30630
Seq. No.
                   218694 1.R1040
Contig ID
                   zhf700959525.h1
5'-most EST
                   30631
Seq. No.
                   218789 1.R1040
Contig ID
                   zhf700\overline{9}59683.h1
5'-most EST
```

Seq. No. 30632

Contig ID 218809\_1.R1040 5'-most EST zhf700959715.h1



Seq. No. 30633

Contig ID 218864\_1.R1040 5'-most EST jC-gmf102220065d12d1

Seq. No. 30634

Contig ID 218891\_1.R1040 5'-most EST epx701106945.h1

Seq. No. 30635

Contig ID 218931\_1.R1040

5'-most EST uC-gmflminsoy007e06b1

Seq. No. 30636

Contig ID 218945 1.R1040

5'-most EST uC-gmrominsoy241g07b1

Method BLASTX
NCBI GI g2072986
BLAST score 684
E value 5.0e-72
Match length 182
% identity 73

% identity 73
NCBI Description (U95142) putative G-protein-coupled receptor [Arabidopsis

thaliana] >gi\_2072988 (U95143) putative G-protein-coupled

receptor [Arabidopsis thaliana]

Seq. No. 30637

Contig ID 219009 1.R1040

5'-most EST jC-gmle01810071a01a1

Method BLASTX
NCBI GI g100226
BLAST score 229
E value 7.0e-19
Match length 103
% identity 38

NCBI Description hypothetical protein - tomato >gi\_19275\_emb\_CAA78112\_

(Z12127) protein of unknown function [Lycopersicon esculentum] >gi 445619 prf 1909366A Leu zipper protein

[Lycopersicon esculentum]

Seq. No. 30638

Contig ID 219031 1.R1040

NCBI Description (U78721) cadmium-induced protein isolog [Arabidopsis

thaliana]

Seq. No. 30639

Contig ID 219034\_1.R1040

5'-most EST jC-gmst02400014e01a1

Seq. No. 30640

Contig ID 219048\_1.R1040

4696



5'-most EST jC-gmst02400032d01a1

Method BLASTX
NCBI GI g4056421
BLAST score 834
E value 1.0e-89
Match length 183
% identity 81

NCBI Description (AC005322) Similar to gb Z30094 basic transcripion factor

2, 44 kD subunit from Homo sapiens. EST gb\_W43325 comes

from this gene. [Arabidopsis thaliana]

Seq. No. 30641

Contig ID 219064\_1.R1040

5'-most EST uC-gmrominsoy224g05b1

Method BLASTX
NCBI GI g4559384
BLAST score 146
E value 5.0e-09
Match length 112
% identity 32

NCBI Description (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No. 30642

Contig ID 219139\_1.R1040 5'-most EST jC-gmf102220103e11a1

Seq. No. 30643

Contig ID 219147\_1.R1040

5'-most EST uC-gmflminsoy008d02b1

Seq. No. 30644

Contig ID 219153\_1.R1040

5'-most EST jC-gmle01810010d12a1

Method BLASTX
NCBI GI g4006867
BLAST score 168
E value 1.0e-11
Match length 72
% identity 43

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 30645

Contig ID 219168\_1.R1040

5'-most EST g5509222

Seq. No. 30646

Contig ID 219233 1.R1040 5'-most EST zhf700960282.h1

Seq. No. 30647

Contig ID 219249\_1.R1040 5'-most EST rlr700898788.h1

Seq. No. 30648

Contig ID 219259 1.R1040 5'-most EST leu701147216.h1



```
30649
Seq. No.
                   219277 1.R1040
Contig ID
                   zhf700960342.h1
5'-most EST
                   30650
Seq. No.
                   219284 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400025a03a1
Method
                   BLASTX
                   q2832241
NCBI GI
                   505
BLAST score
                   3.0e-51
E value
                   145
Match length
                   50
% identity
                   (AF030864) nonphototropic hypocotyl 1 [Arabidopsis
NCBI Description
                   thaliana]
                   30651
Seq. No.
                   219302 1.R1040
Contig ID
                   zhf700\overline{9}60376.h1
5'-most EST
                   30652
Seq. No.
                   219326 1.R1040
Contig ID
                   leu701155385.hl
5'-most EST
Seq. No.
                   30653
                   219332 1.R1040
Contig ID
                   asn701134881.h2
5'-most EST
                   30654
Seq. No.
                   219338 1.R1040
Contig ID
                   jC-gmle01810047e03a1
5'-most EST
                   BLASTX
Method
                   q2113914
NCBI GI
BLAST score
                   149
                   1.0e-09
E value
                   81
Match length
                   21
% identity
NCBI Description (Z95554) rpsA [Mycobacterium tuberculosis]
                   30655
Seq. No.
                   219413 1.R1040
Contig ID
                   zhf700960602.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2661676
BLAST score
                   161
                   8.0e-11
E value
                   100
Match length
```

40 % identity

(AL009199) hypothetical ATP/GTP binding protein NCBI Description

[Streptomyces coelicolor]

30656 Seq. No.

219413 2.R1040 Contig ID

jC-gmf102220114e02d1 5'-most EST

30657 Seq. No.

219483 1.R1040 Contig ID



5'-most EST zhf700960719.h1

Method BLASTX
NCBI GI g3608127
BLAST score 319
E value 3.0e-29
Match length 66

Match length 66 % identity 77

NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 30658

Contig ID 219487\_1.R1040 5'-most EST hrw701058931.h1

Seq. No. 30659

Contig ID 219489\_1.R1040 5'-most EST zhf700960845.h1

Method BLASTX
NCBI GI g3367537
BLAST score 172
E value 9.0e-19
Match length 63
% identity 73

NCBI Description (AC004392) Contains similarity to ANK repeat region of

Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi\_485107 from Caenorhabditis elegans cosmid gb\_U00049. This gene is continued from unannotated gene on BAC F19K23 gb\_AC000375.

[Arabid

Seq. No. 30660

Contig ID 219632\_1.R1040 5'-most EST zhf700960978.h1

Seq. No. 30661

Contig ID 219675\_1.R1040 5'-most EST asn701136803.h1

Seq. No. 30662

Contig ID 219695 1.R1040 5'-most EST zhf700961072.h1

Method BLASTX
NCBI GI g3142303
BLAST score 299
E value 4.0e-27
Match length 114
% identity 61

NCBI Description (AC002411) Strong similarity to MRP-like ABC transporter

gb\_U92650 from A. thaliana and canalicular multi-drug resistance protein gb\_L49379 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No. 30663

Contig ID 219726 1.R1040

5'-most EST jC-gmf\(\bar{1}\)02220064b01d1

Seq. No. 30664

Contig ID 219730 1.R1040

5'-most EST jC-gmf102220112c05d1

```
BLASTX
Method
NCBI GI
                  g2315983
BLAST score
                  180
                   5.0e-13
E value
                   148
Match length
                   35
% identity
                   (U82087) calmodulin-like domain protein kinase [Tortula
NCBI Description
                   ruralis]
                   30665
Seq. No.
                   219741 1.R1040
Contig ID
5'-most EST
                   zhf700964314.h1
                   30666
Seq. No.
                   219785 1.R1040
Contig ID
                   jC-gmf102220113e03a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2244996
                   439
BLAST score
                   1.0e-43
E value
                   117
Match length
                   31
% identity
                   (Z97341) similarity to a membrane-associated salt-inducible
NCBI Description
                   protein [Arabidopsis thaliana]
                   30667
Seq. No.
                   219792 1.R1040
Contig ID
                   uC-gmrominsoy306d05b1
5'-most EST
                   30668
Seq. No.
                   219800 1.R1040
Contig ID
5'-most EST
                   zsg701129832.h1
                   BLASTX
Method
                   g100226
NCBI GI
BLAST score
                   355
                   5.0e-34
E value
Match length
                   97
                   71
% identity
                   hypothetical protein - tomato >gi_19275_emb_CAA78112_
NCBI Description
                   (Z12127) protein of unknown function [Lycopersicon
                   esculentum] >gi_445619_prf__1909366A Leu zipper protein
                   [Lycopersicon esculentum]
                   30669
Seq. No.
                   219825 1.R1040
Contig ID
                   jC-gmst02400043c08d1
 5'-most EST
 Seq. No.
                   30670
                   219868 1.R1040
 Contig ID
                   g5058245
 5'-most EST
                   BLASTX
Method
```

g3786004 NCBI GI 267 BLAST score 1.0e-27 E value 92 Match length 70 % identity

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

BLAST score

E value

274 7.0e-24



```
30671
Seq. No.
                  219916 2.R1040
Contig ID
                  leu701153836.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2905893
                  183
BLAST score
                  6.0e-14
E value
                  58
Match length
                  59
% identity
NCBI Description (U66424) fimbrin-like protein [Arabidopsis thaliana]
                  30672
Seq. No.
                  219934 1.R1040
Contig ID
5'-most EST
                  uC-qmflminsoy100c12b1
                  BLASTX
Method
NCBI GI
                  g4006913
BLAST score
                  388
E value
                  1.0e-37
                  100
Match length
                  80
% identity
NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  30673
                  219936 1.R1040
Contig ID
5'-most EST
                  kl1701215367.h1
                  BLASTN
Method
NCBI GI
                  q2656028
BLAST score
                  47
                  3.0e-17
E value
                  107
Match length
                  86
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNF13
Seq. No.
                  30674
                  219939 1.R1040
Contig ID
5'-most EST
                  zhf700961477.h1
Method
                  BLASTX
NCBI GI
                  g3935187
BLAST score
                  515
E value
                  2.0e-52
Match length
                  138
% identity
                  38
NCBI Description (AC004557) F17L21.30 [Arabidopsis thaliana]
                  30675
Seq. No.
Contig ID
                   219982 1.R1040
5'-most EST
                   zhf700961553.h1
Seq. No.
                   30676
                   220022 1.R1040
Contig ID
                   jC-gmst02400070a11a1
5'-most EST
Method
                  BLASTX
                  g1749686
NCBI GI
```



Match length 180
% identity 36
NCBI Description (D89239) similar to Saccharomyces cerevisiae unknown, EMBL Accession Number Z68194 [Schizosaccharomyces pombe]

Seq. No. 30677
Contig ID 220038\_1.R1040
5'-most EST pmv700890656.h1

 Seq. No.
 30678

 Contig ID
 220070\_1.R1040

 5'-most EST
 leu701144949.h1

 Method
 BLASTX

NCBI GI g1778145
BLAST score 415
E value 8.0e-41
Match length 123
% identity 67

NCBI Description (U66402) phosphate/phosphoenolpyruvate translocator

precursor [Nicotiana tabacum]

 Seq. No.
 30679

 Contig ID
 220205\_1.R1040

 5'-most EST
 zhf700965015.h1

Method BLASTX
NCBI GI g4263822
BLAST score 167
E value 9.0e-12
Match length 84
% identity 46

NCBI Description (AC006067) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 30680

Contig ID 220246\_2.R1040 5'-most EST asn701134689.h2

Seq. No. 30681

Contig ID 220248\_1.R1040 5'-most EST zhf700961933.h1

Method BLASTX
NCBI GI g2501011
BLAST score 445
E value 3.0e-44
Match length 147
% identity 57

NCBI Description ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)

>gi\_1652625\_dbj\_BAA17545\_ (D90907) isoleucyl-tRNA

synthetase [Synechocystis sp.]

Seq. No. 30682

Contig ID 220254\_1.R1040 5'-most EST zhf700961942.h1

Method BLASTX
NCBI GI g2266985
BLAST score 220
E value 1.0e-34



Match length 94 % identity 82

NCBI Description (Y13943) METRS [Arabidopsis thaliana]

Seq. No. 30683

Contig ID 220310\_1.R1040

5'-most EST uC-gmflminsoy031c01b1

Method BLASTX
NCBI GI g4415942
BLAST score 364
E value 9.0e-35
Match length 134
% identity 54

NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30684

Contig ID 220319\_1.R1040 5'-most EST fua701039125.h1

Method BLASTX
NCBI GI g2832629
BLAST score 497
E value 5.0e-50
Match length 174
% identity 53

NCBI Description (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis

thaliana]

Seq. No. 30685

Contig ID 220344 2.R1040 5'-most EST pxt700945686.h1

Seq. No. 30686

Contig ID 220353 1.R1040 5'-most EST zhf700962060.h1

Seq. No. 30687

Contig ID 220379\_1.R1040 5'-most EST dpv701101245.h1

Seq. No. 30688

Contig ID 220424 1.R1040

5'-most EST jC-gmst02400013a01a1

Method BLASTX
NCBI GI 94220534
BLAST score 404
E value 2.0e-39
Match length 125
% identity 67

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 30689

Contig ID 220427\_1.R1040 5'-most EST zhf700962154.h1

Seq. No. 30690

Contig ID 220432\_1.R1040 5'-most EST jC-gmro02910039g11d1



```
Seq. No.
                  30691
                  220438 1.R1040
Contig ID
5'-most EST
                  zhf700962171.h1
                  30692
Seq. No.
Contig ID
                  220448 1.R1040
                  zhf700962183.h1
5'-most EST
Seq. No.
                  30693
Contig ID
                  220454 1.R1040
5'-most EST
                  zhf700962463.h1
Seq. No.
                  30694
Contiq ID
                  220489 1.R1040
5'-most EST
                  jC-gmle01810094f02a1
Method
                  BLASTX
NCBI GI
                  g2497542
BLAST score
                  393
                  9.0e-53
E value
Match length
                  164
% identity
                  67
NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR
                  >gi 629696_pir__S44287 pyruvate kinase, plastid - common
                  tobacco >gi_482938_emb_CAA82223_ (Z28374) Pyruvate kinase;
                  plastid isozyme [Nicotiana tabacum]
Seq. No.
                  30695
                  220501 1.R1040
Contig ID
5'-most EST
                  pmv700891893.h1
Seq. No.
                  30696
                  220508_1.R1040
Contig ID
5'-most EST
                  zhf700962260.h1
Method
                  BLASTX
NCBI GI
                  g126306
BLAST score
                  352
E value
                  3.0e-33
Match length
                  179
% identity
                  44
                  TRIACYLGLYCEROL LIPASE PRECURSOR (LIPASE, GASTRIC)
NCBI Description
                  >gi_106904_pir__S07145 triacylglycerol lipase (EC 3.1.1.3)
                  precursor, gastric - human >gi 758063 emb CAA29413
                  (X05997) gastric lipase precursor [Homo sapiens]
Seq. No.
                  30697
Contig ID
                  220535 1.R1040
```

5'-most EST uC-gmflminsoy119e02b1

Method BLASTX NCBI GI g3096930 BLAST score 353 E value 3.0e - 33Match length 88 % identity 74

NCBI Description (AL023094) Homeodomain - like protein [Arabidopsis

thaliana]



Seq. No. 3069

Contig ID 220551\_1.R1040 5'-most EST zhf700962319.h1

Method BLASTX
NCBI GI g2642448
BLAST score 204
E value 4.0e-16
Match length 114
% identity 46

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

>gi\_3169187 (AC004401) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 30699

Contig ID 220610\_1.R1040 5'-most EST gsv701049810.h1

Method BLASTX
NCBI GI g3549652
BLAST score 477
E value 3.0e-48
Match length 104
% identity 88

NCBI Description (AJ224982) MAP3K epsilon protein kinase [Arabidopsis

thaliana]

Seq. No. 30700

Contig ID 220629 1.R1040 5'-most EST lus701015830.h1

Seq. No. 30701

Contig ID 220642\_1.R1040 5'-most EST uC-gmropic032e05b1

Seq. No. 30702

Contig ID 220667\_1.R1040 5'-most EST zhf700962475.h1

Seq. No. 30703

Contig ID 220721\_1.R1040 5'-most EST zhf700962540.h1

Method BLASTX
NCBI GI g2655098
BLAST score 263
E value 5.0e-23
Match length 98
% identity 46

NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

Seq. No. 30704

Contig ID 220723\_1.R1040 5'-most EST fua701038983.h1

Seq. No. 30705

Contig ID 220747\_1.R1040 5'-most EST zhf700962571.h1

Method BLASTX NCBI GI g861299

```
BLAST score
                  2.0e-21
E value
                  107
Match length
                  47
% identity
                  (U28742) highly similar to alpha-adaptin (rat and mouse)
NCBI Description
                  [Caenorhabditis elegans]
                  30706
```

Seq. No. 220765 1.R1040 Contiq ID dpv701096980.hl 5'-most EST

30707 Seq. No. 220766 1.R1040 Contig ID epx701110249.hl 5'-most EST

30708 Seq. No. 220819 1.R1040 Contig ID

 $jC-gms\overline{t}02400015h12a1$ 5'-most EST 30709

Seq. No. 220859 1.R1040 Contig ID  $gsv701\overline{0}45933.h1$ 5'-most EST

30710 Seq. No.

220860 1.R1040 Contig ID  $zhf700\overline{9}62718.h1$ 5'-most EST

30711 Seq. No.

220918 1.R1040 Contig ID zhf700962796.hl 5'-most EST

30712 Seq. No.

220919 1.R1040 Contig ID zhf700962801.h1 5'-most EST

BLASTX Method q3135274 NCBI GI 169 BLAST score 3.0e-12 E value 48 Match length 65 % identity

(AC003058) putative beta-1,3-endoglucanase [Arabidopsis NCBI Description

thaliana]

30713 Seq. No.

220930 1.R1040 Contig ID asn701138573.h1 5'-most EST

BLASTX Method q1881268 NCBI GI 190 BLAST score 2.0e-14 E value Match length 104 40 % identity

(AB001488) ATP-DEPENDENT RNA HELICASE DEAD HOMOLOG. NCBI Description [Bacillus subtilis] >gi\_2632758\_emb\_CAB12265\_ (Z99106)

similar to ATP-dependent RNA helicase [Bacillus subtilis]

30714 Seq. No.

4706



Contig ID 220955\_1.R1040 5'-most EST uC-gmronoir007g06b1

Seq. No. 30715

Contig ID 220981\_1.R1040

5'-most EST g5058284

Method BLASTX

NCBI GI g1709347

BLAST score 198

E value 2.0e-28

Match length 135
% identity 47

NCBI Description SERINE/THREONINE-PROTEIN KINASE NRK2 (SERINE/THREONINE

KINASE 2) >gi\_348245 (L20321) protein serine/threonine kinase [Homo sapiens] >gi 4507277\_ref\_NP\_003148.1\_pSTK2\_

serine/threonine kinase

Seq. No. 30716

Contig ID 221054 1.R1040 5'-most EST leu701149692.h1

Method BLASTX
NCBI GI g3335359
BLAST score 213
E value 6.0e-17
Match length 97
% identity 43

NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 30717

Contig ID 221056\_1.R1040 5'-most EST zhf700962968.h1

Seq. No. 30718

Contig ID 221077\_1.R1040 5'-most EST zhf700962990.h1

Seq. No. 30719

Contig ID 221083\_1.R1040 5'-most EST fjg700968335.h1

Seq. No. 30720

Contig ID 221133\_1.R1040 5'-most EST zhf700963053.h1

Method BLASTX
NCBI GI g4099835
BLAST score 212
E value 6.0e-20
Match length 72
% identity 56

NCBI Description (U90266) bifunctional nuclease [Zinnia elegans]

Seq. No. 30721

Contig ID 221199 1.R1040

5'-most EST uC-gmrominsoy088d07b1

Method BLASTN NCBI GI g3873174 BLAST score 33

4707



E value 7.0e-09 Match length 129 % identity 81

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14N23,

complete sequence [Arabidopsis thaliana]

Seq. No. 30722

Contig ID 221220 1.R1040 5'-most EST zhf700964947.h1

Method BLASTX
NCBI GI g1086249
BLAST score 338
E value 4.0e-32
Match length 90
% identity 70

NCBI Description subtilisin-like protease - Alnus glutinosa

>gi\_757522\_emb\_CAA59964\_ (X85975) subtilisin-like protease

[Alnus glutinosa]

Seq. No. 30723

Contig ID 221222\_1.R1040 5'-most EST zhf700963158.h1

Method BLASTX
NCBI GI g4539460
BLAST score 166
E value 1.0e-11
Match length 108
% identity 4

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 30724

Contig ID 221242 1.R1040 5'-most EST zhf700963180.h1

Method BLASTX
NCBI GI g1711512
BLAST score 311
E value 1.0e-28
Match length 59
% identity 95

NCBI Description SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54)

>gi\_1076577\_pir\_\_S51598 signal recognition particle 54K
protein - tomato (cv. UC82-B) >gi\_556902\_emb\_CAA84288\_
(Z34527) 54-kD signal recognition particle (SRP) specific

protein [Lycopersicon esculentum]

Seq. No. 30725

Contig ID 221353\_1.R1040 5'-most EST pxt700941791.h1

Method BLASTX
NCBI GI g1707019
BLAST score 216
E value 1.0e-17
Match length 114
% identity 37

NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30726



Contig ID 221360\_1.R1040 5'-most EST zhf700963625.h1

Seq. No. 30727

Contig ID 221367\_1.R1040 5'-most EST zhf700963334.h1

Seq. No. 30728

Contig ID 221370\_1.R1040

5'-most EST jC-gmle01810093h12d1

Method BLASTX
NCBI GI g1841468
BLAST score 339
E value 8.0e-32
Match length 87
% identity 67

NCBI Description (Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]

Seq. No. 30729

Contig ID 221434 1.R1040 5'-most EST zhf700963418.h1

Seq. No. 30730

Contig ID 221469 1.R1040 5'-most EST zhf700963457.h1

Method BLASTX
NCBI GI g1778015
BLAST score 554
E value 9.0e-57
Match length 217
% identity 53

NCBI Description (U59508) osmotic stress-induced proline dehydrogenase

[Arabidopsis thaliana]

Seq. No. 30731

Contig ID 221472\_1.R1040

5'-most EST uC-gmflminsoy028b06b1

Seq. No. 30732

Contig ID 221487\_1.R1040 5'-most EST uC-gmropic073g07b1

Seq. No. 30733

Contig ID 221501 1.R1040 5'-most EST zhf700963596.h1

Method BLASTX
NCBI GI g2213884
BLAST score 259
E value 2.0e-22
Match length 91
% identity 57

NCBI Description (AF004166) 2-isopropylmalate synthase [Lycopersicon

pennellii]

Seq. No. 30734

Contig ID 221566 1.R1040 5'-most EST zhf700963591.h1

Method

NCBI GI

E value

BLAST score

BLASTX

169

q4220461

9.0e-12



```
30735
Seq. No.
Contig ID
                  221576 1.R1040
5'-most EST
                  q5606666
Method
                  BLASTX
NCBI GI
                  q3004564
BLAST score
                  193
E value
                  1.0e-14
Match length
                  79
% identity
                  52
                  (AC003673) putative receptor Ser/Thr protein kinase
NCBI Description
                  [Arabidopsis thaliana]
                  30736
Seq. No.
                  221590_1.R1040
Contig ID
5'-most EST
                  epx701106304.h1
                  BLASTX
Method
NCBI GI
                  g3269289
BLAST score
                  152
                  4.0e-10
E value
                  50
Match length
                  64
% identity
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                  30737
Contig ID
                  221624 1.R1040
                  jC-gmf\overline{1}02220084f12a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2842496
BLAST score
                  147
                  2.0e-09
E value
Match length
                  32
% identity
                  81
NCBI Description (AL021749) NAM / CUC2 -like protein [Arabidopsis thaliana]
                  30738
Seq. No.
                  221631 1.R1040
Contig ID
5'-most EST
                  zhf700964218.h1
                  BLASTX
Method
                  g2979544
NCBI GI
BLAST score
                  238
                  7.0e-20
E value
Match length
                  96
                  47
% identity
NCBI Description (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]
                  30739
Seq. No.
                  221687 1.R1040
Contig ID
5'-most EST
                  zhf700963743.h1
                  30740
Seq. No.
                  221730 1.R1040
Contig ID
                  zhf700963803.h1
5'-most EST
```



Match length 114 % identity 37

NCBI Description (AC006216) ESTs gb\_T75642 and gb\_AA650997 come from this

gene. [Arabidopsis thaliana]

Seq. No. 30741

Contig ID 221741\_1.R1040 5'-most EST leu701156407.h1

Seq. No. 30742

Contig ID 221754\_1.R1040

5'-most EST uC-gmrominsoy061f11b1

Method BLASTN
NCBI GI g556421
BLAST score 53
E value 6.0e-21
Match length 113
% identity 87

NCBI Description Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1)

mRNA, complete cds

Seq. No. 30743

Contig ID 221773\_1.R1040 5'-most EST jC-gmle01810084d05a1

Method BLASTX
NCBI GI g4249412
BLAST score 582
E value 3.0e-60
Match length 146
% identity 76

NCBI Description (AC006072) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30744

Contig ID 221801\_1.R1040 5'-most EST zhf700963882.h1

Method BLASTX
NCBI GI g2252836
BLAST score 355
E value 5.0e-34
Match length 95
% identity 77

NCBI Description (AF013293) contains weak similarity to S. cerevisiae BOB1

protein (PIR:S45444) [Arabidopsis thaliana]

Seq. No. 30745

Contig ID 221828\_1.R1040 5'-most EST zhf700963921.h1

Method BLASTX
NCBI GI g4206209
BLAST score 320
E value 5.0e-30
Match length 74
% identity 80

NCBI Description (AF071527) putative glucan synthase component [Arabidopsis

thaliana] >gi\_4263042\_gb\_AAD15311\_ (AC005142) putative

glucan synthase component [Arabidopsis thaliana]



Seg. No. 30746

Contig ID 221845\_1.R1040 5'-most EST uC-gmropic099h12b1

Method BLASTX
NCBI GI g2285885
BLAST score 516
E value 1.0e-52
Match length 118
% identity 84

NCBI Description (D89631) sulfate transporter [Arabidopsis thaliana]

Seq. No. 30747

Contig ID 221845\_2.R1040 5'-most EST jsh701063802.h1

Method BLASTX
NCBI GI g2285885
BLAST score 407
E value 4.0e-40
Match length 97
% identity 79

NCBI Description (D89631) sulfate transporter [Arabidopsis thaliana]

Seq. No. 30748

Contig ID 221873 1.R1040

5'-most EST uC-qmflminsoy077h05b1

Seq. No. 30749

Contig ID 221884 1.R1040 5'-most EST dpv701102641.h1

Seq. No. 30750

Contig ID 221915\_1.R1040 5'-most EST zhf700964031.h1

Seq. No. 30751

Contig ID 221943\_1.R1040 5'-most EST zhf700964063.h1

Method BLASTX
NCBI GI g2252840
BLAST score 456
E value 3.0e-45
Match length 202
% identity 44

NCBI Description (AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No. 30752

Contig ID 221950\_1.R1040

5'-most EST uC-gmflminsoy077g11b1

Seq. No. 30753

Contig ID 222002\_1.R1040 5'-most EST fua701043085.h1

Method BLASTX
NCBI GI g3250679
BLAST score 282
E value 8.0e-26



Match length 86 % identity 64

NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 30754

Contig ID 222071\_1.R1040 5'-most EST uC-gmronoir030d08b1

Seq. No. 30755

Contig ID 222081\_1.R1040 5'-most EST zhf700964239.h1

Seq. No. 30756

Contig ID 222132\_1.R1040

5'-most EST jC-gmf102220108d01d1

Seq. No. 30757

Contig ID 222148\_1.R1040 5'-most EST zhf700964326.h1

Method BLASTX
NCBI GI g2108252
BLAST score 343
E value 2.0e-32
Match length 123
% identity 25

NCBI Description (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]

>gi\_2108254\_emb\_CAA71276\_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi\_4538925\_emb\_CAB39661.1\_

(AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No. 30758

Contig ID 222167\_1.R1040 5'-most EST fua701040929.h1

Seq. No. 30759

Contig ID 222211\_1.R1040 5'-most EST zhf700964402.h1

Seq. No. 30760

Contig ID 222220\_1.R1040 5'-most EST zsg701127981.h1

Method BLASTX
NCBI GI g629602
BLAST score 476
E value 5.0e-92
Match length 302
% identity 58

NCBI Description probable imbibition protein - wild cabbage

>gi\_488787\_emb\_CAA55893\_ (X79330) putative imbibition

protein [Brassica oleracea]

Seq. No. 30761

Contig ID 222252 1.R1040 5'-most EST zhf700964451.h1

Seq. No. 30762

Contig ID 222263 1.R1040



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zhf700964464.h1
5'-most EST
Seq. No.
                  30763
Contig ID
                  222273 1.R1040
5'-most EST
                  zsg701123360.h1
                  30764
Seq. No.
                  222292 1.R1040
Contig ID
                  zhf700964501.h1
5'-most EST
                  BLASTX
Method
                  g3540181
NCBI GI
BLAST score
                  561
E value
                  7.0e-76
Match length
                  203
% identity
                  70
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
                  30765
Seq. No.
                  222300 1.R1040
Contig ID
5'-most EST
                  uC-gmropic104h05b1
                  BLASTN
Method
NCBI GI
                  g2330650
BLAST score
                  141
E value
                  2.0e-73
Match length
                  377
% identity
                  84
NCBI Description Pisum sativum mRNA for topoisomerase II
                  30766
Seq. No.
                  222338 1.R1040
Contig ID
5'-most EST
                  zhf700964559.h1
Method
                  BLASTN
                  g3786500
NCBI GI
BLAST score
                  33
E value
                  4.0e-09
Match length
                  59
% identity
NCBI Description Caenorhabditis elegans cosmid T06A4
Seq. No.
                  30767
                  222412 1.R1040
Contig ID
5'-most EST
                  zhf700964650.hl
Method
                  BLASTX
NCBI GI
                  g2642448
BLAST score
                  161
E value
                  6.0e-11
Match length
                  131
% identity
                  12
NCBI Description
                  (AC002391) hypothetical protein [Arabidopsis thaliana]
                  >gi_3169187 (AC004401) hypothetical protein [Arabidopsis
                  thalianal
```

Seq. No. 30768

222417 1.R1040 Contig ID zhf700964656.hl 5'-most EST

Seq. No. 30769



Contig ID 222493\_1.R1040 5'-most EST asj700967309.h1

Method BLASTX
NCBI GI g728868
BLAST score 197
E value 2.0e-15
Match length 52
% identity 69

NCBI Description ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)

>gi\_99824\_pir\_\_S16748 proline-rich protein - rape

(fragment) >gi\_22597\_emb\_CAA42924\_ (X60376) proline-rich

protein [Brassica napus]

Seq. No. 30770

Contig ID 222514\_1.R1040 5'-most EST zhf700964776.h1

Method BLASTX
NCBI GI g2921340
BLAST score 668
E value 7.0e-70
Match length 201
% identity 66

NCBI Description (AF034134) MYB-like DNA-binding domain protein [Gossypium

hirsutum]

Seq. No. 30771

Contig ID 222527\_1.R1040 5'-most EST leu701156718.h1

Seq. No. 30772

Contig ID 222546\_1.R1040 5'-most EST zhf700964815.h1

Method BLASTX
NCBI GI g3811347
BLAST score 163
E value 1.0e-11
Match length 62
% identity 47

NCBI Description (AF065215) cytosolic phospholipase A2 beta [Homo sapiens]

Seq. No. 30773

Contig ID 222548 1.R1040 5'-most EST jC-gmle01810082b01a1

Method BLASTX
NCBI GI g3337366
BLAST score 339
E value 1.0e-31
Match length 122
% identity 26

NCBI Description (AC004481) unknown protein [Arabidopsis thaliana]

Seq. No. 30774

Contig ID 222569\_1.R1040 5'-most EST jC-gmfl02220060c12d1

Method BLASTX NCBI GI g960289 BLAST score 415



E value 2.0e-40
Match length 104
% identity 74

NCBI Description (L34343) anthranilate synthase alpha subunit [Ruta

graveolens]

Seq. No. 30775

Contig ID 222674\_1.R1040 5'-most EST zhf700964974.h1

Method BLASTX
NCBI GI g2739385
BLAST score 246
E value 5.0e-21
Match length 75
% identity 63

NCBI Description (AC002505) putative beta-1,3-glucanase [Arabidopsis

thaliana]

Seq. No. 30776

Contig ID 222699 1.R1040 5'-most EST zhf700965008.h1

Seq. No. 30777

Contig ID 222702 1.R1040

5'-most EST uC-gmrominsoy100b02b1

Seq. No. 30778

Contig ID 222753 1.R1040

5'-most EST uC-gmflminsoy036h05b1

Seq. No. 30779

Contig ID 222809\_1.R1040 5'-most EST zhf700965140.h1

Seq. No. 30780

Contig ID 222817 1.R1040 5'-most EST epx701107471.h1

Method BLASTX
NCBI GI g1172633
BLAST score 485
E value 7.0e-49
Match length 135
% identity 67

NCBI Description PROLIFERA PROTEIN >gi\_675491 (L39954) contains MCM2/3/5

family signature; PROSITE; PS00847; disruption leads to early lethal phenotype; similar to MCM2/3/5 family, most

similar to YBR1441 [Arabidopsis thaliana]

Seq. No. 30781

Contig ID 222827\_1.R1040 5'-most EST zhf700965161.h1

Method BLASTX
NCBI GI g4572671
BLAST score 216
E value 2.0e-17
Match length 75
% identity 56



(AC006954) putative cyclic nucleotide regulated ion channel NCBI Description [Arabidopsis thaliana]

30782 Seq. No.

222830 1.R1040 Contig ID

 $jC-gmf\overline{1}02220126d11a1$ 5'-most EST

BLASTX Method g3341693 NCBI GI 151 BLAST score 6.0e-10 E value 88 Match length 38 % identity

(AC003672) unknown protein [Arabidopsis thaliana] NCBI Description

30783 Seq. No.

222830 2.R1040 Contig ID zhf700965166.hl 5'-most EST

30784 Seq. No.

222843 1.R1040 Contig ID zhf700965182.hl 5'-most EST

30785 Seq. No.

222845 1.R1040 Contig ID zhf700965184.h1 5'-most EST

BLASTN Method g2654107 NCBI GI 280 BLAST score 1.0e-156 E value Match length 528 88 % identity

Pisum sativum cytosine-5 DNA methyltransferase mRNA, NCBI Description

complete cds

30786 Seq. No.

222853 1.R1040 Contig ID 5'-most EST zhf700965201.hl

Method BLASTX q3953457 NCBI GI 187 BLAST score 5.0e-14 E value 72 Match length 50 % identity

(AC002328) F20N2.2 [Arabidopsis thaliana] NCBI Description

30787 Seq. No.

222876 1.R1040 Contig ID zhf700965225.h1 5'-most EST

BLASTX Method q3024898 NCBI GI BLAST score 400 E value 4.0e-39 109 Match length 69 % identity

PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA NCBI Description HELICASE KIAA0224 (HA4657) >gi\_1504028\_dbj\_BAA13213



KO3H1.2 of C.elegans(S41025) [Homo sapiens] >gi\_3123906 (AF038391) pre-mRNA splicing factor [Homo sapiens]

30788 Seq. No. 222891 1.R1040 Contig ID  $\texttt{fC-gmro}\overline{\texttt{700565636z3}}$ 5'-most EST BLASTX Method g2924516 NCBI GI 761 BLAST score 2.0e-99 E value 234 Match length 52 % identity (AL022023) WD-40 repeat protein (MSI3) [Arabidopsis NCBI Description thaliana] 30789 Seq. No. 222891 2.R1040 Contig ID fC-gmro700565636r2 5'-most EST BLASTX Method q3122389 NCBI GI 198 BLAST score 9.0e-16 E value 53 Match length 79 % identity WD-40 REPEAT PROTEIN MSI3 >gi 2394233 (AF016848) WD-40 NCBI Description repeat protein [Arabidopsis thaliana] 30790 Seq. No. 222912 1.R1040 Contig ID zhf700965271.h1 5'-most EST BLASTX Method g3165536 NCBI GI 358 BLAST score 2.0e-34 E value 83 Match length 80 % identity (AF067608) similar to DEAD-box helicases (Pfam: DEAD.hmm, NCBI Description score: 262.89) (Pfam: helicase\_C.hmm, score: 76.21) [Caenorhabditis elegans] 30791 Seq. No. 222925 1.R1040 Contig ID g5678025 5'-most EST 30792 Seq. No. 222980 1.R1040 Contig ID all700863157.hl 5'-most EST BLASTX Method q2739002 NCBI GI 172 BLAST score E value 1.0e-12 81 Match length 37 % identity NCBI Description (AF022460) CYP83D1p [Glycine max]

4718

30793

223039 1.R1040

Seq. No.

Contig ID

```
jC-qmst02400072b08d1
5'-most EST
                  BLASTX
Method
                  g3874495
NCBI GI
                  242
BLAST score
                  2.0e-20
E value
                  70
Match length
                  66
% identity
                  (Z92826) predicted using Genefinder; cDNA EST EMBL:C09402
NCBI Description
                  comes from this gene [Caenorhabditis elegans]
                  30794
Seq. No.
                  223177 1.R1040
Contig ID
                  jC-gmle01810006b08d1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4106395
BLAST score
                  348
                  7.0e-33
E value
                  118
Match length
                   58
% identity
                  (AF073744) raffinose synthase [Cucumis sativus]
NCBI Description
                   30795
Seq. No.
                   223253 1.R1040
Contig ID
                  pmv700889558.h1
5'-most EST
                   30796
Seq. No.
                   223334 1.R1040
Contig ID
                   leu701152196.h1
5'-most EST
                   BLASTX
Method
                   g461735
NCBI GI
                   496
BLAST score
                   2.0e-50
E value
                   103
Match length
                   97
% identity
                   MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR
NCBI Description
                   >gi_478785_pir__S29315 chaperonin 60 - cucurbit
                   >gi_12544_emb_CAA50217_ (X70867) chaperonin 60 [Cucurbita
                   sp.]
                   30797
Seq. No.
                   223368 1.R1040
Contig ID
                   g4105688
 5'-most EST
                   BLASTX
Method
                   q3790677
NCBI GI
BLAST score
                   249
                   8.0e-35
 E value
                   307
Match length
                   35
 % identity
                   (AF099002) similar to human 5'-nucleotidase (SW:P49902)
 NCBI Description
                    [Caenorhabditis elegans]
                    30798
 Seq. No.
```

223373 1.R1040 Contig ID

jC-gmr002910006a09a1 5'-most EST

30799 Seq. No.

223463 1.R1040 Contig ID

```
kl1701214569.hl
5'-most EST
                   30800
Seq. No.
                   223518 1.R1040
Contig ID
```

pxt700942813.h1 5'-most EST BLASTX Method g2980773 NCBI GI 148 BLAST score 1.0e-09 E value 57

Match length 27 % identity

(AL022198) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 223520 1.R1040 Contig ID crh700850473.hl 5'-most EST BLASTX Method g2160163 NCBI GI 270 BLAST score

30801

5.0e-24 E value 70 Match length 45 % identity

(AC000132) No definition line found [Arabidopsis thaliana] NCBI Description

30802 Seq. No. 223612 2.R1040 Contig ID pxt700942360.hl 5'-most EST

30803 Seq. No. 223620 1.R1040 Contig ID crh700850690.h1 5'-most EST BLASTN Method g4220643 NCBI GI

35 BLAST score 4.0e-10 E value 51 Match length 92 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MWD22, complete sequence [Arabidopsis thaliana]

30804 Seq. No. 223624 1.R1040 Contig ID jC-gmro02910062f05a1 5'-most EST

30805 Seq. No. 223633 1.R1040 Contig ID

zsq701124347.h1 5'-most EST 30806 Seq. No.

Contig ID 5'-most EST uC-qmrominsoy095a06b1 Method BLASTX q2244799 NCBI GI 430 BLAST score 3.0e-42 E value

223730 1.R1040

Match length 191 % identity 46



NCBI Description (Z97336) carnitine racemase homolog [Arabidopsis thaliana]

Seq. No. 30807

Contig ID 223748\_1.R1040 5'-most EST crh700850888.h1

Method BLASTX
NCBI GI g3334489
BLAST score 208
E value 9.0e-17
Match length 67

Match length 67 % identity 60

NCBI Description DNA-DIRECTED RNA POLYMERASE I 190 KD POLYPEPTIDE

>gi\_82799\_pir\_\_JS0080 DNA-directed RNA polymerase (EC
2.7.7.6) T 189K chain - fission yeast (Schizosaccharomyces
pombe) >gi\_173433 (M37411) RNA polymerase I largest subunit

[Schizosaccharomyces pombe] >gi\_2832886\_emb\_CAA16827\_ (AL021730) dna-directed rna polymerase i 190 kd subunit

[Schizosaccharomyces pombe]

Seq. No. 30808

Contig ID 223759 1.R1040 5'-most EST zsg701124765.h1

Seq. No. 30809

Contig ID 223827\_1.R1040 5'-most EST crh700851110.h1

Seq. No. 30810

Contig ID 223833\_1.R1040 5'-most EST crh700851118.h1

Seq. No. 30811

Contig ID 223874\_1.R1040 5'-most EST crh700851178.h1

Seq. No. 30812

Contig ID 223880\_1.R1040 5'-most EST crh700851184.h1

Seq. No. 30813

Contig ID 223889\_1.R1040 5'-most EST crh700851202.h1

Seq. No. 30814

Contig ID 223893\_1.R1040

5'-most EST jC-gmro02800034c08a1

Seq. No. 30815

Contig ID 223931\_1.R1040 5'-most EST crh700851424.h1

Method BLASTX
NCBI GI g3377805
BLAST score 168
E value 4.0e-17
Match length 73
% identity 59

NCBI Description (AF075597) contains similarity to several apoptosis or



programmed cell death proteins such as rat apoptosis
protein RP-8 (GB:M80601) [Arabidopsis thaliana]
>gi\_3912928\_gb\_AAC78712.1\_ (AF001308) putative zinc finger
protein [Arabidopsis thaliana]

Seq. No. 30816

Contig ID 224061\_1.R1040

5'-most EST jC-gmle01810022f06d1

Seq. No. 30817

Contig ID 224107\_1.R1040 5'-most EST crh700851516.h1

Method BLASTX
NCBI GI g3913425
BLAST score 635
E value 2.0e-66
Match length 144
% identity 88

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi\_2275203 (AC002337) RNA helicase isolog

[Arabidopsis thaliana]

Seq. No. 30818

Contig ID 224227\_1.R1040 5'-most EST kl1701215344.h1

Method BLASTX
NCBI GI g4454048
BLAST score 285
E value 2.0e-25
Match length 142
% identity 44

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 30819

Contig ID 224272\_1.R1040 5'-most EST crh700851772.h1

Method BLASTX
NCBI GI g3757515
BLAST score 510
E value 7.0e-52
Match length 146
% identity 69

NCBI Description (AC005167) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30820

Contig ID 224315\_1.R1040 5'-most EST crh700851837.h1

Seq. No. 30821

Contig ID 224329\_1.R1040 5'-most EST crh700851896.h1

Method BLASTN
NCBI GI 94519195
BLAST score 59
E value 1.0e-24
Match length 175
% identity 83

4722



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No. 30822

Contig ID 224343\_1.R1040 5'-most EST fC-gmse700851887f1

Method BLASTX
NCBI GI g4164145
BLAST score 451
E value 7.0e-45
Match length 158
% identity 54

NCBI Description (AB012205) gibberelin 3beta-hydroxylase [Lactuca sativa]

Seq. No. 30823

Contig ID 224366\_1.R1040 5'-most EST crh700856137.h1

Method BLASTX
NCBI GI g3004555
BLAST score 317
E value 3.0e-29
Match length 136
% identity 5

NCBI Description (AC003673) similar to salt inducible protein [Arabidopsis

thaliana]

Seq. No. 30824

Contig ID 224375\_1.R1040 5'-most EST crh700852006.h1

Method BLASTN
NCBI GI g2104682
BLAST score 81
E value 8.0e-38
Match length 245
% identity 84

NCBI Description V.faba mRNA for putative transciption factor (2861bp)

Seq. No. 30825

Contig ID 224379\_1.R1040 5'-most EST fC-gmse700851947f1

Method BLASTX
NCBI GI g2652938
BLAST score 521
E value 4.0e-53
Match length 132
% identity 47

NCBI Description (Z47554) orf [Zea mays]

Seq. No. 30826

Contig ID 224413\_1.R1040 5'-most EST gsv701049938.h1

Method BLASTX
NCBI GI g3183347
BLAST score 249
E value 8.0e-21
Match length 178
% identity 35

4723



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NCBI Description HYPOTHETICAL 48.5 KD PROTEIN C23C11.04C IN CHROMOSOME I

>gi\_2330768\_emb\_CAB11157\_ (Z98559) SPAC23C11.04c;
len:421aa, similar eg. to C. elegans Q19683, F21D5.5,
(250aa), fasta scores, opt:395, E():1.1e-32, (41.7%
identity in 223 aa overlap)also similar eg. to YMR156C,

YM31 YEAST, Q03796, hypothetical 27.4 kd

Seq. No. 30827

Contig ID 224473\_1.R1040 5'-most EST pxt700943889.h1

Seq. No. 30828

Contig ID 224498\_1.R1040 5'-most EST crh700852121.h1

Seq. No. 30829

Contig ID 224510\_1.R1040 5'-most EST crh700852272.h1

Seq. No. 30830

Contig ID 224522 1.R1040 5'-most EST fua701037333.h1

Seq. No. 30831

Contig ID 224546 1.R1040

5'-most EST uC-gmflminsoy043d11b1

Method BLASTX
NCBI GI g1130682
BLAST score 498
E value 1.0e-50
Match length 118
% identity 77

NCBI Description (Z46959) acetohydroxyacid synthase [Gossypium hirsutum]

Seq. No. 30832

Contig ID 224569 1.R1040 5'-most EST kll701206318.h1

Seq. No. 30833

Contig ID 224580\_1.R1040 5'-most EST fC-gmse700852258f1

Method BLASTX
NCBI GI g3980380
BLAST score 493
E value 4.0e-59
Match length 151
% identity 81

NCBI Description (AC004561) putative enolase [Arabidopsis thaliana]

Seq. No. 30834

Contig ID 224600\_1.R1040 5'-most EST crh700852284.h1

Method BLASTX
NCBI GI g4263791
BLAST score 504
E value 3.0e-51
Match length 137



% identity

(AC006068) putative receptor protein kinase [Arabidopsis NCBI Description

thaliana]

Seq. No. Contig ID 5'-most EST 30835 224708 1.R1040 epx701109365.hl

Seq. No.

30836

Contig ID 5'-most EST 224713 1.R1040 fC-qmse700852469f1

Method BLASTX q2497752 NCBI GI 320 BLAST score 1.0e-29 E value

116 Match length % identity 53

NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) NCBI Description

>gi 1321911\_emb\_CAA65475\_ (X96714) lipid transfer protein

[Prunus dulcis]

Seq. No.

30837

Contig ID 5'-most EST 224742 1.R1040 rlr700901185.hl

Seq. No.

30838

Contig ID 5'-most EST 224744 1.R1040 uC-gmropic016a07b1

Seq. No.

30839

Contig ID 5'-most EST 224806 1.R1040 crh700852610.hl

Seq. No.

30840

Contig ID 5'-most EST 224846 1.R1040 fC-gmro700844279d3

Seq. No.

30841

Contig ID 5'-most EST 224900 1.R1040  $leu701\overline{1}55145.h1$ 

BLASTX Method g3080375 NCBI GI 496 BLAST score 3.0e-50 E value Match length 124

75 % identity

NCBI Description (AL022580) putative protein [Arabidopsis thaliana]

Seq. No.

30842

Contig ID 5'-most EST 224907 1.R1040 crh700852746.h1

Seq. No.

30843

Contig ID 5'-most EST 224964 1.R1040 fC-qmse700839629g1

Seq. No.

30844



Contig ID 224998\_1.R1040

5'-most EST uC-gmrominsoy315b09b1

Seq. No. 30845

Contig ID 225100\_1.R1040 5'-most EST fC-gmse700852993a1

Method BLASTX
NCBI GI g2245136
BLAST score 503
E value 4.0e-51
Match length 111
% identity 74

NCBI Description (Z97344) trehalose-6-phosphate synthase homolog

[Arabidopsis thaliana]

Seq. No. 30846

Contig ID 225200\_1.R1040 5'-most EST kl1701207083.h1

Method BLASTX
NCBI GI g4538928
BLAST score 156
E value 2.0e-10
Match length 37
% identity 81

NCBI Description (AL049483) putative protein [Arabidopsis thaliana]

Seq. No. 30847

Contig ID 225226\_1.R1040 5'-most EST pmv700888944.h1

Seq. No. 30848

Contig ID 225254\_1.R1040 5'-most EST gsv701052672.h1

Seq. No. 30849

Contig ID 225292 1.R1040 5'-most EST crh700853334.h1

Method BLASTX
NCBI GI g2244986
BLAST score 257
E value 2.0e-22
Match length 94
% identity 28

NCBI Description (Z97340) FCA gamma [Arabidopsis thaliana]

Seq. No. 30850

Contig ID 225297\_1.R1040 5'-most EST crh700853339.h1

Seq. No. 30851

Contig ID 225363\_1.R1040 5'-most EST crh700853454.h1

Seq. No. 30852

Contig ID 225390 1.R1040 5'-most EST crh700853504.h1

Method BLASTN



```
g2330648
NCBI GI
                  154
BLAST score
                  5.0e-81
E value
                  321
Match length
                  88
% identity
                  Pisum sativum mRNA for topoisomerase I
NCBI Description
                  30853
Seq. No.
                   225444 1.R1040
Contig ID
                   asn701142024.h1
5'-most EST
                   30854
Seq. No.
                   225466 1.R1040
Contig ID
                   fC-gmse700853718a1
5'-most EST
                   BLASTX
Method
                   q3860250
NCBI GI
BLAST score
                   213
                   7.0e-17
E value
Match length
                   67
```

% identity 63 (AC005824) putative chloroplast prephenate dehydratase NCBI Description

[Arabidopsis thaliana]

30855 Seq. No. 225530 1.R1040 Contig ID jC-gmst02400051a07d1 5'-most EST

30856 Seq. No. 225584 1.R1040 Contig ID crh700853988.h1 5'-most EST BLASTX Method

g2129662 NCBI GI BLAST score 202 1.0e-21 E value 75 Match length 75 % identity

ovule-specific homeotic protein homolog A20 - Arabidopsis NCBI Description thaliana >gi\_1881536 (U37589) A20 [Arabidopsis thaliana]

30857 Seq. No.

225642 1.R1040 Contig ID crh700854105.h15'-most EST

Seq. No. 30858

225674 1.R1040 Contig ID jC-gmle01810067e07d1 5'-most EST

BLASTX Method q3819699 NCBI GI BLAST score 259 E value 3.0e-22 109 Match length 52 % identity

(AJ009609) BnMAP4K alpha2 [Brassica napus] NCBI Description

30859 Seq. No.

Contig ID 225722 1.R1040 uC-gmropic070e11b1 5'-most EST



Seq. No. 30860

Contig ID 225738\_1.R1040 5'-most EST crh700854306.h1

Seq. No. 30861

Contig ID 225747\_1.R1040 5'-most EST crh700854318.h1

Seq. No. 30862

Contig ID 225787\_1.R1040 5'-most EST crh700854410.h1

Seq. No. 30863

Contig ID 225837\_1.R1040 5'-most EST fC-gmse700854493a1

Method BLASTX
NCBI GI g4098647
BLAST score 382
E value 9.0e-37
Match length 94
% identity 76

NCBI Description (U80668) homogentisate 1,2-dioxygenase [Arabidopsis

thaliana]

Seq. No. 30864

Contig ID 225845\_1.R1040 5'-most EST crh700854505.h1

Seq. No. 30865

Contig ID 225882 1.R1040 5'-most EST crh700854563.h1

Seq. No. 30866

Contig ID 225890 1.R1040 5'-most EST leu701156924.h1

Method BLASTX
NCBI GI g4454018
BLAST score 224
E value 3.0e-18
Match length 101
% identity 48

NCBI Description (AL035396) SRG1-like protein [Arabidopsis thaliana]

Seq. No. 30867

Contig ID 225892\_1.R1040

5'-most EST jC-gmf102220144d07a1

Seq. No. 30868

Contig ID 225920\_1.R1040 5'-most EST crh700854630.h1

Seq. No. 30869

Contig ID 226016\_1.R1040

5'-most EST g4291148

Seq. No. 30870



Contig ID 226018\_1.R1040 5'-most EST gsv701054582.h1 Method BLASTX

Method BLASTX
NCBI GI g688423
BLAST score 122
E value 3.0e-11
Match length 90
% identity 41

NCBI Description (D26453) tumor-related protein [Nicotiana glauca X

Nicotiana langsdorffii]

Seq. No. 30871

Contig ID 226047\_1.R1040 5'-most EST leu701155547.h1

Seq. No. 30872

Contig ID 226056\_1.R1040 5'-most EST crh700854933.h1

Seq. No. 30873

Contig ID 226077 1.R1040

5'-most EST  $g56064\overline{49}$ 

Seq. No. 30874

Contig ID 226077 2.R1040 5'-most EST gsv701046666.h1

Seq. No. 30875

Contig ID 226092\_1.R1040 5'-most EST crh700855006.h1

Seq. No. 30876

Contig ID 226104\_1.R1040 5'-most EST crh700855024.h1

Seq. No. 30877

Contig ID 226218\_1.R1040 5'-most EST crh700855435.h1

Seq. No. 30878

Contig ID 226277\_1.R1040 5'-most EST kll701206295.h1

Method BLASTX
NCBI GI g4325342
BLAST score 238
E value 3.0e-20
Match length 89
% identity 58

NCBI Description (AF128393) No definition line found [Arabidopsis thaliana]

Seq. No. 30879

Contig ID 226372\_1.R1040 5'-most EST fC-gmse700855772a1

Method BLASTX
NCBI GI g3822223
BLAST score 562
E value 6.0e-58



Match length 142 % identity 73

NCBI Description (AF077955) branched-chain alpha keto-acid dehydrogenase El alpha subunit [Arabidopsis thaliana]

Seq. No. 30880

Contig ID 226380\_1.R1040 5'-most EST crh700855811.h1

Seq. No. 30881

Contig ID 226414\_1.R1040 5'-most EST gsv701056785.h1

Seq. No. 30882

Contig ID 226476\_1.R1040 5'-most EST crh700856007.h1

Seq. No. 30883

Contig ID 226506\_1.R1040 5'-most EST crh700856088.h1

Method BLASTX
NCBI GI 94468984
BLAST score 323
E value 7.0e-30
Match length 107
% identity 59

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 30884

Contig ID 226510 1.R1040

5'-most EST jC-gmro02800042c09d1

Seq. No. 30885

Contig ID 226524\_1.R1040

5'-most EST jC-gmle01810002e05d1

Method BLASTX
NCBI GI g4056493
BLAST score 234
E value 2.0e-19
Match length 56
% identity 71

NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 30886

Contig ID 226561\_1.R1040

5'-most EST jC-gmf102220068e03a1

Method BLASTX
NCBI GI g2281090
BLAST score 437
E value 2.0e-43
Match length 114
% identity 76

NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30887

Contig ID 226756\_1.R1040 5'-most EST jC-gmst02400067d10d1



Seq. No. 30889

Contig ID 226783\_1.R1040

5'-most EST jC-gmle01810046b08d1

Seq. No. 30890

Contig ID 226821\_1.R1040

5'-most EST g5752647

Seq. No. 30891

Contig ID 226858\_1.R1040

5'-most EST jC-gmst02400073f08a1

Method BLASTX
NCBI GI g3395440
BLAST score 392
E value 2.0e-43
Match length 138
% identity 65

NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30892

Contig ID 226866\_1.R1040

5'-most EST uC-gmflminsoy065b03b1

Method BLASTX
NCBI GI g2623296
BLAST score 367
E value 5.0e-35
Match length 150
% identity 52

NCBI Description (AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30893

Contig ID 226877 1.R1040

5'-most EST jC-gmst02400023c07a1

Seq. No. 30894

Contig ID 226881\_1.R1040 5'-most EST pmv700888211.h1

Method BLASTX
NCBI GI g2435522
BLAST score 537
E value 4.0e-55
Match length 127
% identity 74

NCBI Description (AF024504) contains similarity to other AMP-binding enzymes

[Arabidopsis thaliana]

Seq. No. 30895

Contig ID 226885\_1.R1040 5'-most EST pmv700888216.h1

Method BLASTX NCBI GI g4263795 BLAST score 156



E value 5.0e-12 Match length 58

% identity 66

NCBI Description (AC006068) putative glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 30896

Contig ID 226934\_1.R1040

5'-most EST jC-gmst02400033g10d1

Method BLASTX
NCBI GI g1711618
BLAST score 263
E value 2.0e-36
Match length 132
% identity 61

NCBI Description LOW AFFINITY SULPHATE TRANSPORTER 3 >gi 1085993 pir S51765

low affinity sulphate transporter - Stylosanthes hamata
>gi\_607188\_emb\_CAA57831\_ (X82454) low affinity sulphate

transporter [Stylosanthes hamata]

Seq. No. 30897

Contig ID 226960 1.R1040

5'-most EST jC-gmle01810053e09a1

Method BLASTX
NCBI GI g4335734
BLAST score 362
E value 3.0e-34
Match length 185
% identity 42

NCBI Description (AC006248) putative calmodulin [Arabidopsis thaliana]

Seq. No. 30898

Contig ID 226961\_1.R1040 5'-most EST pmv700888312.h1

Seq. No. 30899

Contig ID 226967 1.R1040

5'-most EST jC-gmst02400025f05a1

Method BLASTX
NCBI GI 94220462
BLAST score 903
E value 1.0e-97
Match length 211
% identity 84

NCBI Description (AC006216) Strong similarity to gb\_Z50851 HD-zip (athb-8)

gene from Arabidopsis thaliana containing Homeobox PF\_00046

and bZIP PF\_00170 domains. [Arabidopsis thaliana]

Seq. No. 30900

Contig ID 226977\_1.R1040 5'-most EST pmv700890884.h1

Seq. No. 30901

Contig ID 226981\_1.R1040 5'-most EST pmv700888336.h1

Seq. No. 30902

227026 1.R1040 Contig ID 5'-most EST pmv700892102.h1 30903 Seq. No. 227040 2.R1040 Contig ID pmv700888509.hl 5'-most EST 30904 Seq. No. 227045 1.R1040 Contig ID pmv700888414.h1 5'-most EST 30905 Seq. No. Contig ID 227057 1.R1040 g4284686 5'-most EST BLASTX Method g1755192 NCBI GI BLAST score 201 5.0e-26 E value Match length 95 66 % identity (U75207) germin-like protein [Arabidopsis thaliana] NCBI Description 30906 Seq. No. Contig ID 227060 1.R1040 5'-most EST uC-gmropic018d03b1 30907 Seq. No. 227081 1.R1040 Contig ID 5'-most EST jsh701069769.h1 BLASTX Method g1703376 NCBI GI 297 BLAST score 3.0e-27 E value Match length 67 85 % identity ADP-RIBOSYLATION FACTOR 1 >gi 480121 pir S36453 NCBI Description ADP-ribosylation factor 1 - potato >gi\_396808 emb\_CAA52468 (X74461) ADP-ribosylation factor 1 [Solanum tuberosum] 30908 Seq. No. 227097 1.R1040 Contig ID pmv700888489.h1 5'-most EST Seq. No. 30909 227101 1.R1040 Contig ID 5'-most EST pmv700888494.h1 Method BLASTN

Method BLASTN
NCBI GI 9429107
BLAST score 100
E value 4.0e-49
Match length 248
% identity 85

NCBI Description L.esculentum S-adenosyl-L-methionine synthetase mRNA,

complete CDS

Seq. No. 30910

Contig ID 227192 1.R1040



5'-most EST jC-gmf102220089a09d1

Seq. No. 30911

Contig ID 227194\_1.R1040 5'-most EST leu701155561.h1

Seq. No. 30912

Contig ID 227202\_1.R1040

5'-most EST jC-gmst02400034g02d2

Seq. No. 30913

Contig ID 227289\_1.R1040 5'-most EST pmv700888746.h1

Seq. No. 30914

Contig ID 227328\_1.R1040 5'-most EST pmv700888821.h1

Method BLASTX
NCBI GI g4249411
BLAST score 210
E value 1.0e-16
Match length 42
% identity 93

NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 30915

Contig ID 227329\_1.R1040 5'-most EST pmv700888822.h1

Seq. No. 30916

Contig ID 227360\_1.R1040 5'-most EST leu701154547.h1

Seq. No. 30917

Contig ID 227369\_1.R1040 5'-most EST uC-gmropic007h11b1

Method BLASTX
NCBI GI g1076315
BLAST score 172
E value 3.0e-12
Match length 101
% identity 40

NCBI Description cytochrome P450 - Arabidopsis thaliana

>qi 853719 emb CAA60793 (X87367) CYP90 protein

[Arabidopsis thaliana] >gi\_871988\_emb\_CAA60794\_ (X87368)

CYP90 protein [Arabidopsis thaliana]

Seq. No. 30918

Contig ID 227373\_1.R1040 5'-most EST pmv700888873.h1

Seq. No. 30919

Contig ID 227387\_1.R1040 5'-most EST rlr700896045.h1

Seq. No. 30920

Contig ID 227421\_1.R1040



```
pmv700888935.h1
5'-most EST
Method
                  BLASTX
                  q4539369
NCBI GI
                  189
BLAST score
                  4.0e-14
E value
                  65
Match length
                  62
% identity
                  (AL049525) putative protein [Arabidopsis thaliana]
NCBI Description
                  30921
Seq. No.
                  227423 1.R1040
Contig ID
                  jC-gmle01810031a08d1
5'-most EST
Seq. No.
                  30922
                  227431 1.R1040
Contig ID
                  uC-gmropic034h09b1
5'-most EST
                  BLASTX
Method
                   g3548802
NCBI GI
BLAST score
                   502
                   6.0e-51
E value
                   146
Match length
                   63
% identity
                  (AC005313) axi 1-like protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4335769 gb AAD17446 (AC006284) putative axil protein
                   [Nicotiana tabacum] [Arabidopsis thaliana]
                   30923
Seq. No.
                   227446 1.R1040
Contig ID
                   pmv700888964.hl
5'-most EST
                   BLASTX
Method
                   q3522956
NCBI GI
BLAST score
                   238
                   2.0e-22
E value
Match length
                   88
% identity
                   58
                  (AC004411) putative pectinacetylesterase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   30924
Seq. No.
                   227451 1.R1040
Contig ID
                   fC-qmro700869490f2
 5'-most EST
                   BLASTX
Method
                   g1703318
NCBI GI
BLAST score
                   483
                   2.0e-48
E value
                   119
Match length
 % identity
                   77
                   ANNEXIN-LIKE PROTEIN RJ4 >gi 1362037_pir__S56674 annexin
 NCBI Description
                   homolog RJ4 (clone RJ4) - garden strawberry (fragment)
                   >gi 643076 (U19941) annexin [Fragaria x ananassa]
```

30925 Seq. No.

227452 1.R1040 Contig ID pmv700888972.h1 5'-most EST

Method BLASTX g2494231 NCBI GI 182 BLAST score



E value 7.0e-14
Match length 89
% identity 47

musculus]

Seq. No. 30926

Contig ID 227471\_1.R1040 5'-most EST pxt700944495.h1

Seq. No. 30927

Contig ID 227472\_1.R1040 5'-most EST pmv700888994.h1

Seq. No. 30928

Contig ID 227528\_1.R1040 5'-most EST pxt700942665.h1

Method BLASTX
NCBI GI g1420936
BLAST score 1002
E value 1.0e-109
Match length 237
% identity 76

NCBI Description (U61396) Vigna unguiculata aspartic proteinase mRNA,

complete cds. [Vigna unguiculata]

Seg. No. 30929

Contig ID 227532 1.R1040 5'-most EST asn701134848.h2

Method BLASTX
NCBI GI g3386605
BLAST score 168
E value 5.0e-22
Match length 86
% identity 57

NCBI Description (AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30930

Contig ID 227551\_1.R1040 5'-most EST pmv700889088.h1

Seq. No. 30931

Contig ID 227554\_1.R1040 5'-most EST pxt700941410.h1

Seq. No. 30932

Contig ID 227589 1.R1040

5'-most EST jC-gmle01810049a08d1

Seq. No. 30933

Contig ID 227602\_1.R1040 5'-most EST pmv700889151.h1

Method BLASTX
NCBI GI g1742955
BLAST score 667
E value 4.0e-70



Match length 202 % identity 67

NCBI Description (Z71446) CLC-b chloride channel protein [Arabidopsis

thaliana]

Seq. No. 30934

Contig ID 227643\_1.R1040 5'-most EST rlr700898408.h1

Method BLASTX
NCBI GI g584861
BLAST score 159
E value 7.0e-11
Match length 57
% identity 54

NCBI Description CYTOCHROME P450 71A2 (CYPLXXIA2) (P-450EG4)

>qi\_480396\_pir\_\_\_S36806 cytochrome P450 71A2 - eggplant
>gi\_408140\_emb\_CAA50645\_ (X71654) P450 hydroxylase [Solanum melongena] >gi\_441185\_dbj\_BAA03635\_ (D14990) Cytochrome

P-450EG4 [Solanum melongena]

Seq. No. 30935

Contig ID 227697\_1.R1040 5'-most EST jC-gmst02400036e11d2

Seq. No. 30936

Contig ID 227708\_1.R1040

5'-most EST jC-gmst02400006f10d1

Seq. No. 30937

Contig ID 227723\_1.R1040 5'-most EST fC-gmro700869757f5

Method BLASTX
NCBI GI g2511693
BLAST score 608
E value 6.0e-63
Match length 170
% identity 62

NCBI Description (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No. 30938

Contig ID 227731\_1.R1040 5'-most EST kl1701214248.h1

Seq. No. 30939

Contig ID 227737 1.R1040

5'-most EST uC-gmrominsoy247f08b1

Seq. No. 30940

Contig ID 227742\_1.R1040 5'-most EST pmv700889626.h1

Seq. No. 30941

Contig ID 227747\_1.R1040 5'-most EST pmv700893691.h1

Method BLASTX NCBI GI g3892057 BLAST score 252



```
4.0e-22
E value
                  69
Match length
                  32
% identity
                  (AC002330) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  30942
Seq. No.
                  227769 1.R1040
Contig ID
                  pmv700889360.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3258569
                  465
BLAST score
                  1.0e-46
E value
                  121
Match length
                  79
% identity
                  (U89959) Similar to yeast general negative regulator of
NCBI Description
                  transcription subunit 1 [Arabidopsis thaliana]
                  30943
Seq. No.
                  227797 1.R1040
Contig ID
                  pmv700889393.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3327271
BLAST score
                  231
                  3.0e-19
E value
                  100
Match length
                  52
% identity
                  (AB016000) PKn2 [Ipomoea nil]
NCBI Description
                  30944
Seq. No.
                  227918 1.R1040
Contig ID
                  g4300792
5'-most EST
                  30945
Seq. No.
                  227960 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910047b01a1
                  BLASTX
Method
                  g4490300
NCBI GI
                   430
BLAST score
E value
                  2.0e-42
                  121
Match length
                   73
% identity
                  (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   30946
Seq. No.
                   227989 1.R1040
Contig ID
5'-most EST
                  pxt700940986.h1
                   BLASTX
Method
                   q1360090
NCBI GI
                   300
BLAST score
                   2.0e-27
E value
                   106
Match length
                   60
```

% identity (X95576) C1C-Nt1 [Nicotiana tabacum] NCBI Description

30947

Seq. No. Contig ID 228004 1.R1040 5'-most EST leu701154017.h1



Seq. No. 30948

Contig ID 228031\_1.R1040 5'-most EST fC-gmro700870127f3

Method BLASTX
NCBI GI g3269291
BLAST score 417
E value 8.0e-41
Match length 181
% identity 49

NCBI Description (AL030978) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 30949

Contig ID 228040\_1.R1040 5'-most EST gsv701054529.h1

Seq. No. 30950

Contig ID 228042\_1.R1040 5'-most EST fC-gmro700870195a4

Method BLASTX
NCBI GI g2853078
BLAST score 147
E value 4.0e-09
Match length 161
% identity 19

NCBI Description (AL021768) TMV resistance protein N-like [Arabidopsis

thaliana]

Seq. No. 30951

Contig ID 228046\_1.R1040 5'-most EST pmv700889742.h1

Method BLASTX
NCBI GI g2914698
BLAST score 388
E value 8.0e-40
Match length 190
% identity 45

NCBI Description (AC003974) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30952

Contig ID 228054\_1.R1040 5'-most EST dkc700968025.h1

Seq. No. 30953

Contig ID 228054\_2.R1040 5'-most EST jsh701064341.h1

Seq. No. 30954

Contig ID 228054\_3.R1040 5'-most EST pxt700942158.h1

Seq. No. 30955

Contig ID 228064\_1.R1040 5'-most EST hrw701063230.h1

Seq. No. 30956



Contig ID 228066\_1.R1040 5'-most EST pmv700889774.h1

Seq. No. 30957

Contig ID 228121\_1.R1040 5'-most EST epx701106844.h1

Method BLASTX
NCBI GI g3695019
BLAST score 287
E value 6.0e-26
Match length 97
% identity 57

NCBI Description (AF055848) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 30958

Contig ID 228141\_1.R1040 5'-most EST jC-gmle01810063e05a1

Seq. No. 30959

Contig ID 228145\_1.R1040 5'-most EST fC-gmle700870650f3

Method BLASTX
NCBI GI g2129698
BLAST score 669
E value 2.0e-93
Match length 219
% identity 79

NCBI Description protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana

->qi 1054633 emb CAA63387 (X92728) protein kinase

[Arabidopsis thaliana]

Seq. No. 30960

Contig ID 228152 1.R1040

5'-most EST jC-gmst02400005g06a1

Seq. No. 30961

Contig ID 228155 1.R1040

5'-most EST jC-gmro02910004e07a1

Seq. No. 30962

Contig ID 228157\_1.R1040 5'-most EST pmv700889894.h1

Method BLASTX
NCBI GI g3935181
BLAST score 184
E value 4.0e-20
Match length 60
% identity 83

NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No. 30963

Contig ID 228167\_1.R1040 5'-most EST pmv700889912.h1

Method BLASTX
NCBI GI g2832661
BLAST score 323
E value 4.0e-30



Match length 59 % identity

(AL021710) pherophorin - like protein [Arabidopsis NCBI Description

thaliana]

30964 Seq. No.

228182 1.R1040 Contig ID 5'-most EST pmv700889931.h1

Seq. No. 30965

228189 1.R1040 Contig ID 5'-most EST pxt700943687.hl

30966 Seq. No.

228211 1.R1040 Contig ID fua701037866.h1 5'-most EST

30967 Seq. No.

228351 1.R1040 Contig ID r1r700899917.h15'-most EST

Seq. No. 30968

228353 1.R1040 Contig ID

uC-gmflminsoy043h09b1 5'-most EST

Method BLASTX g2498329 NCBI GI BLAST score 435 E value 4.0e-43 Match length 139 % identity 63

NCBI Description

PATTERN FORMATION PROTEIN EMB30 >gi 2129665 pir S65571 pattern-formation protein GNOM - Arabidopsis thaliana

>gi\_1209633 (U36433) GNOM gene product [Arabidopsis

thaliana] >qi 1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi 1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession

Number J03918 [Arabidopsis thaliana]

30969 Seq. No.

228366 1.R1040 Contig ID

5'-most EST uC-gmflminsoy035g07b1

Seq. No. 30970

228375 1.R1040 Contig ID uC-gmropic045h04b1 5'-most EST

BLASTX Method NCBI GI q3695059 BLAST score 531 E value 3.0e-54155 Match length 70 % identity

(AF064787) rac GTPase activating protein 1 [Lotus NCBI Description

japonicus]

Seq. No. 30971

228393 1.R1040 Contig ID



5'-most EST uC-gmrominsoy277g05b1

Method BLASTX
NCBI GI g4218120
BLAST score 231
E value 5.0e-19
Match length 144
% identity 35

NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis

thaliana]

Seq. No. 30972

Contig ID 228398\_1.R1040 5'-most EST jC-gmst02400044f01a1

Method BLASTX
NCBI GI g1350783
BLAST score 667
E value 8.0e-70
Match length 321
% identity 48

NCBI Description RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR

>gi\_282883\_pir\_\_S27756 receptor-like protein kinase
precursor - Arabidopsis thaliana >gi\_166850 (M84660)
receptor-like protein kinase [Arabidopsis thaliana]

>qi 2842492 emb CAA16889 (AL021749) receptor-like protein

kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No. 30973

Contig ID 228435\_1.R1040 5'-most EST fC-gmle700871051f3

Method BLASTX
NCBI GI g4539383
BLAST score 379
E value 9.0e-37
Match length 93
% identity 76

NCBI Description (AL035526) putative protein (fragment) [Arabidopsis

thaliana]

Seq. No. 30974

Contig ID 228442\_1.R1040

5'-most EST jC-gmst02400047d09a1

Seq. No. 30975

Contig ID 228471\_1.R1040 5'-most EST pmv700892204.h1

Seq. No. 30976

Contig ID 228489\_1.R1040 5'-most EST pmv700892264.h1

Method BLASTX
NCBI GI g4115563
BLAST score 268
E value 2.0e-26
Match length 82
% identity 71

NCBI Description (AB013598) UDP-glucose:anthocyanin 5-0-glucosyltransferase

[Verbena x hybrida]



```
      Seq. No.
      30977

      Contig ID
      228491_1.R1040

      5'-most EST
      pmv700890335.h1

      Method
      BLASTX

      NCBI GI
      g3258575

      BLAST score
      225
```

E value 2.0e-22 Match length 79 % identity 71

NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 30978

Contig ID 228499\_1.R1040 5'-most EST pmv700892214.h1

Seq. No. 30979

Contig ID 228503\_1.R1040 5'-most EST pmv700892258.h1

Seq. No. 30980

Contig ID 228506\_1.R1040 5'-most EST pmv700890392.h1

Seq. No. 30981

Contig ID 228509 1.R1040 5'-most EST kl1701203832.h1

Seq. No. 30982

Contig ID 228524\_1.R1040 5'-most EST pmv700892272.h1

Method BLASTX
NCBI GI g1865677
BLAST score 326
E value 8.0e-31
Match length 74
% identity 76

NCBI Description (Y08568) trehalose-6-phosphate synthase [Arabidopsis

thaliana]

Seq. No. 30983

Contig ID 228578\_1.R1040 5'-most EST gsv701052775.h1

Method BLASTX
NCBI GI g2578818
BLAST score 168
E value 7.0e-12
Match length 75
% identity 51

NCBI Description (AB000121) TBPIP [Mus musculus]

Seq. No. 30984

Contig ID 228691\_1.R1040 5'-most EST jC-gmst02400011b05d1

Method BLASTX NCBI GI g3327178 BLAST score 224



E value 3.0e-18
Match length 139
% identity 15

NCBI Description (AB014582) KIAA0682 protein [Homo sapiens]

Seq. No. 30985

Contig ID 228736\_1.R1040 5'-most EST pmv700890653.h1

Seq. No. 30986

Contig ID 228747 1.R1040

5'-most EST uC-gmflminsoy030g05b1

Method BLASTX
NCBI GI 94522005
BLAST score 193
E value 1.0e-19
Match length 125
% identity 43

NCBI Description (AC007069) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 30987

Contig ID 228774\_1.R1040 5'-most EST pmv700890711.h1

Seq. No. 30988

Contig ID 228780 1.R1040

5'-most EST jC-qmle01810022d12d1

Seq. No. 30989

Contig ID 228784\_1.R1040

5'-most EST jC-gmst02400054e12a1

Seq. No. 30990

Contig ID 228875\_1.R1040 5'-most EST uC-gmropic059g07b1

Seq. No. 30991

Contig ID 228929\_1.R1040 5'-most EST uC-gmropic059h02b1

Method BLASTX
NCBI GI g3695019
BLAST score 277
E value 1.0e-24
Match length 101
% identity 54

NCBI Description (AF055848) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 30992

Contig ID 228979 1.R1040 5'-most EST fC-gmf1700898910f1

Method BLASTX
NCBI GI g629722
BLAST score 227
E value 2.0e-18
Match length 188
% identity 37

4744



NCBI Description finger protein pcpl - potato >gi\_563623\_emb\_CAA57772\_ (X82328) putative DNA/RNA binding protein [Solanum

tuberosum]

Seq. No. 30993

Contig ID 229088\_1.R1040 5'-most EST fC-gmro7000749140r1

Seq. No. 30994

Contig ID 229101\_1.R1040 5'-most EST pmv700891126.h1

Seq. No. 30995

Contig ID 229117\_1.R1040 5'-most EST uC-gmropic025h05b1

Method BLASTX
NCBI GI g2104534
BLAST score 596
E value 5.0e-62
Match length 129
% identity 84

NCBI Description (AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30996

Contig ID 229131 1.R1040 5'-most EST kl1701213809.h1

Seq. No. 30997

Contig ID 229150\_1.R1040 5'-most EST zsg701124540.h1

Method BLASTX
NCBI GI g3880026
BLAST score 277
E value 1.0e-25
Match length 101
% identity 55

NCBI Description (Z75550) Similarity with Schizosaccharomyces hypothetical gene (TREMBL ID G847708); cDNA EST EMBL:M89418 comes from

this gene [Caenorhabditis elegans]

Seq. No. 30998

Contig ID 229155\_1.R1040 5'-most EST asn701133270.h1

Method BLASTX
NCBI GI g3763933
BLAST score 715
E value 1.0e-75
Match length 187
% identity 85

NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

Seq. No. 30999

Contig ID 229165\_1.R1040 5'-most EST pmv700891209.h1

Seq. No. 31000

Contig ID 229271 1.R1040

Seq. No.

Contig ID

31007

229425\_1.R1040



```
5'-most EST
                   q4284566
                   31001
Seq. No.
                   229294 1.R1040
Contig ID
                  pmv700891358.hl
5'-most EST
                  BLASTX
Method
                   g2827528
NCBI GI
BLAST score
                   333
                   6.0e-31
E value
Match length
                   108
% identity
                   64
                   (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
                   31002
Seq. No.
                   229303 1.R1040
Contig ID
                   kl1701202962.hl
5'-most EST
Method
                   BLASTX
                   g1747310
NCBI GI
BLAST score
                   158
E value
                   2.0e-17
Match length
                   73
% identity
                   73
NCBI Description
                   (D58424) Myb-like DNA binding protein [Arabidopsis
Seq. No.
                   31003
                   229314 1.R1040
Contig ID
5'-most EST
                   zsq701118417.h1
                   31004
Seq. No.
                   229330 1.R1040
Contig ID
5'-most EST
                   dpv701101822.h1
Seq. No.
                   31005
                   229365_1.R1040
Contig ID
                   pmv700891445.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2098709
BLAST score
                   426
                   4.0e-42
E value
                   118
Match length
                   68
% identity
                  (U82975) pectinesterase [Citrus sinensis]
NCBI Description
                   31006
Seq. No.
                   229382 1.R1040
Contig ID
                   pmv700891466.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3184285
BLAST score
                   143
                   5.0e-09
E value
                   49
Match length
                   55
% identity
                  (AC004136) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```



```
dpv701100873.h1
5'-most EST
                  BLASTX
Method
                  g4115384
NCBI GI
                  459
BLAST score
                   4.0e-46
E value
Match length
                  106
                  79
% identity
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  31008
                   229445 1.R1040
Contig ID
5'-most EST
                  pmv700891569.h1
Method
                  BLASTX
                   g3786021
NCBI GI
BLAST score
                   191
                   1.0e-14
E value
Match length
                   66
% identity
                   58
                  (AC005499) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   31009
Seq. No.
Contig ID
                   229465 1.R1040
5'-most EST
                   fC-gmle700872274f7
Method
                   BLASTX
                   q2760839
NCBI GI
                   756
BLAST score
                   4.0e-86
E value
Match length
                   252
% identity
                   67
                  (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
                   31010
Seq. No.
                   229503_1.R1040
Contig ID
                   jC-gmst02400001b07a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2827143
BLAST score
                   286
E value
                   6.0e-26
Match length
                   64
                   72
% identity
                   (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   31011
                   229607 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910024g02d1
Seq. No.
                   31012
                   229643 1.R1040
Contig ID
                   jC-gmro02910048b02a1
5'-most EST
                   BLASTX
Method
                   g3360289
NCBI GI
BLAST score
                   164
E value
                   3.0e-11
Match length
                   54
                   54
% identity
```



## 1 [Zea mays]

Seq. No. 31014

Contig ID 229658\_1.R1040 5'-most EST fC-gmle700873056f3

Method BLASTX
NCBI GI g2795809
BLAST score 319
E value 3.0e-29
Match length 64
% identity 88

NCBI Description (AC003674) putative expansin [Arabidopsis thaliana]

Seq. No. 31015

Contig ID 229664\_1.R1040 5'-most EST uC-gmropic096a08b1

Method BLASTX
NCBI GI g4539314
BLAST score 193
E value 2.0e-14
Match length 89
% identity 51

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 31016

Contig ID 229704\_1.R1040 5'-most EST pmv700891910.h1

Method BLASTN
NCBI GI g1850545
BLAST score 34
E value 2.0e-09
Match length 115
% identity 89

NCBI Description Arabidopsis thaliana syntaxin related protein AtVam3p

(AtVAM3) mRNA, complete cds

Seq. No. 31017

Contig ID 229839\_1.R1040 5'-most EST fC-gmle700873194f3

Method BLASTX
NCBI GI g1350783
BLAST score 400
E value 6.0e-39
Match length 149
% identity 9

NCBI Description RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR

>gi\_282883\_pir\_\_S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >gi\_166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana]

>gi 2842492\_emb\_CAA16889\_ (AL021749) receptor-like protein

kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No. 31018



Contig ID 229855\_1.R1040 5'-most EST rlr700896085.h1

Method BLASTX
NCBI GI g1946360
BLAST score 249
E value 1.0e-21
Match length 84
% identity 57

NCBI Description (U93215) elicitor response element binding protein WRKY3

isolog [Arabidopsis thaliana]

Seq. No. 31019

Contig ID 229856\_1.R1040 5'-most EST asn701130917.h1

Seq. No. 31020

Contig ID 229905 1.R1040 5'-most EST kl1701213279.h1

Seq. No. 31021

Contig ID 229939\_1.R1040 5'-most EST pmv700892206.h1

Seq. No. 31022

Contig ID 229947\_1.R1040 5'-most EST pmv700892225.h1

Seq. No. 31023

Contig ID 229952\_1.R1040 5'-most EST pmv700892231.h1

Seq. No. 31024

Contig ID 230015 1.R1040 5'-most EST pmv700892338.h1

Seq. No. 31025

Contig ID 230039 1.R1040 5'-most EST pmv700892367.h1

Seq. No. 31026

Contig ID 230045 1.R1040 5'-most EST hrw701058029.h1

Seq. No. 31027

Contig ID 230056\_1.R1040 5'-most EST pmv700892390.h1

Seq. No. 31028

Contig ID 230060\_1.R1040 5'-most EST pmv700892395.h1

Seq. No. 31029

Contig ID 230085\_1.R1040 5'-most EST fC-gmle700873426f3

Method BLASTX NCBI GI g729775 BLAST score 288



E value 2.0e-25 Match length 99 % identity 57

NCBI Description HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR)

>gi\_100264\_pir\_\_S25481 heat shock transcription factor 8 - Peruvian tomato >gi\_19492\_emb\_CAA47869\_ (X67600) heat shock

transcription factor 8 [Lycopersicon peruvianum]

Seq. No. 31030

Contig ID 230087\_1.R1040 5'-most EST leu701154633.h1

Method BLASTX
NCBI GI g3386609
BLAST score 385
E value 2.0e-37
Match length 106
% identity 70

NCBI Description (AC004665) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 31031

Contig ID 230100\_1.R1040 5'-most EST pmv700892449.h1

Method BLASTX
NCBI GI g4432857
BLAST score 285
E value 3.0e-25
Match length 159
% identity 38

NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31032

Contig ID 230108\_1.R1040 5'-most EST pmv700892457.h1

Seq. No. 31033

Contig ID 230110\_1.R1040

5'-most EST jC-gmle01810062h09d1

Seq. No. 31034

Contig ID 230129 1.R1040 5'-most EST fua701043214.h1

Seq. No. 31035

Contig ID 230150\_1.R1040 5'-most EST pmv700892549.h1

Seq. No. 31036

Contig ID 230189 1.R1040

5'-most EST jC-gmst02400002b06a1

Seq. No. 31037

Contig ID 230231\_1.R1040 5'-most EST pmv700892623.h1

Seq. No. 31038



Contig ID 230253\_2.R1040 5'-most EST jC-gmst02400020c12a1

Method BLASTX
NCBI GI g3757521
BLAST score 268
E value 2.0e-23
Match length 98
% identity 52

NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 31039

Contig ID 230258\_1.R1040 5'-most EST pmv700892661.h1

Seq. No. 31040

Contig ID 230264\_1.R1040 5'-most EST pmv700892668.h1

Method BLASTX
NCBI GI g1730133
BLAST score 158
E value 4.0e-10
Match length 87
% identity 38

NCBI Description ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE

3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV) (ELAM-1 LIGAND FUCOSYLTRANSFERASE) >gi\_105261\_pir\_\_A40976

alpha(1,3)-fucosyltransferase (EC  $2.4.\overline{1.-}$ ) -  $\overline{\text{human}}$ 

>gi\_1236720 (M65030) alpha(1,3)-fucosyltransferase [Homo

sapīens]

Seq. No. 31041

Contig ID 230319\_1.R1040 5'-most EST pmv700892794.h1

Seq. No. 31042

Contig ID 230343 2.R1040 5'-most EST gsv701048887.h1

Seq. No. 31043

Contig ID 230382\_1.R1040 5'-most EST pmv700892877.h1

Method BLASTX
NCBI GI g3434969
BLAST score 168
E value 2.0e-11
Match length 107
% identity 44

NCBI Description (AB008104) ethylene responsive element binding factor 2

[Arabidopsis thaliana]

Seq. No. 31044

Contig ID 230410\_1.R1040 5'-most EST pmv700892924.h1

Method BLASTX
NCBI GI g2191193
BLAST score 183
E value 2.0e-13



Match length 153 % identity 29

NCBI Description (AF007271) contain similarity to type 1 inositol 1,4,5-triphosphate receptors [Arabidopsis thaliana]

Seq. No. 31045

Contig ID 230429\_2.R1040

5'-most EST  $jC-gmf\overline{1}02220131e01d1$ 

Method BLASTX
NCBI GI g4006831
BLAST score 165
E value 3.0e-11
Match length 82
% identity 43

NCBI Description (AC005970) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 31046

Contig ID 230430\_1.R1040 5'-most EST fC-gmle700877271f1

Method BLASTX
NCBI GI g2961358
BLAST score 231
E value 3.0e-19
Match length 105
% identity 48

NCBI Description (AL022140) serine/threonine protein kinase like protein

[Arabidopsis thaliana]

Seq. No. 31047

Contig ID 230467\_1.R1040 5'-most EST pmv700894827.h1

Seq. No. 31048

Contig ID 230484\_1.R1040 5'-most EST gsv701048525.h1

Seq. No. 31049

Contig ID 230496\_1.R1040 5'-most EST leu701148894.h1

Method BLASTX
NCBI GI g2160694
BLAST score 666
E value 3.0e-70
Match length 138
% identity 90

NCBI Description (U73528) B' regulatory subunit of PP2A [Arabidopsis

thaliana]

Seq. No. 31050

Contig ID 230500\_1.R1040 5'-most EST asn701141708.h1

Seq. No. 31051

Contig ID 230507\_1.R1040 5'-most EST pmv700893055.h1

Method BLASTX



NCBI GI g2618698 BLAST score 324 E value 4.0e-32 Match length 104 % identity 61

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 31052

Contig ID 230521\_1.R1040 5'-most EST pmv700893071.h1

Seq. No. 31053

Contig ID 230522\_1.R1040 5'-most EST pmv700893072.h1

Seq. No. 31054

Contig ID 230527\_1.R1040 5'-most EST pmv700893083.h1

Seq. No. 31055

Contig ID 230545\_1.R1040 5'-most EST pmv700893117.h1

Method BLASTX
NCBI GI g3334200
BLAST score 390
E value 4.0e-38
Match length 94
% identity 80

NCBI Description GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE

DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) >gi\_2894362\_emb\_CAB16918\_ (Z99770) P-Protein precursor

[Solanum tuberosum]

Seq. No. 31056

Contig ID 230550\_1.R1040 5'-most EST zsg701122283.h1

Seq. No. 31057

Contig ID 230635\_1.R1040 5'-most EST rlr700896343.h1

Seq. No. 31058

Contig ID 230690 1.R1040

5'-most EST g4282637
Method BLASTX
NCBI GI g1346792
BLAST score 186
E value 7.0e-14
Match length 119
% identity 36

NCBI Description DNA PRIMASE SMALL SUBUNIT (DNA PRIMASE 49 KD SUBUNIT) (P49)

>gi 631124 pir S45630 DNA primase chain p48 - human

>gi\_510406\_emb\_CAA52377 (X74330) DNA primase (subunit p48)
[Homo sapiens] >gi\_4506051\_ref\_NP\_000937.1\_pPRIM1\_ primase,

polypeptide 1 (49kD)

Seq. No. 31059



Contig ID 230692\_1.R1040 5'-most EST pmv700893312.h1

Method BLASTX
NCBI GI g2911073
BLAST score 440
E value 1.0e-43
Match length 108
% identity 77

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 31060

Contig ID 230743\_1.R1040 5'-most EST kl1701205938.h1 Method BLASTX

NCBI GI g4220514 BLAST score 359 E value 5.0e-34 Match length 115 % identity 62

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 31061

Contig ID 230759\_1.R1040

5'-most EST uC-gmrominsoy142f10b1

Seq. No. 31062

Contig ID 230783\_1.R1040

5'-most EST jC-gmfl02220080a08a1

Seq. No. 31063

Contig ID 230792\_1.R1040 5'-most EST pmv700893471.h1

Seq. No. 31064

Contig ID 230814\_1.R1040 5'-most EST pmv700893535.h1

Seq. No. 31065

Contig ID 230818 1.R1040

5'-most EST jC-gmle01810009b11d1

Seq. No. 31066

Contig ID 230875 1.R1040

5'-most EST jC-gmf102220062d09a1

Seg. No. 31067

Contig ID 230886\_1.R1040 5'-most EST pmv700893608.h1

Seq. No. 31068

Contig ID 231037 1.R1040

5'-most EST jC-gmle01810025d02a1

Method BLASTX
NCBI GI g3928084
BLAST score 316
E value 5.0e-29
Match length 100



% identity 64
NCBI Description (AC005770) retrotransposon-like protein [Arabidopsis thaliana]

Seq. No. 31069

Contig ID 231050\_1.R1040 5'-most EST kl1701213823.h1

Method BLASTX
NCBI GI g2245066
BLAST score 245
E value 5.0e-21
Match length 108
% identity 48

NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 31070

Contig ID 231057\_1.R1040 5'-most EST pmv700893864.h1

Seq. No. 31071

Contig ID 231103\_1.R1040 5'-most EST pxt700942790.h1

Method BLASTX
NCBI GI g2114104
BLAST score 653
E value 2.0e-68
Match length 167
% identity 70

NCBI Description (AB003590) sulfate transporter [Arabidopsis thaliana]

>gi\_2114106\_dbj\_BAA20085\_ (AB003591) sulfate transporter

[Arabidopsis thaliana]

Seq. No. 31072

Contig ID 231134\_1.R1040 5'-most EST gsv701045634.h1

Method BLASTX
NCBI GI g4455340
BLAST score 281
E value 2.0e-25
Match length 70
% identity 73

NCBI Description (AL035522) putative protein [Arabidopsis thaliana]

Seq. No. 31073

Contig ID 231164\_1.R1040

5'-most EST jC-gmro02800031b11a1

Seq. No. 31074

Contig ID 231329\_1.R1040 5'-most EST pmv700894208.h1

Seq. No. 31075

Contig ID 231330\_1.R1040 5'-most EST hrw701062070.h1

Seq. No. 31076

Contig ID 231337\_1.R1040



5'-most EST pmv700894217.h1 Method BLASTX

NCBI GI g1730630

BLAST score 298
E value 6.0e-27
Match length 164
% identity 41

NCBI Description HYPOTHETICAL 82.6 KD PROTEIN B0361.8 IN CHROMOSOME III >qi 458956 (U00031) similar to cytoplasmic domain of

synaptobrevin [Caenorhabditis elegans]

Seq. No. 31077

Contig ID 231353\_1.R1040 5'-most EST fua701041207.h1

Seq. No. 31078

Contig ID 231383\_1.R1040 5'-most EST pmv700894269.h1

Seq. No. 31079

Contig ID 231396 1.R1040

5'-most EST uC-gmflminsoy082f10b1

Seq. No. 31080

Contig ID 231404\_1.R1040 5'-most EST pmv700894293.h1

Seq. No. 31081

Contig ID 231435\_1.R1040 5'-most EST pmv700894335.h1

Method BLASTX
NCBI GI g3063469
BLAST score 185
E value 9.0e-14
Match length 127
% identity 40

NCBI Description (AC003981) F22013.31 [Arabidopsis thaliana]

Seq. No. 31082

Contig ID 231458 1.R1040

Seq. No. 31083

Contig ID 231476\_1.R1040 5'-most EST kl1701202873.h1

Seq. No. 31084

Contig ID 231494\_1.R1040

5'-most EST jC-gmst02400053h06d1

Method BLASTN
NCBI GI g2293111
BLAST score 100
E value 7.0e-49
Match length 284
% identity 86

NCBI Description V.faba mRNA for potassium channel



Seq. No. 31085

Contig ID 231495\_1.R1040 5'-most EST asn701138631.h1

Method BLASTX
NCBI GI g3367519
BLAST score 197
E value 3.0e-23
Match length 82
% identity 68

NCBI Description (AC004392) Contains similarity to gb\_U51898

Ca2+-independent phospholipase A2 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No. 31086

Contig ID 231498\_1.R1040

5'-most EST jC-gmst02400052h08a1

Method BLASTX
NCBI GI g2894600
BLAST score 268
E value 2.0e-23
Match length 117
% identity 45

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 31087

Contig ID 231506\_1.R1040

5'-most EST uC-gmflminsoy046g09b1

Method BLASTX
NCBI GI g3142295
BLAST score 335
E value 3.0e-31
Match length 98
% identity 63

NCBI Description (AC002411) Strong similarity to phosphoribosylanthranilate

transferase gb\_D86180 from Pisum sativum. [Arabidopsis

thaliana]

Seq. No. 31088

Contig ID 231540\_1.R1040 5'-most EST pmv700894468.h1

Seq. No. 31089

Contig ID 231568\_1.R1040 5'-most EST zsg701127162.h1

Method BLASTN
NCBI GI g3860320
BLAST score 83
E value 1.0e-38
Match length 190
% identity 87

NCBI Description Cicer arietinum mRNA for beta-galactosidase, clone

CanBGal-5

Seq. No. 31090

Contig ID 231568\_2.R1040 5'-most EST rlr700901926.h1

Method BLASTN



NCBI GI g3860320 BLAST score 253 E value 1.0e-140 Match length 648 % identity 85

NCBI Description Cicer arietinum mRNA for beta-galactosidase, clone

CanBGal-5

Seq. No. 31091

Contig ID 231588\_1.R1040 5'-most EST pmv700894539.h1

Seq. No. 31092

Contig ID 231639\_1.R1040

5'-most EST jC-gmst02400061h01a1

Method BLASTX
NCBI GI g4567304
BLAST score 340
E value 9.0e-32
Match length 183
% identity 43

NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]

Seq. No. 31093

Contig ID 231691 1.R1040

5'-most EST uC-gmflminsoy007g03b1

Seq. No. 31094

Contig ID 231761\_1.R1040 5'-most EST pmv700894763.h1

Seq. No. 31095

Contig ID 231800\_1.R1040 5'-most EST rlr700896970.h1

Method BLASTX
NCBI GI g3128210
BLAST score 316
E value 4.0e-54
Match length 198
% identity 56

NCBI Description (AC004077) putative cytochrome P450 protein [Arabidopsis

thaliana] >gi 3337378 (AC004481) putative cytochrome P450

protein [Arabidopsis thaliana]

Seq. No. 31096

Contig ID 231803 1.R1040

5'-most EST g4304935

Seq. No. 31097

Contig ID 231810\_1.R1040 5'-most EST asn701133583.h2

Method BLASTN
NCBI GI g1223915
BLAST score 203
E value 1.0e-110
Match length 255
% identity 95



NCBI Description Vigna radiata carboxypeptidase II mRNA, partial cds

Seq. No. 31098

Contig ID 231856\_1.R1040 5'-most EST pmv700894885.h1

Method BLASTX
NCBI GI 94455284
BLAST score 410
E value 4.0e-40
Match length 112
% identity 69

NCBI Description (AL035527) beta-glucosidase-like protein [Arabidopsis

thaliana]

Seq. No. 31099

Contig ID 231857 1.R1040

5'-most EST uC-gmrominsoy229c05b1

Seq. No. 31100

Contig ID 231881\_1.R1040 5'-most EST pmv700894927.h1

Seq. No. 31101

Contig ID 231887\_1.R1040 5'-most EST pmv700894938.h1

Seq. No. 31102

Contig ID 231981\_1.R1040 5'-most EST pmv700895087.h1

Method BLASTN
NCBI GI g22738
BLAST score 147
E value 4.0e-77
Match length 259
% identity 94

NCBI Description G.max mitochondrial atpA

Seq. No. 31103

Contig ID 231984\_1.R1040 5'-most EST pmv700895091.h1

Seq. No. 31104

Contig ID 232044\_1.R1040 5'-most EST pmv700895173.h1

Method BLASTX
NCBI GI g2160156
BLAST score 578
E value 8.0e-60
Match length 145
% identity 76

NCBI Description (AC000132) Strong similarity to S. pombe leucyl-tRNA

synthetase (gb Z73100). [Arabidopsis thaliana]

Seq. No. 31105

Contig ID 232062\_1.R1040 5'-most EST pmv700895196.h1

Method BLASTX

4759



NCBI GI g4508068 BLAST score 390 E value 1.0e-37 Match length 142 % identity 58

NCBI Description (AC005882) 3063 [Arabidopsis thaliana]

Seq. No. 31106

Contig ID 232119\_1.R1040 5'-most EST uC-gmropic006c04b1

Seq. No. 31107

Contig ID 232120\_1.R1040 5'-most EST zsg701127724.h1

Method BLASTN
NCBI GI g2924733
BLAST score 46
E value 1.0e-16
Match length 230
% identity 80

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUF9, complete sequence [Arabidopsis thaliana]

Seq. No. 31108

Contig ID 232159 1.R1040

5'-most EST uC-gmrominsoy188g02b1

Method BLASTX
NCBI GI g4468985
BLAST score 152
E value 9.0e-10
Match length 60
% identity 45

NCBI Description (AL035605) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31109

Contig ID 232207\_1.R1040 5'-most EST rry700808389.h1

Method BLASTX
NCBI GI g4249404
BLAST score 295
E value 6.0e-27
Match length 89
% identity 64

NCBI Description (AC006072) putative nuclear protein SA-1 [Arabidopsis

thaliana]

Seq. No. 31110

Contig ID 232221 1.R1040 5'-most EST leu701155274.h1

Seq. No. 31111

Contig ID 232294 1.R1040

5'-most EST jC-gmr002910023e01d1

Method BLASTX
NCBI GI g3080420
BLAST score 751
E value 5.0e-80



Match length 173 % identity 82

NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis

thaliana]

Seq. No. 31112

Contig ID 232321 1.R1040

Match length 147 % identity 54

NCBI Description (AF020833) eukaryotic translation initiation factor 3

subunit [Homo sapiens]

Seq. No. 31113

Contig ID 232321 2.R1040

5'-most EST uC-gmrominsoy180f04b1

Seq. No. 31114

Contig ID 232377\_1.R1040 5'-most EST uC-gmropic058d02b1

Method BLASTX
NCBI GI g2501011
BLAST score 495
E value 5.0e-50
Match length 159
% identity 56

NCBI Description ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)

>gi\_1652625\_dbj\_BAA17545\_ (D90907) isoleucyl-tRNA

synthetase [Synechocystis sp.]

Seq. No. 31115

Contig ID 232381\_1.R1040 5'-most EST pxt700941004.h1

Seq. No. 31116

Contig ID 232394\_1.R1040 5'-most EST uC-gmronoir043h04b1

Method BLASTX
NCBI GI g1407705
BLAST score 721
E value 2.0e-76
Match length 158
% identity 79

NCBI Description (U60202) lipoxygenase [Solanum tuberosum]

Seq. No. 31117

Contig ID 232397\_1.R1040 5'-most EST zsg701122060.h1

Seq. No. 31118

Contig ID 232422\_1.R1040 5'-most EST pxt700941055.h1 Method BLASTX



```
NCBI GI
                   g2501231
                   392
BLAST score
E value
                   2.0e-47
Match length
                   118
                   76
% identity
```

HYPOTHETICAL 38.1 KD PROTEIN >gi\_99505\_pir\_\_S24930 NCBI Description

hypothetical protein - pink corydalis >gi\_18258\_emb\_CAA45139\_ (X63595) protein of unknown

function [Corydalis sempervirens] >gi 444333 prf 1906382A

pCSC71 protein [Corydalis sempervirens]

```
31119
Seq. No.
```

232443 1.R1040 Contig ID

5'-most EST jC-qmro02910006a02d1

Seq. No. 31120

232474 1.R1040 Contig ID 5'-most EST pxt700941117.h1 Method BLASTX

NCBI GI g4406819 BLAST score 549 3.0e-56 E value Match length 155

72 % identity

(AC006201) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 31121

232503 1.R1040 Contig ID 5'-most EST pxt700941149.h1

Seq. No. 31122

232518 1.R1040 Contig ID 5'-most EST kl1701211586.h1

Seq. No. 31123

Contig ID 232519 1.R1040 5'-most EST leu701148185.h1

BLASTN Method NCBI GI g3688527 BLAST score 185 E value 1.0e-99 Match length 512 % identity 84

NCBI Description Pisum sativum mRNA for TPE4A thiol-protease

Seq. No. 31124

Contig ID 232560 1.R1040 5'-most EST zsq701128408.h1

Method BLASTX NCBI GI q2285885 BLAST score 327 E value 9.0e-31 Match length 90 70 % identity

NCBI Description (D89631) sulfate transporter [Arabidopsis thaliana]

Seq. No. 31125



```
232565 1.R1040
 Contig ID
                   pxt700941226.hl
 5'-most EST
                   BLASTX
Method
                   g3236235
NCBI GI
 BLAST score
                   215
                   3.0e-17
 E value
                   79
Match length
                   44
 % identity
                   (AC004684) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   >gi 4056501 (AC005896) unknown protein [Arabidopsis
                   thaliana]
                   31126
 Seq. No.
                   232574 1.R1040
 Contig ID
                   jC-gmle01810078d12d1
 5'-most EST
                   BLASTN
 Method
 NCBI GI
                   g169956
                   91
 BLAST score
                   2.0e-43
 E value
 Match length
                    280
 % identity
                    90
 NCBI Description Glycine max G-box binding factor (GBF1) mRNA, complete cds
 Seq. No.
                    31127
                    232634 1.R1040
 Contig ID
 5'-most EST
                    g4305763
                    BLASTX
Method
 NCBI GI
                    g4510381
                    203
 BLAST score
                    8.0e-16
 E value
                    98
 Match length
                    45
 % identity
                   (AC007017) unknown protein [Arabidopsis thaliana]
 NCBI Description
                    31128
 Seq. No.
                    232640 1.R1040
 Contig ID
 5'-most EST
                    jC-gmst02400028e04a1
                    BLASTX
 Method
                    g3046815
 NCBI GI
                    162
 BLAST score
                    3.0e-11
 E value
                    118
 Match length
                    36
 % identity
                   (AL021687) cytochrome P450 [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    31129
                    232656 1.R1040
 Contig ID
 5'-most EST
                    pxt700941358.hl
                    31130
 Seq. No.
                    232738 1.R1040
```

Contig ID

5'-most EST jC-gmf102220102e12a1

Seq. No. 31131

Contig ID 232777 1.R1040

5'-most EST q4292653



Seq. No. 31132

Contig ID 232787\_1.R1040 5'-most EST uC-gmronoir033h06b1

Method BLASTX
NCBI GI g3033375
BLAST score 546
E value 7.0e-56
Match length 190
% identity 57

NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis

thaliana]

Seq. No. 31133

Contig ID 232794\_1.R1040 5'-most EST jC-gmle01810066c12a1

Seq. No. 31134

Contig ID 232814\_1.R1040 5'-most EST pxt700942401.h1

Method BLASTX
NCBI GI g3176686
BLAST score 394
E value 1.0e-38
Match length 89
% identity 82

NCBI Description (AC003671) Similar to high affinity potassium transporter,

HAK1 protein gb\_U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 31135

Contig ID 232849 1.R1040 5'-most EST pxt700941795.h1

Seq. No. 31136

Contig ID 232888\_1.R1040 5'-most EST uC-gmropic074d08b1

Method BLASTN
NCBI GI g4159703
BLAST score 34
E value 1.0e-09
Match length 58
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K5F14, complete sequence [Arabidopsis thaliana]

Seq. No. 31137

Contig ID 232892\_1.R1040 5'-most EST epx701109856.h1

Seq. No. 31138

Contig ID 232954\_1.R1040 5'-most EST pxt700942963.h1

Method BLASTX
NCBI GI g4539404
BLAST score 343
E value 6.0e-32
Match length 127



% identity 53

NCBI Description (AL049524) putative protein [Arabidopsis thaliana]

Seq. No. 31139

Contig ID 232976\_1.R1040 5'-most EST kl1701206489.h1

Method BLASTX
NCBI GI g1169128
BLAST score 284
E value 9.0e-26
Match length 87
% identity 62

NCBI Description SERINE/THREONINE-PROTEIN KINASE CTR1 >gi\_166680 (L08789) protein kinase [Arabidopsis thaliana] >gi\_166682 (L08790)

protein kinase [Arabidopsis thaliana]

Seq. No. 31140

Contig ID 232995 1.R1040

5'-most EST uC-gmrominsoy262b07b1

Seq. No. 31141

Contig ID 233012\_1.R1040 5'-most EST leu701151389.h1

Seq. No. 31142

Contig ID 233044 1.R1040

5'-most EST uC-qmflminsoy012f10b1

Method BLASTX
NCBI GI g3687833
BLAST score 317
E value 2.0e-30
Match length 90

% identity 12

NCBI Description (AF069737) notchless [Xenopus laevis]

Seq. No. 31143

Contig ID 233047\_1.R1040 5'-most EST pxt700942390.h1

Seq. No. 31144

Contig ID 233103\_1.R1040 5'-most EST pxt700945970.h1

Method BLASTX
NCBI GI g3426048
BLAST score 221
E value 2.0e-18
Match length 88
% identity 49

NCBI Description (AC005168) putative hydroxymethylglutaryl-CoA lyase

precursor [Arabidopsis thaliana]

Seq. No. 31145

Contig ID 233110\_1.R1040 5'-most EST gsv701046923.h1

Method BLASTX NCBI GI g4522004 BLAST score 229



3.0e-19 E value 53 Match length 77 % identity

(AC007069) putative histidine kinase, sensory transduction NCBI Description

[Arabidopsis thaliana]

31146 Seq. No.

233177 1.R1040 Contig ID

jC-gmro02910037d08d1 5'-most EST

Method BLASTX q1049022 NCBI GI 207 BLAST score 4.0e-16 E value 96 Match length

51 % identity

(U25696) transcription factor SaMADS A [Sinapis alba] NCBI Description

31147 Seq. No.

233203 2.R1040 Contig ID pxt700942656.h1 5'-most EST

Seq. No. 31148

233291 1.R1040 Contig ID pxt700942779.hl 5'-most EST

31149 Seq. No.

233324 1.R1040 Contig ID

g4289918 5'-most EST BLASTN Method g4388714 NCBI GI BLAST score 36 2.0e-10 E value Match length 40

97 % identity

Arabidopsis thaliana chromosome II BAC F5K7 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

31150 Seq. No.

233406 1.R1040 Contig ID 5'-most EST pxt700942954.hl

Seq. No. 31151

233424 1.R1040 Contig ID leu701156434.hl 5'-most EST

31152 Seq. No.

Contig ID 233429 1.R1040

g5510163 5'-most EST

31153 Seq. No.

233434 1.R1040 Contig ID 5'-most EST pxt700942995.hl

BLASTX Method NCBI GI q4467108 BLAST score 359 E value 1.0e-34 Match length 75



% identity 81
NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31154

Contig ID 233447\_1.R1040 5'-most EST zsg701121850.h1

Method BLASTX
NCBI GI g3738339
BLAST score 698
E value 7.0e-74
Match length 157
% identity 85

NCBI Description (AC005170) putative kinase [Arabidopsis thaliana]

Seq. No. 31155

Contig ID 233460\_1.R1040 5'-most EST pxt700943027.h1

Seq. No. 31156

Contig ID 233463\_1.R1040 5'-most EST pxt700943031.h1

Seq. No. 31157

Contig ID 233497\_1.R1040

NCBI Description (AF069442) putative phospho-ser/thr phosphatase

[Arabidopsis thaliana]

Seq. No. 31158

Contig ID 233600\_1.R1040

5'-most EST jC-gmst02400027e10a1

Seq. No. 31159

Contig ID 233619\_1.R1040 5'-most EST pxt700943247.h1

Method BLASTN
NCBI GI g1752733
BLAST score 95
E value 4.0e-46
Match length 258
% identity 84

NCBI Description Glycine max mRNA for beta-glucan-elicitor receptor,

complete cds

Seq. No. 31160

Contig ID 233644\_1.R1040 5'-most EST pxt700943279.h1

Seq. No. 31161

Contig ID 233691\_1.R1040 5'-most EST uC-gmropic021g02b1



Method BLASTX NCBI GI q3025447 BLAST score 175 E value 2.0e-12 116 Match length 29 % identity

NCBI Description (AC004528) R32184\_3 [Homo sapiens]

31162 Seq. No.

233776 1.R1040 Contig ID pxt700943441.hl 5'-most EST

Method BLASTN q603870 NCBI GI BLAST score 36 1.0e-10 E value 99 Match length 89 % identity

NCBI Description P.hybrida mRNA for MAP/ERK kinase

31163 Seq. No.

233810 1.R1040 Contig ID

jC-gmro02800041g06a1 5'-most EST

Method BLASTX NCBI GI a3193316 BLAST score 328 6.0e-44 E value 138 Match length % identity

(AF069299) contains similarity to nucleotide sugar NCBI Description

epimerases [Arabidopsis thaliana]

Seq. No. 31164

233811 1.R1040 Contig ID

g5057551 5'-most EST Method BLASTN g4336435 NCBI GI BLAST score 83 1.0e-38 E value Match length 207 % identity 85

Lotus japonicus protein phosphatase type 2C (PP2C2) mRNA, NCBI Description

complete cds

31165 Seq. No.

233849 1.R1040 Contig ID

5'-most EST jC-gmf102220114f05d1

31166 Seq. No.

233865 1.R1040 Contig ID pxt700944432.h1 5'-most EST

31167 Seq. No.

233890 1.R1040 Contig ID 5'-most EST pxt700943586.h1

Seq. No. 31168

233891\_1.R1040 Contig ID



```
leu701151322.hl
5'-most EST
Method
                  BLASTN
                   q3046856
NCBI GI
                   37
BLAST score
                   2.0e-11
E value
                   45
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXI22, complete sequence [Arabidopsis thaliana]
                   31169
Seq. No.
Contig ID
                   233892 1.R1040
5'-most EST
                   pxt700943588.h1
                   31170
Seq. No.
                   233947 1.R1040
Contig ID
                   pxt700943659.h1
5'-most EST
Seq. No.
                   31171
                   233982 1.R1040
Contig ID
                   pxt700943708.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2832300
BLAST score
                   430
                   2.0e-42
E value
Match length
                   114
% identity
                   (AF044285) adenosine-5'-phosphosulfate-kinase [Catharanthus
NCBI Description
                   roseus]
Seq. No.
                   31172
Contig ID
                   233985 1.R1040
5'-most EST
                   pxt700943711.h1
Method
                   BLASTX
NCBI GI
                   g2194125
BLAST score
                   307
                   4.0e-28
E value
Match length
                   104
                   63
% identity
                   (AC002062) ESTs gb R30459, gb N38441 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   31173
                   233992 1.R1040
Contig ID
                   pxt700943718.h1
5'-most EST
                   BLASTX
Method
                   q3885344
NCBI GI
                   157
BLAST score
                   9.0e-11
E value
                   77
Match length
```

42 % identity (AC005623) unknown protein [Arabidopsis thaliana] NCBI Description

>gi 4557057\_gb\_AAD22497.1\_AC007154\_1 (AC007154) unknown

protein [Arabidopsis thaliana]

31174 Seq. No.

234013 2.R1040 Contig ID



```
pxt700943740.h1
5'-most EST
                  31175
Seq. No.
                  234033 1.R1040
Contig ID
                  pxt700943766.hl
5'-most EST
Method
                  BLASTN
                  g1816649
NCBI GI
                  322
BLAST score
                  0.0e + 00
E value
Match length
                  437
% identity
                  94
                  Lupinus luteus NADH plastiquinone oxidoreductase subunit J
NCBI Description
                  (ndhJ) gene, chloroplast gene encoding chloroplast protein,
                  complete cds
                  31176
Seq. No.
                  234054 1.R1040
Contig ID
                  gsv701053970.h1
5'-most EST
Seq. No.
                  31177
                  234083 1.R1040
Contig ID
5'-most EST
                  fua701038173.hl
                  31178
Seq. No.
                  234101 1.R1040
Contig ID
                  fC-qmst700652534d5
5'-most EST
                  BLASTN
Method
NCBI GI
                  q294667
                  47
BLAST score
                  3.0e-17
E value
                  59
Match length
                  95
% identity
                  Castor bean chloroplast beta-ketoacyl-ACP synthase (50 kDa
NCBI Description
                  synthase) mRNA, complete cds
                  31179
Seq. No.
                  234102 1.R1040
Contig ID
                  q4285233
5'-most EST
                  BLASTX
Method
                  g2130073
NCBI GI
BLAST score
                   269
E value
                   8.0e-24
                   60
Match length
                   85
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
NCBI Description
                   cytosolic - rice >gi_786178 dbj BAA08845 (D50307) aldolase
                   C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301)
                   aldolase C-1 [Oryza sativa]
                   31180
Seq. No.
                   234107 1.R1040
Contig ID
```

Contig ID 234107\_1.RI040 5'-most EST pxt700943860.h1

Seq. No. 31181

Contig ID 234181\_1.R1040 5'-most EST jC-gmro02910056b03a1



Seq. No. 31182

Contig ID 234235\_1.R1040 5'-most EST pxt700944032.h1

Method BLASTX
NCBI GI g3540207
BLAST score 617
E value 3.0e-64
Match length 157
% identity 75

NCBI Description (AC004260) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 31183

Contig ID 234236 1.R1040

5'-most EST uC-gmflminsoy100h09b1

Seq. No. 31184

Contig ID 234264\_1.R1040 5'-most EST dpv701098034.h1

Method BLASTX
NCBI GI g2344889
BLAST score 208
E value 5.0e-17
Match length 92
% identity 48

NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 31185

Contig ID 234286\_1.R1040 5'-most EST pxt700944094.h1

Seq. No. 31186

Contig ID 234329\_1.R1040 5'-most EST fua701037891.h1

Method BLASTX
NCBI GI g4522009
BLAST score 293
E value 8.0e-27
Match length 87
% identity 57

NCBI Description (AC007069) unknown protein [Arabidopsis thaliana]

Seq. No. 31187

Contig ID 234346\_1.R1040 5'-most EST uC-gmropic020d05b1

Seq. No. 31188

Contig ID 234356 1.R1040

5'-most EST jC-gmst02400036b09a1

Method BLASTX
NCBI GI g2281090
BLAST score 183
E value 8.0e-16
Match length 82
% identity 52

NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31189



```
234451 1.R1040
Contig ID
                   q42604\overline{3}7
5'-most EST
                   BLASTX
Method
                   g1698548
NCBI GI
                   752
BLAST score
                   4.0e-80
E value
                   170
Match length
                   82
% identity
                  (U58971) calmodulin-binding protein [Nicotiana tabacum]
NCBI Description
                   31190
Seq. No.
                   234520 1.R1040
Contig ID
                   jC-gmf\overline{1}02220144g09d1
5'-most EST
Seq. No.
                   31191
                   234550 1.R1040
Contig ID
                   pxt700944454.hl
5'-most EST
                   31192
Seq. No.
                   234605 1.R1040
Contig ID
                   pxt700944523.hl
5'-most EST
                   31193
Seq. No.
                   234645 1.R1040
Contig ID
                   jC-gmst02400031g10d1
5'-most EST
                   31194
Seq. No.
                   234648 1.R1040
Contig ID
                   jC-gmst02400067g01d1
5'-most EST
                   31195
Seq. No.
                   234712 1.R1040
Contig ID
                   uC-gmflminsoy041d08b1
5'-most EST
                   BLASTX
Method
                   q2462931
NCBI GI
BLAST score
                   527
                   7.0e-54
E value
Match length
                   141
                   76
% identity
                   (Z83833) UDP-glucose:sterol glucosyltransferase
NCBI Description
                    [Arabidopsis thaliana]
                   31196
Seq. No.
                   234735 1.R1040
Contig ID
                   pxt700944676.hl
5'-most EST
                   BLASTX
Method
                   q3758859
NCBI GI
                    199
BLAST score
                    3.0e-15
E value
                    104
Match length
                    35
 % identity
                   (Z98551) predicted using hexExon; MAL3P6.7 (PFC0730w),
NCBI Description
                    Hypothetical protein, len: 222 aa [Plasmodium falciparum]
```

Seq. No. 31197

Contig ID 234778\_1.R1040 5'-most EST uC-gmronoir005h03b1



Method BLASTX
NCBI GI g3176686
BLAST score 459
E value 4.0e-46
Match length 106
% identity 81

NCBI Description (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 31198

Contig ID 234805 1.R1040

5'-most EST uC-gmflminsoy098b01b1

Seq. No. 31199

Contig ID 234825\_1.R1040 5'-most EST gsv701046932.h1

Method BLASTX
NCBI GI g3395428
BLAST score 217
E value 3.0e-17
Match length 88
% identity 52

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 31200

Contig ID 234834\_1.R1040 5'-most EST pxt700944808.h1

Seq. No. 31201

Contig ID 234852\_1.R1040

5'-most EST uC-gmflminsoy100c03b1

Method BLASTX
NCBI GI g4580395
BLAST score 547
E value 3.0e-56
Match length 124
% identity 87

NCBI Description (AC007171) putative kinesin-related protein [Arabidopsis

thaliana]

Seq. No. 31202

Contig ID 234895\_1.R1040 5'-most EST uC-gmropic112b01b1

Method BLASTX
NCBI GI g3420052
BLAST score 686
E value 2.0e-72
Match length 166
% identity 80

NCBI Description (AC004680) putative ubiqinone reductase [Arabidopsis

thaliana]

Seq. No. 31203

Contig ID 234907\_1.R1040 5'-most EST kl1701208476.h1

Method BLASTX



NCBI GI g2914710
BLAST score 421
E value 1.0e-41
Match length 69
NCBI Description (AC003974) putative beta-D-galactosidase [Arabidopsis thaliana]

Seq. No. 31204

Contig ID 234960\_1.R1040

5'-most EST g5342711

Seq. No. 31205

Contig ID 234975\_1.R1040 5'-most EST pxt700944980.h1

Seq. No. 31206

Contig ID 234998\_1.R1040

5'-most EST jC-gmle01810042c03a1

Seq. No. 31207

Contig ID 235000\_1.R1040 5'-most EST kl1701206129.h1

Seq. No. 31208

Contig ID 235028\_1.R1040 5'-most EST asn701137793.h1

Method BLASTX
NCBI GI g3080427
BLAST score 425
E value 3.0e-42
Match length 96
% identity 79

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 31209

Contig ID 235048\_1.R1040 5'-most EST pxt700945073.h1

Seq. No. 31210

Contig ID 235121\_1.R1040 5'-most EST pxt700945164.h1

Seq. No. 31211

Contig ID 235134\_1.R1040

5'-most EST uC-gmflminsoy057h02b1

Method BLASTN
NCBI GI g4193319
BLAST score 131
E value 2.0e-67
Match length 325
% identity 88

NCBI Description Zea mays histone deacetylase (hdlb) mRNA, complete cds

Seq. No. 31212

Contig ID 235173\_1.R1040 5'-most EST jC-gmf102220130c12d1



31213 Seq. No. 235182\_1.R1040 Contig ID uC-gmrominsoy201a03b1 5'-most EST BLASTX Method g4567311 NCBI GI 176 BLAST score 1.0e-12 E value 52 Match length 63 % identity (AC005956) putative protein kinase [Arabidopsis thaliana] NCBI Description 31214 Seq. No. 235238 1.R1040 Contig ID jC-gmf102220073e02a1 5'-most EST BLASTX Method g2827621 NCBI GI 411 BLAST score 5.0e-40E value 207 Match length 49 % identity (AL021636) putative protein [Arabidopsis thaliana] NCBI Description 31215 Seq. No. 235281 1.R1040 Contig ID pxt700945368.h1 5'-most EST BLASTN Method g1946219 NCBI GI 120 BLAST score 1.0e-60 E value 284 Match length 86 % identity NCBI Description M.domestica mRNA for kn1-like protein (1791 bp) 31216 Seq. No. 235318 1.R1040 Contig ID 5'-most EST pxt700945415.h131217 Seq. No. 235357 1.R1040 Contig ID 5'-most EST uC-gmflminsoy025e06b1 31218 Seq. No. 235369 1.R1040 Contig ID jC-gmle01810025a10a1 5'-most EST 31219 Seq. No. 235441 1.R1040 Contig ID jC-qmle01810005h06a1 5'-most EST 31220 Seq. No. 235573 1.R1040

Contig ID 235573\_1.R1040 5'-most EST uC-gmropic103d04b1

Method BLASTX
NCBI GI g3608154
BLAST score 334
E value 3.0e-31



Match length 173 % identity 42

NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 31221

Contig ID 235586\_1.R1040 5'-most EST jC-gmro02910046d04d1

Method BLASTX
NCBI GI g1698582
BLAST score 459
E value 1.0e-45
Match length 133

% identity 68
NCBI Description (U60767) integral membrane protein OsNramp3 [Oryza sativa]

Seq. No. 31222

Contig ID 235648\_1.R1040

5'-most EST jC-gmle01810071e05a1

Method BLASTX
NCBI GI g3549665
BLAST score 174
E value 2.0e-12
Match length 54
% identity 59

NCBI Description (AL031394) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31223

Contig ID 235667\_1.R1040 5'-most EST pxt700945888.h1

Method BLASTX
NCBI GI g3176965
BLAST score 513
E value 3.0e-52
Match length 149
% identity 66

NCBI Description (AF067967) pyrroline-5-carboxylate synthetase

[Mesembryanthemum crystallinum]

Seq. No. 31224

Contig ID 235750\_1.R1040 5'-most EST pxt700946018.h1

Seq. No. 31225

Contig ID 235765\_1.R1040 5'-most EST pxt700946037.h1

Seq. No. 31226

Contig ID 235818\_1.R1040 5'-most EST pxt700946108.h1

Seq. No. 31227

Contig ID 235819\_1.R1040 5'-most EST pxt700946110.h1

Method BLASTX
NCBI GI g2160190
BLAST score 239
E value 2.0e-23



Match length 85 % identity 66

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 31228

Contig ID 235845\_1.R1040 5'-most EST zsg701125748.h1

Seq. No. 31229

Contig ID 235851\_1.R1040 5'-most EST pxt700946153.h1

Seq. No. 31230

Contig ID 235908\_1.R1040

5'-most EST jC-gmro02800025a03a1

Seq. No. 31231

Contig ID 235917\_1.R1040

5'-most EST g4405652
Method BLASTX
NCBI GI g2244989
BLAST score 480
E value 4.0e-48
Match length 143
% identity 66

NCBI Description (Z97340) strong similarity to naringenin 3-dioxygenase

[Arabidopsis thaliana]

Seq. No. 31232

Contig ID 235958\_1.R1040 5'-most EST pxt700946285.h1

Method BLASTX
NCBI GI g2102679
BLAST score 371
E value 2.0e-35
Match length 91
% identity 75

NCBI Description (U07424) putative tRNA synthetase-like protein [Homo

sapiens] >gi\_4104935\_gb\_AAD02221\_ (AF042347) putative phenylalanyl-tRNA synthetase alpha-subunit; PheHA [Homo

sapiens]

Seq. No. 31233

Contig ID 235998\_1.R1040

5'-most EST uC-gmrominsoy048f03b1

Seq. No. 31234

Contig ID 236021\_1.R1040 5'-most EST pxt700946367.h1

Seq. No. 31235

Contig ID 236047\_1.R1040 5'-most EST pxt700946396.h1

Method BLASTX
NCBI GI g4538929
BLAST score 223
E value 4.0e-18

4777



31236

Match length 60 % identity (AL049483) putative nucleic acid binding protein NCBI Description [Arabidopsis thaliana]

236062 1.R1040 Contig ID pxt700946416.h1 5'-most EST BLASTX Method q4510421 NCBI GI 169 BLAST score E value 1.0e-11 Match length 52 62 % identity

NCBI Description (AC006929) unknown protein [Arabidopsis thaliana]

31237 Seq. No. 236072 1.R1040 Contig ID

Seq. No.

pxt700946428.h1 5'-most EST BLASTX Method

g4455260 NCBI GI 515 BLAST score E value 1.0e-52 Match length 102 93 % identity

(AL035353) protein kinase-like protein [Arabidopsis NCBI Description

thaliana]

31238 Seq. No.

236084 1.R1040 Contig ID pxt700946462.hl 5'-most EST

31239 Seq. No.

236133 1.R1040 Contig ID jC-gmro02910039c11d1 5'-most EST

31240 Seq. No.

236168 1.R1040 Contig ID cf1700863553.h1 5'-most EST

BLASTX Method g2213592 NCBI GI 386 BLAST score 4.0e-38 E value 139 Match length 30 % identity

(AC000348) T7N9.12 [Arabidopsis thaliana] NCBI Description

31241 Seq. No.

236208 1.R1040 Contig ID

uC-gmrominsoy216g12b1 5'-most EST

BLASTX Method g4191789 NCBI GI BLAST score 270 1.0e-42 E value 119 Match length 76 % identity

NCBI Description (AC005917) putative transmembrane transport protein



## [Arabidopsis thaliana]

Seq. No. 31242

Contig ID 236251\_1.R1040 5'-most EST uC-gmronoir006c12b1

Method BLASTX
NCBI GI g4454039
BLAST score 247
E value 5.0e-21
Match length 151
% identity 39

NCBI Description (AL035394) putative Na+/H+-exchanging protein [Arabidopsis

thaliana]

Seq. No. 31243

Contig ID 236262 1.R1040

5'-most EST uC-gmrominsoy207a08b1

Seq. No. 31244

Contig ID 236269\_1.R1040 5'-most EST fC-gmf1700863687y1

Method BLASTX
NCBI GI g2494742
BLAST score 775
E value 1.0e-158
Match length 334
% identity 78

NCBI Description GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE)

>gi 2104791 emb CAA73235 (Y12704) glutamine synthetase

[Agaricus bisporus]

Seq. No. 31245

Contig ID 236290\_1.R1040 5'-most EST epx701104704.h1

Seq. No. 31246

Contig ID 236341 1.R1040

5'-most EST jC-gmro02910069g10d1

Seq. No. 31247

Contig ID 236348\_1.R1040 5'-most EST asn701135735.h1

Seq. No. 31248

Contig ID 236406 1.R1040

5'-most EST g5057320
Method BLASTX
NCBI GI g4559340
BLAST score 174
E value 2.0e-12
Match length 51
% identity 76

NCBI Description (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31249

Contig ID 236412 1.R1040

5'-most EST uC-gmrominsoy268h10b1



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31250
Seq. No.
                  236477 1.R1040
Contig ID
                  r1r700895772.h1
5'-most EST
                  31251
Seq. No.
                  236492 1.R1040
Contig ID
                  rlr700895654.h1
5'-most EST
                  BLASTX
Method
                  q1255448
NCBI GI
                   316
BLAST score
E value
                   6.0e-29
                   90
Match length
                   71
% identity
                   (D50468) mitogen-activated protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   31252
Seq. No.
                   236524 1.R1040
Contig ID
                   asn701139977.h1
5'-most EST
                   BLASTX
Method
                   g2252840
NCBI GI
BLAST score
                   308
                   8.0e-36
E value
                   158
Match length
                   47
% identity
                   (AF013293) contains regions of similarity to Haemophilus
NCBI Description
                   influenzae permease (SP:P38767) [Arabidopsis thaliana]
                   31253
Seq. No.
                   236544 1.R1040
Contig ID
                   rlr700895727.h1
5'-most EST
Method
                   BLASTX
                   q2462822
NCBI GI
                   333
BLAST score
                   5.0e-31
E value
                   110
Match length
                   19
% identity
                  (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   31254
Seq. No.
                   236620 1.R1040
Contig ID
                   rlr700895846.hl
5'-most EST
                   31255
Seq. No.
                   236631 1.R1040
Contig ID
                   rlr700895865.h1
5'-most EST
                   BLASTX
Method
                   g4467359
NCBI GI
                   182
BLAST score
                   8.0e-14
E value
                   82
Match length
                   11
% identity
```

NCBI Description

(AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis thaliana]

31256 Seq. No.



Contig ID 236651\_1.R1040 5'-most EST gsv701045260.h1

Seq. No. 31257

Contig ID 236721\_1.R1040

NCBI Description (AC002329) putative RING zinc-finger protein [Arabidopsis

thaliana] >qi 3790573 (AF078824) RING-H2 finger protein

RHA3a [Arabidopsis thaliana]

Seq. No. 31258

Contig ID 236809 1.R1040

5'-most EST uC-gmrominsoy248d01b1

Method BLASTX
NCBI GI g4049410
BLAST score 619
E value 2.0e-64
Match length 168
% identity 67

NCBI Description (Y10225) L-ascorbate oxidase [Cucumis melo]

Seq. No. 31259

Contig ID 236916\_1.R1040 5'-most EST uC-gmronoir007c08b1

Method BLASTX
NCBI GI g3935183
BLAST score 405
E value 3.0e-39

Match length 158 % identity 56

NCBI Description (AC004557) F17L21.26 [Arabidopsis thaliana]

Seq. No. 31260

Contig ID 236942\_1.R1040 5'-most EST rlr700896352.h1

Method BLASTX
NCBI GI g542812
BLAST score 148
E value 2.0e-09
Match length 95
% identity 36

NCBI Description estrogen-responsive finger protein, efp (RING finger,

coiled-coil domains) - human >gi\_458726\_dbj\_BAA04747\_
(D21205) estrogen responsive finger protein (efp) [Homo

sapiens]

Seq. No. 31261

Contig ID 236964\_1.R1040 5'-most EST rlr700896382.h1

Seq. No. 31262



```
Contig ID
                   237012 1.R1040
5'-most EST
                   rlr700900992.h1
Seq. No.
                   31263
Contig ID
                   237075 1.R1040
5'-most EST
                   zsg701130250.h1
Method
                   BLASTX
NCBI GI
                   q3859659
BLAST score
                   330
E value
                   6.0e-31
Match length
                   111
% identity
                   63
NCBI Description
                   (AL031394) putative potassium transporter AtKT5p (AtKT5)
                   [Arabidopsis thaliana]
Seq. No.
                   31264
Contig ID
                   237098 1.R1040
5'-most EST
                   asn701133396.h1
Seq. No.
                   31265
                   237105 1.R1040
Contig ID
5'-most EST
                   r1r700896607.h1
Method
                   BLASTX
NCBI GI
                   g3434971
BLAST score
                   208
                   3.0e-16
E value
Match length
                   120
% identity
                   45
NCBI Description
                   (AB008105) ethylene responsive element binding factor 3
                   [Arabidopsis thaliana]
Seq. No.
                   31266
Contig ID
                   237186 1.R1040
5'-most EST
                   rlr700896731.h1
Seq. No.
                   31267
Contig ID
                   237191 1.R1040
5'-most EST
                   jC-gmst02400039a10a1
Method
                   BLASTX
NCBI GI
                   g2950476
BLAST score
                   166
E value
                   2.0e-11
Match length
                   102
% identity
                   36
NCBI Description
                   (AL022070) vesicle transport v-snare protein
                   [Schizosaccharomyces pombe]
Seq. No.
                  31268
```

Contig ID 237259 1.R1040 5'-most EST g4397154

Seq. No. 31269

Contig ID 237270 1.R1040

5'-most EST uC-gmrominsoy294h03b1

Seq. No. 31270

Contig ID 237352 1.R1040

Method

NCBI GI

BLASTX

q4415914



```
5'-most EST
                   zsg701119837.h1
Seq. No.
                   31271
Contig ID
                   237372 1.R1040
5'-most EST
                   uC-gmropic046b04b1
Method
                   BLASTX
NCBI GI
                   g3641863
BLAST score
                   229
E value
                   4.0e-19
Match length
                   99
% identity
                   51
                  (AJ005042) beta-galactosidase [Cicer arietinum]
NCBI Description
Seq. No.
                   31272
Contig ID
                   237426 1.R1040
5'-most EST
                   kl1701202488.h1
Method
                   BLASTX
NCBI GI
                   g1814424
BLAST score
                   405
E value
                   1.0e-39
Match length
                   97
                   76
% identity
NCBI Description
                   (U85254) homeodomain protein AHDP [Arabidopsis thaliana]
Seq. No.
                   31273
Contig ID
                   237455 1.R1040
5'-most EST
                   rlr700897282.h1
Seq. No.
                   31274
Contig ID
                   237506 1.R1040
5'-most EST
                   gsv701051920.h1
Method
                   BLASTX
NCBI GI
                   g3461836
BLAST score
                   379
E value
                   3.0e-36
Match length
                   189
% identity
                   42
                   (AC005315) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >gi_3927841 (AC005727) putative protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   31275
Contig ID
                   237520 1.R1040
5'-most EST
                   rlr700897244.h1
Method
                   BLASTX
NCBI GI
                   q2781359
BLAST score
                   162
                   5.0e-16
E value
Match length
                   105
% identity
                   54
NCBI Description
                   (AC003113) F2501.15 [Arabidopsis thaliana]
Seq. No.
                   31276
Contig ID
                   237524 1.R1040
5'-most EST
                  fC-qmf1700897731a1
```

4783





BLAST score 387 E value 2.0e-37 Match length 134 % identity 48

NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]

Seq. No. 31277

Contig ID 237531\_1.R1040 5'-most EST rlr700898266.h1

Seq. No. 31278

Contig ID 237555 1.R1040

5'-most EST uC-gmflminsoy074c06b1

Seq. No. 31279

Contig ID 237581\_1.R1040 5'-most EST gsv701043841.h1

Seq. No. 31280

Contig ID 237637 1.R1040

5'-most EST  $g42898\overline{9}4$ 

Seq. No. 31281

Contig ID 237687 1.R1040

5'-most EST jC-gmfl02220065g10a1 Method BLASTX

NCBI GI g3402693
BLAST score 385
E value 2.0e-37
Match length 101
% identity 83

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 31282

Contig ID 237706 1.R1040

5'-most EST uC-gmrominsoy081g10b1

Method BLASTX
NCBI GI g3776029
BLAST score 628
E value 1.0e-65
Match length 141
% identity 84

NCBI Description (AJ010476) RNA helicase [Arabidopsis thaliana]

Seq. No. 31283

Contig ID 237738\_1.R1040 5'-most EST rlr700897565.h1

Method BLASTX
NCBI GI g1619321
BLAST score 188
E value 2.0e-14
Match length 83
% identity 42

NCBI Description (Y07563) hin1 [Nicotiana tabacum]

Seq. No. 31284

Contig ID 237767\_1.R1040



5 -most EST g5677100

Method BLASTX

NCBI GI g4138581

BLAST score 499

E value 3.0e-91

Match length 239

% identity 39

NCBI Description (X98474) mitochondrial energy transfer protein [Solanum

tuberosum]

Seq. No. 31285

Contig ID 237845\_1.R1040 5'-most EST dpv701101422.h1

Seq. No. 31286

Contig ID 237846\_1.R1040 5'-most EST rlr700897740.h1

Method BLASTX
NCBI GI g4220537
BLAST score 146
E value 3.0e-09
Match length 67
% identity 39

NCBI Description (AL035356) PsRT17-1 like protein [Arabidopsis thaliana]

Seq. No. 31287

Contig ID 237931\_1.R1040 5'-most EST uC-gmronoir041e06b1

Method BLASTX
NCBI GI 94309698
BLAST score 1085
E value 1.0e-119
Match length 243
% identity 83

NCBI Description (AC006266) putative glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 31288

Contig ID 237942\_1.R1040 5'-most EST fC-gmfl700901262a1

Method BLASTX
NCBI GI g3687224
BLAST score 496
E value 3.0e-50
Match length 138
% identity 69

NCBI Description (AC005169) putative N-acetyl-gamma-glutamyl-phosphate

reductase [Arabidopsis thaliana]

Seq. No. 31289

Contig ID 237961\_1.R1040 5'-most EST rlr700897919.h1

Seq. No. 31290

Contig ID 238024 1.R1040

5'-most EST uC-qmflminsoy032g07b1

```
Seq. No.
Contig ID
                   238093 1.R1040
5'-most EST
                   dpv701102606.hl
Seq. No.
                   31292
Contig ID
                   238126 1.R1040
5'-most EST
                   uC-gmrominsoy176e11b1
Method
                   BLASTX
NCBI GI
                   g3522931
BLAST score
                   203
E value
                   7.0e-16
Match length
                   67
% identity
NCBI Description
                   (AC002535) putative Na+/Ca2+ exchanger [Arabidopsis
                   thaliana]
                   31293
Seq. No.
Contig ID
                   238166 1.R1040
5'-most EST
                   rlr700898308.h1
Method
                   BLASTX
NCBI GI
                   g2146739
BLAST score
                   335
E value
                   1.0e-31
Match length
                   100
% identity
                   64
                  hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521
NCBI Description
                   (U28214) hexokinase 1 [Arabidopsis thaliana]
                   31294
Seq. No.
                   238167 1.R1040
Contig ID
5'-most EST
                   jC-gms\(\overline{t}\)02400074b11d1
Seq. No.
                   31295
                   238172 1.R1040
Contig ID
5'-most EST
                   r1r700898315.h1
Method
                   BLASTX
NCBI GI
                   g3882239
BLAST score
                   287
E value
                   1.0e-25
Match length
                   154
% identity
NCBI Description
                   (AB018302) KIAA0759 protein [Homo sapiens]
Seq. No.
                   31296
Contig ID
                   238239 1.R1040
5'-most EST
                   uC-gmrominsoy107b04b1
Method
                   BLASTX
NCBI GI
                   g2970034
BLAST score
                   436
E value
                   4.0e-43
Match length
                   144
% identity
                   50
```

(D88536) delta 9 desaturase [Arabidopsis thaliana] 31297

Contig ID 238260 1.R1040 5'-most EST rlr700898478.h1

NCBI Description

Seq. No.



```
BLASTX.
Method
                   g404688
NCBI GI
                   605
BLAST score
E value
                   1.0e-62
                   188
Match length
                   56
% identity
                  (L19074) cytochrome P450 [Catharanthus roseus]
NCBI Description
                   31298
Seq. No.
                   238322 1.R1040
Contig ID
                   rlr700898576.h1
5'-most EST
                   BLASTX
Method
                   g3269289
NCBI GI
                   239
BLAST score
                   4.0e-20
E value
Match length
                   71
                   68
% identity
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   31299
Seq. No.
                   238434 1.R1040
Contig ID
5'-most EST
                   rlr700898745.hl
                   BLASTX
Method
                   q3219271
NCBI GI
BLAST score
                   192
                   5.0e-15
E value
Match length
                   64
% identity
                   55
                  (AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]
NCBI Description
                   31300
Seq. No.
Contig ID
                   238469 1.R1040
5'-most EST
                   rlr700898803.h1
                   31301
Seq. No.
                   238534 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810073a12d1
                   31302
Seq. No.
                   238568 1.R1040
Contig ID
5'-most EST
                   zsg701118545.h1
                   31303
Seq. No.
                   238638 1.R1040
Contig ID
                   rlr700899094.h1
5'-most EST
                   BLASTX
Method
                   g4490730
NCBI GI
BLAST score
                   253
                   4.0e-22
E value
                   73
Match length
% identity
```

Seq. No. 31304

NCBI Description

Contiq ID 238650 1.R1040

5'-most EST uC-gmrominsoy212d09b1

Method BLASTX

4787

(AL035709) putative protein [Arabidopsis thaliana]



NCBI GI g3114573 BLAST score 334 E value 4.0e-31 Match length 146 % identity 47 NCBI Description (AF01938

NCBI Description (AF019383) 1-deoxyxylulose-5-phosphate synthase [Mentha x

piperita]

Seq. No. 31305

Contig ID 238652\_1.R1040 5'-most EST rlr700899120.h1

Method BLASTX
NCBI GI g2443876
BLAST score 183
E value 1.0e-13
Match length 60
% identity 63

NCBI Description (AC002294) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 31306

Contig ID 238670 1.R1040

5'-most EST uC-gmrominsoy265b09b1

Seq. No. 31307

Contig ID 238682\_1.R1040 5'-most EST rlr700899168.h1

Method BLASTX
NCBI GI g3150416
BLAST score 257
E value 1.0e-22
Match length 90
% identity 56

NCBI Description (AC004165) putative protein kinase, 5' partial [Arabidopsis

thaliana]

Seq. No. 31308

Contig ID 238771\_1.R1040 5'-most EST jC-gmro02910034c02a1

Seq. No. 31309

Contig ID 238847 1.R1040 5'-most EST rlr700899452.h1

Seq. No. 31310

Contig ID 238854\_1.R1040

5'-most EST jC-gmro02910051d12d1

Seq. No. 31311

Contig ID 238866\_1.R1040 5'-most EST rlr700899483.h1

Seq. No. 31312

Contig ID 238902 1.R1040

5'-most EST uC-gmflminsoy014c03b1

Method BLASTN NCBI GI g3821780

BLAST score 36



E value 1.0e-10 Match length 50 % identity 51

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 31313

Contig ID 238987\_1.R1040 5'-most EST rlr700899662.h1

Seq. No. 31314

Contig ID 239004\_1.R1040 5'-most EST rlr700899684.h1

Seq. No. 31315

Contig ID 239066\_1.R1040 5'-most EST rlr700899820.h1

Seq. No. 31316

Contig ID 239073\_1.R1040 5'-most EST rlr700899832.h1

Method BLASTX
NCBI GI 94006829
BLAST score 188
E value 2.0e-14
Match length 74
% identity 54

NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No. 31317

Contig ID 239116\_1.R1040 5'-most EST rlr700899964.h1

Method BLASTX
NCBI GI g3355473
BLAST score 152
E value 2.0e-13
Match length 89
% identity 56

% identity 56
NCBI Description (AC004218) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31318

Contig ID 239175\_1.R1040 5'-most EST zsg701121593.h1

Seq. No. 31319

Contig ID 239185\_1.R1040 5'-most EST rlr700900113.h1

Method BLASTX
NCBI GI g3426039
BLAST score 288
E value 4.0e-26
Match length 82
% identity 68

NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 31320

Contig ID 239247\_1.R1040 5'-most EST rlr700900254.h1



15

% identity

NCBI Description

```
975.
                       31321
    Seq. No.
                       239299 1.R1040
    Contig ID
    5'-most EST
                       g4297487
    Seq. No.
                       31322
                       239371 1.R1040
    Contig ID
                       rlr700900511.hl
    5'-most EST
    Method
                       BLASTX
                       q3355467
    NCBI GI
                       203
    BLAST score
                       7.0e-16
    E value
                       99
    Match length
                       45
    % identity
                       (AC004218) hypothetical protein [Arabidopsis thaliana]
    NCBI Description
                       31323
    Seq. No.
                       239388 1.R1040
    Contig ID
    5'-most EST
                       r1r700\overline{9}00537.h1
    Method
                       BLASTX
    NCBI GI
                       g3096947
    BLAST score
                       481
    E value
                       1.0e-48
    Match length
                       105
                       86
    % identity
                       (Y16327) putative cyclic nucleotide-regulated ion channel
    NCBI Description
                       [Arabidopsis thaliana]
                       31324
    Seq. No.
                       239402 1.R1040
    Contig ID
    5'-most EST
                       rlr700900553.h1
                       31325
    Seq. No.
                       239407 1.R1040
    Contig ID
                       r1r700\overline{9}00558.h1
    5'-most EST
    Method
                       BLASTX
    NCBI GI
                       g2129635
    BLAST score
                       443
                       5.0e-44
    E value
    Match length
                       141
                       62
    % identity
    NCBI Description
                       light repressible receptor protein kinase - Arabidopsis
                       thaliana >gi_1321686_emb_CAA66376_ (X97774) light
                       repressible receptor protein kinase [Arabidopsis thaliana]
                       31326
    Seq. No.
    Contig ID
                       239451 1.R1040
                       rlr700900625.h1
    5'-most EST
    Method
                       BLASTX
    NCBI GI
                       q1710628
    BLAST score
                       185
    E value
                       1.0e-13
    Match length
                       78
```

4790

(L28010) HnRNP F protein [Homo sapiens]

HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F)

>qi 631210 pir S43484 hnRNP F protein - human >qi 452048



43

```
Seq. No.
                   31327
Contig ID
                   239462 1.R1040
5'-most EST
                   rlr700900644.hl
Method
                   BLASTX
NCBI GI
                   g2288994
BLAST score
                   160
E value
                   5.0e-24
Match length
                   155
```

NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

 Seq. No.
 31328

 Contig ID
 239564\_1.R1040

 5'-most EST
 rlr700900813.h1

Seq. No. 31329

% identity

Contig ID 239565 1.R1040 5'-most EST rlr700900850.h1

Seq. No. 31330

Contig ID 239566\_1.R1040

5'-most EST  $jC-gmf\overline{1}02220069b11d1$ 

Method BLASTX
NCBI GI g464900
BLAST score 291
E value 3.0e-26
Match length 68
% identity 81

NCBI Description PUTATIVE KINASE-LIKE PROTEIN TMKL1 PRECURSOR

>gi\_539008\_pir\_\_S39476 kinase-like transmembrane protein

TMKL1 precursor - Arabidopsis thaliana

>gi\_313190\_emb\_CAA51385\_ (X72863) TMKL1 [Arabidopsis

thaliana]

Seq. No. 31331

Contig ID 239609 1.R1040 5'-most EST rlr700900878.h1

Seq. No. 31332

Contig ID 239621 1.R1040

5'-most EST uC-gmrominsoy079h09b1

Seq. No. 31333

Contig ID 239761\_1.R1040 5'-most EST gsv701047017.h1

Method BLASTX
NCBI GI g2244869
BLAST score 156
E value 2.0e-10
Match length 84

% identity 44

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31334

Contig ID 239812\_1.R1040 5'-most EST epx701107156.h1

% identity

43



```
Method
                   BLASTX
NCBI GI
                  g3114573
BLAST score
                   507
E value
                   1.0e-51
Match length
                  105
% identity
                   88
                   (AF019383) 1-deoxyxylulose-5-phosphate synthase [Mentha x
NCBI Description
                  piperita]
Seq. No.
                   31335
                  239842 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810085b09d1
Method
                  BLASTX
NCBI GI
                  g2191127
BLAST score
                   517
                  1.0e-52
E value
Match length
                  111
                  94
% identity
NCBI Description
                  (AF007269) A_IG002N01.1 gene product [Arabidopsis thaliana]
Seq. No.
                  31336
                  239857 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910008d04d1
Method
                  BLASTX
NCBI GI
                  g4468994
BLAST score
                  657
E value
                  1.0e-102
Match length
                  268
% identity
                  67
NCBI Description
                  (AL035605) putative protein [Arabidopsis thaliana]
Seq. No.
                  31337
Contig ID
                  239859 1.R1040
5'-most EST
                  uC-gmrominsoy105d02b1
Seq. No.
                  31338
                  239871 1.R1040
Contig ID
5'-most EST
                  hrw701058964.h1
Method
                  BLASTX
NCBI GI
                  g2244993
BLAST score
                  623
E value
                  5.0e-65
Match length
                  146
                  77
% identity
NCBI Description
                  (Z97341) similarity to AMP-activated protein kinase beta
                  [Arabidopsis thaliana]
Seq. No.
                  31339
Contig ID
                  239879 1.R1040
5'-most EST
                  asn701142909.h2
Method
                  BLASTX
NCBI GI
                  q3319357
BLAST score
                  147
E value
                  1.0e-09
Match length
                  94
```

NCBI Description (AF077407) contains similarity to phosphoenolpyruvate



## synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]

```
Seq. No.
  Contig ID
                     239880 1.R1040
  5'-most EST
                     rlr700901284.h1
  Seq. No.
                     31341
                     239912 1.R1040
  Contig ID
  5'-most EST
                     dpv701101235.h1
                     31342
  Seq. No.
                     239922 1.R1040
  Contig ID
  5'-most EST
                     g5605974
  Method
                     BLASTX
  NCBI GI
                     g1781299
  BLAST score
                     186
                     9.0e-14
  E value
  Match length
                     56
  % identity
                     66
  NCBI Description
                     (Y09506) transformer-SR ribonucleoprotein [Nicotiana
                     tabacum]
                     31343
  Seq. No.
                     239956 1.R1040
  Contig ID
  5'-most EST
                     jC-gmro02910027c06a1
  Method
                     BLASTX
  NCBI GI
                     g3335359
  BLAST score
                     188
  E value
                     4.0e-14
  Match length
                     96
  % identity
                     35
  NCBI Description
                     (AC003028) unknown protein [Arabidopsis thaliana]
  Seq. No.
                     31344
  Contig ID
                     239968 1.R1040
  5'-most EST
                     gsv701052113.h1
  Seq. No.
                     31345
  Contig ID
                     240065_1.R1040
  5'-most EST
                     g4305686
  Method
                     BLASTX
  NCBI GI
                     g2911077
  BLAST score
                     284
  E value
                     2.0e-25
  Match length
                     106
  % identity
                     48
  NCBI Description
                     (AL021960) gibberellin 20-oxidase - like protein
                     [Arabidopsis thaliana]
  Seq. No.
                     31346
  Contig ID
                     240079 1.R1040
  5'-most EST
                     rlr700901591.h1
  Method
                     BLASTX
  NCBI GI
                     g285741
  BLAST score
```

4.0e-09

145

Match length 45

E value



% identity 62

NCBI Description (D14550) EDGP precursor [Daucus carota]

Seq. No. 31347

Contig ID 240178\_1.R1040 5'-most EST gsv701055354.h1

Method BLASTX
NCBI GI g2444231
BLAST score 196
E value 3.0e-15
Match length 62
% identity 58

NCBI Description (AF026267) ethylene receptor homolog [Nicotiana tabacum]

Seq. No. 31348

Contig ID 240208\_1.R1040 5'-most EST rlr700901829.h1

Seq. No. 31349

Contig ID 240268 1.R1040 5'-most EST rlr700901923.h1

Seq. No. 31350

Contig ID 240298\_1.R1040 5'-most EST rlr700902304.h1

Seq. No. 31351

Contig ID 240373 1.R1040 5'-most EST kl1701210880.h1

Method BLASTX
NCBI GI g3688284
BLAST score 233
E value 8.0e-20
Match length 61
% identity 69

NCBI Description (AJ011567) lanatoside 15'-O-acetylesterase [Digitalis

lanata]

31352

Seq. No.

Contig ID 240385 1.R1040

5'-most EST uC-gmrominsoy258b01b1

Method BLASTX
NCBI GI g3036871
BLAST score 319
E value 1.0e-35
Match length 127
% identity 61

NCBI Description (AJ005340) IAA amidohydrolase [Linum usitatissimum]

Seq. No. 31353

Contig ID 240412\_1.R1040 5'-most EST uC-gmronoir070c10b1

Seq. No. 31354

Contig ID 240412 2.R1040

5'-most EST uC-gmrominsoy127h01b1



Contig ID 240434\_1.R1040 5'-most EST rlr700902244.h1

Seq. No. 31356

Contig ID 240481\_1.R1040 5'-most EST zsg701121831.h1

Method BLASTX
NCBI GI g2194117
BLAST score 379
E value 2.0e-36
Match length 127
% identity 60

NCBI Description (AC002062) Strong similarity to Arabidopsis receptor

protein kinase PR5K (gb\_ATU48698). [Arabidopsis thaliana]

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Seq. No. 31357

Contig ID 240488 1.R1040

5'-most EST jC-gmst02400014a03a1

Seq. No. 31358

Contig ID 240525\_1.R1040 5'-most EST rlr700902392.h1

Seq. No. 31359

Contig ID 240533\_1.R1040 5'-most EST rlr700902407.h1

Seq. No. 31360

Contig ID 240534 1.R1040

5'-most EST jC-gmro02910044b02a1

Seq. No. 31361

Contig ID 240727 1.R1040

5'-most EST uC-gmrominsoy300g02b1

Seq. No. 31362

Contig ID 240789\_1.R1040 5'-most EST uC-gmropic014f12b1

Method BLASTX
NCBI GI g4204295
BLAST score 286
E value 2.0e-25
Match length 173
% identity 38

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 31363

Contig ID 240819\_1.R1040 5'-most EST epx701104050.h1

Seq. No. 31364

Contig ID 240823\_1.R1040

5'-most EST uC-gmrominsoy111g05b1

Seq. No. 31365

% identity

NCBI Description

47



```
Contig ID
                   240830 1.R1040
5'-most EST
                   jC-gmf102220132ag07d1
Seq. No.
                   31366
Contig ID
                   240839 1.R1040
5'-most EST
                   uC-gmronoir011c08b1
Seq. No.
                   31367
Contig ID
                   240935 1.R1040
5'-most EST
                   uC-gmrominsoy262g09b1
Method
                   BLASTX
NCBI GI
                   g1657615
BLAST score
                   379
E value
                   2.0e-36
Match length
                   99
                   72
% identity
NCBI Description
                   (U72502) Glp [Arabidopsis thaliana] >gi 3068706 (AF049236)
                   putative transmembrane protein G1p [Arabidopsis thaliana]
Seq. No.
                   31368
Contig ID
                   240944 1.R1040
5'-most EST
                   dpv701098646.h1
Method
                   BLASTN
NCBI GI
                   g3128137
BLAST score
                   50
E value
                   3.0e-19
Match length
                   126
% identity
                   85
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K9I9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   31369
Contig ID
                   240950 1.R1040
5'-most EST
                   dpv701097313.h1
Seq. No.
                   31370
Contig ID
                   240989 1.R1040
5'-most EST
                   uC-gmrominsoy043h10b1
Method
                   BLASTX
NCBI GI
                   g4335751
BLAST score
                   183
E value
                   1.0e-21
Match length
                   125
% identity
                   45
NCBI Description
                   (AC006284) putative methyltransferase [Arabidopsis
                   thaliana]
Seq. No.
                   31371
Contig ID
                   240993 1.R1040
5'-most EST
                   dpv701097361.h1
Method
                   BLASTX
NCBI GI
                   g4006915
BLAST score
                   143
E value
                   6.0e-09
Match length
                  75
```

(Z99708) hypothetical protein [Arabidopsis thaliana]



Contig ID 241096\_1.R1040

5'-most EST uC-gmflminsoy045a06b1

Method BLASTX
NCBI GI g2129550
BLAST score 146
E value 2.0e-09
Match length 33
% identity 82

NCBI Description calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -

Arabidopsis thaliana >gi 2129554 pir S71901

calcium-dependent protein kinase 6 - Arabidopsis thaliana

£,

>gi\_836940 (U20623) calcium-dependent protein kinase

[Arabidopsis thaliana] >gi 836944 (U20625)

calcium-dependent protein kinase [Arabidopsis thaliana]
>gi\_4454034\_emb\_CAA23031.1\_ (AL035394) calcium-dependent

protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No. 31373

Contig ID 241097 1.R1040

5'-most EST uC-gmrominsoy062e01b1

Method BLASTX
NCBI GI g1666096
BLAST score 249
E value 3.0e-21
Match length 89
% identity 56

NCBI Description (Y09113) dioxygenase [Marah macrocarpus]

Seq. No. 31374

Contig ID 241150\_1.R1040 5'-most EST dpv701098766.h2

Seq. No. 31375

Contig ID 241169\_1.R1040 5'-most EST dpv701097591.h1

Seq. No. 31376

Contig ID 241230 1.R1040

5'-most EST uC-gmrominsoy247a11b1

Method BLASTX
NCBI GI g2191151
BLAST score 246
E value 1.0e-20
Match length 164
% identity 35

NCBI Description (AF007269) contains similarity to membrane associated

salt-inducible protein [Arabidopsis thaliana]

Seq. No. 31377

Contig ID 241242\_1.R1040 5'-most EST dpv701097695.h1

Seq. No. 31378

Contig ID 241259\_1.R1040

5'-most EST g4297977



 Seq. No.
 31379

 Contig ID
 241275\_1.R1040

 5'-most EST
 leu701157858.h1

Seq. No. 31380
Contig ID 241276\_1.R1040
5'-most EST dpv701097780.h1

Seq. No. 31381 Contig ID 241355 1

Contig ID 241355\_1.R1040 5'-most EST dpv701097986.h1 Method BLASTX

NCBI GI g4454019 BLAST score 234 E value 2.0e-19 Match length 95 % identity 53

NCBI Description (AL035396) SRG1-like protein [Arabidopsis thaliana]

Seq. No. 31382

Contig ID 241369\_1.R1040 5'-most EST dpv701098007.h1

Seq. No. 31383

Contig ID 241392\_1.R1040

5'-most EST uC-gmrominsoy241e11b1

Method BLASTX
NCBI GI g4218011
BLAST score 481
E value 3.0e-48
Match length 187
% identity 53

NCBI Description (AC006135) putative protein kinase [Arabidopsis thaliana]

>gi\_4309721 gb AAD15491 (AC006439) putative

serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 31384

Contig ID 241475\_1.R1040 5'-most EST dpv701098205.h1

Method BLASTX
NCBI GI g3522939
BLAST score 260
E value 2.0e-22
Match length 87
% identity 57

NCBI Description (AC004411) putative squamosa-promoter binding protein

[Arabidopsis thaliana]

Seq. No. 31385

Contig ID 241475 2.R1040

5'-most EST jC-gmro02910037h09a1

Seq. No. 31386

Contig ID 241495\_1.R1040 5'-most EST jC-gmle01810042g06a1

Method BLASTN



```
NCBI GI
                   q349158
BLAST score
                   278
E value
                   1.0e-155
Match length
                   436
% identity
                   92
NCBI Description
                  Vigna aconitifolia AIR carboxylase (purE) mRNA, partial cds
Seq. No.
                   31387
                   241512 1.R1040
Contig ID
5'-most EST
                   epx701107812.hl
Method
                   BLASTX
NCBI GI
                   g4432814
BLAST score
                   399
E value
                   1.0e-38
Match length
                   134
% identity
                   57
NCBI Description
                   (AC006593) unknown protein [Arabidopsis thaliana]
Seq. No.
                   31388
Contig ID
                   241513 1.R1040
5'-most EST
                   zsg701123289.h1
Seq. No.
                   31389
Contig ID
                   241531 1.R1040
5'-most EST
                   k11701\overline{2}11402.h1
Method
                   BLASTX
NCBI GI
                   g1809127
BLAST score
                   239
E value
                   2.0e-20
Match length
                   76
% identity
                   54
NCBI Description
                   (U77674) terminal flower 1 [Arabidopsis thaliana]
                   >gi 2208929 dbj BAA20483 (D86932) terminal flower1
                   [Arabidopsis thaliana] >gi 2208931 dbj BAA20484 (D87130)
                   terminal flower1 [Arabidopsis thaliana]
                   >gi 2208933 dbj BAA20485 (D87519) terminal flower1
                   [Arabidopsis thaliana]
Seq. No.
                   31390
Contig ID
                   241534 1.R1040
5'-most EST
                   dpv701098921.h1
Seq. No.
                   31391
                   241540 1.R1040
Contig ID
5'-most EST
                   dpv701102459.h1
Method
                   BLASTX
NCBI GI
                   g1491776
BLAST score
                   201
                   7.0e-16
E value
Match length
                   56
```

% identity

NCBI Description (M37636) cationic peroxidase [Arachis hypogaea]

31392 Seq. No.

241551 1.R1040 Contig ID 5'-most EST dpv701098365.hl

71



Contig ID 241562\_1.R1040 5'-most EST dpv701098389.h1

Method BLASTX
NCBI GI g1086252
BLAST score 380
E value 1.0e-36
Match length 130
% identity 56

NCBI Description sucrose cleavage protein - Potato >gi\_707001\_bbs\_157931

(S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]

. .

[Solanum tuberosum]

Seq. No. 31394

Contig ID 241628\_1.R1040 5'-most EST dpv701098513.h1

Method BLASTX
NCBI GI g3367519
BLAST score 184
E value 6.0e-26
Match length 142
% identity 51

NCBI Description (AC004392) Contains similarity to gb\_U51898

Ca2+-independent phospholipase A2 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No. 31395

Contig ID 241715\_1.R1040 5'-most EST dpv701103463.h1

Method BLASTX
NCBI GI g2765093
BLAST score 227
E value 6.0e-19
Match length 95
% identity 51

NCBI Description (Y10983) putative cytochrome P450 [Glycine max]

Seq. No. 31396

Contig ID 241720\_1.R1040 5'-most EST zsg701123531.h1

Seq. No. 31397

Contig ID 241774 1.R1040 5'-most EST dpv701098794.h2

Method BLASTX
NCBI GI g4454482
BLAST score 283
E value 1.0e-25
Match length 78
% identity 65

NCBI Description (AC006234) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31398

Contig ID 241778\_1.R1040 5'-most EST xzy700966851.h1

Method BLASTX



```
..NCBI GI
                    q1575556
BLAST score
                    224
                    2.0e-54
 E value
                    131
 Match length
                    85
 % identity
                    (U66299) acyl-CoA oxidase homolog [Phalaenopsis sp. 'True
 NCBI Description
                    Lady']
                    31399
 Seq. No.
                    241794 1.R1040
 Contig ID
 5'-most EST
                    uC-gmrominsoy045h04b1
                    31400
 Seq. No.
                    241850 1.R1040
 Contig ID
                    dpv701098934.h1
 5'-most EST
                    BLASTX
 Method
                    g2262116
 NCBI GI
                    143
 BLAST score
                    6.0e-09
 E value
                    116
 Match length
                    36
 % identity
                    (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
 NCBI Description
                    31401
 Seq. No.
                    241891 1.R1040
 Contig ID
 5'-most EST
                    dpv701099004.h1
                    31402
 Seq. No.
                    241898 1.R1040
 Contig ID
 5'-most EST
                    gsv701051813.hl
 Seq. No.
                    31403
                    241909 1.R1040
 Contig ID
                    dpv701\overline{0}99026.h1
 5'-most EST
 Seq. No.
                    31404
                    241912 1.R1040
 Contig ID
                    jC-gmst02400062b05d1
  5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g1346261
 BLAST score
                    240
                    4.0e-20
 E value
 Match length
                    63
  % identity
                    68
                    GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR)
 NCBI Description
                    >gi 1015319 dbj BAA11091 (D67088) glutamyl-tRNA reductase
                    [Cucumis sativus]
```

÷ (

31405 Seq. No.

241950 1.R1040 Contig ID 5'-most EST dpv701099090.h1

31406 Seq. No.

Contig ID 241992 1.R1040 5'-most EST asn701141457.hl

Seq. No. 31407



```
242029 1.R1040
Contig ID
5'-most EST
                   dpv701099213.h1
Seq. No.
                   31408
Contig ID
                   242047 1.R1040
5'-most EST
                   uC-gmrominsoy041c04b1
Method
                   BLASTX
NCBI GI
                   q3252866
BLAST score
                   285
E value
                   2.0e-25
Match length
                   88
                   60
% identity
NCBI Description
                   (AF033535) putative zinc transporter [Arabidopsis thaliana]
Seq. No.
                   31409
Contig ID
                   242047 2.R1040
5'-most EST
                   uC-gmronoir024d04b1
Method
                   BLASTX
NCBI GI
                   g2388566
BLAST score
                   222
E value
                   4.0e-18
Match length
                   93
% identity
                   46
NCBI Description
                   (AC000098) Similar to Arabidopsis Fe(II) transport protein
                   (gb_U27590). [Arabidopsis thaliana]
Seq. No.
                   31410
Contig ID
                   242075 1.R1040
5'-most EST
                   g4290344
Method
                   BLASTX
NCBI GI
                   g1781326
BLAST score
                   372
E value
                   2.0e-35
Match length
                   139
% identity
                   55
NCBI Description
                   (Y10464) peroxidase [Spinacia oleracea]
Seq. No.
                   31411
                   242091 1.R1040
Contig ID
5'-most EST
                   dpv701099303.h1
Method
                   BLASTN
NCBI GI
                   g166929
BLAST score
                   70
E value
                   3.0e - 31
Match length
                   156
% identity
                   91
NCBI Description
                  A.thaliana ubiquitin extension protein (UBQ1) gene,
                   complete cds
Seq. No.
                   31412
Contig ID
                   242156 1.R1040
5'-most EST
                   dpv701099383.h1
```

Method BLASTX
NCBI GI g2642445
BLAST score 205
E value 8.0e-16
Match length 122



% identity (AC002391) putative serine/threonine protein kinase NCBI Description [Arabidopsis thaliana] 31413 Seq. No. 242217 1.R1040 Contig ID fua701043047.hl 5'-most EST BLASTX Method g1781279 NCBI GI 151 BLAST score 4.0e-10 E value 62 Match length 45 % identity (Y10455) MtN13 [Medicago truncatula] NCBI Description 31414 Seq. No. 242300 1.R1040 Contig ID dpv701099685.hl 5'-most EST 31415 Seq. No. 242328 1.R1040 Contig ID  $dpv701\overline{0}99656.h1$ 5'-most EST 31416 Seq. No. 242354 1.R1040 Contig ID dpv701099701.hl 5'-most EST 31417 Seq. No. 242369 1.R1040 Contig ID fua701036913.hl 5'-most EST BLASTN Method g18590 NCBI GI 433 BLAST score 0.0e+00E value 507 Match length 100 % identity NCBI Description G.max GH3 gene for auxin-regulated protein 31418 Seq. No. 242378 1.R1040 Contig ID uC-gmrominsoy126e03b1 5'-most EST 31419 Seq. No. 242378 2.R1040 Contig ID dpv701099729.hl

5'-most EST

31420 Seq. No.

242480 1.R1040 Contig ID

jC-qmst02400049a09a1 5'-most EST

BLASTX Method q2292907 NCBI GI BLAST score 527 8.0e-54E value 151 Match length % identity

NCBI Description (Y10099) P-glycoprotein homologue [Hordeum vulgare]



```
Seq. No.
                   31421
                   242546 1.R1040
Contig ID
                   uC-gmrominsoy256g01b1
5'-most EST
                   BLASTX
Method
                   g2920839
NCBI GI
BLAST score
                   341
                   6.0e-32
E value
                   142
Match length
% identity
                   44
                   (U95136) Os-FIERG2 gene product [Oryza sativa]
NCBI Description
Seq. No.
                   31422
                   242555 1.R1040
Contig ID
                   dpv701099968.hl
5'-most EST
                   31423
Seq. No.
                   242592 1.R1040
Contig ID
                   uC-gmrominsoy109b10b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
                   1.0e-10
E value
Match length
                   48
% identity
                   65
NCBI Description Xenopus laevis cDNA clone 27A6-1
                    31424
 Seq. No.
                    242603 1.R1040
Contig ID
 5'-most EST
                   dpv701100033.h2
                    31425
 Seq. No.
                    242608 1.R1040
 Contig ID
 5'-most EST
                   dpv701100043.h2
                    31426
 Seq. No.
                    242634 1.R1040
 Contig ID
                    q5508996
 5'-most EST
                   BLASTX
 Method
                   g2088647
 NCBI GI
                    473
 BLAST score
                    3.0e-47
 E value
                    163
 Match length
 % identity
                    64
                    (AF002109) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    >qi 3158394 (AF036340) LRR-containing F-box protein
                    [Arabidopsis thaliana]
                    31427
 Seq. No.
                    242758 1.R1040
 Contig ID
                    dpv701100380.h1
 5'-most EST
                    BLASTX
 Method
                    g3868940
 NCBI GI
 BLAST score
                    145
```

Method BLASTX
NCBI GI g3868940
BLAST score 145
E value 1.0e-10
Match length 63
% identity 57

NCBI Description (AB015054) Alg2 [Rhizomucor pusillus]

pusillus]

>gi\_3868942\_dbj\_BAA34297\_ (AB015055) Alg2 [Rhizomucor

31428 Seq. No. 242767 1.R1040 Contig ID dpv701100283.hl 5'-most EST BLASTX Method g2961380 NCBI GI 183 BLAST score 1.0e-13 E value 45 Match length

% identity (AL022141) putative protein [Arabidopsis thaliana] NCBI Description

31429 Seq. No.

242808 1.R1040 Contig ID 5'-most EST dpv701100346.h1

Seq. No. 31430

242861 1.R1040 Contig ID

uC-gmrominsoy180a09b1 5'-most EST

67

Method BLASTX NCBI GI g2465923 270 BLAST score 2.0e-23 E value Match length 91 55 % identity

(AF024648) receptor-like serine/threonine kinase NCBI Description

[Arabidopsis thaliana]

31431 Seq. No.

242862 1.R1040 Contig ID jC-gmf102220085g05a1 5'-most EST

BLASTX Method g3643603 NCBI GI 240 BLAST score 3.0e-20 E value 118 Match length 49 % identity

(AC005395) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 31432

242864 1.R1040 Contig ID

5'-most EST jC-gmst02400008g12d1

BLASTX Method q1170409 NCBI GI BLAST score 190 2.0e-14 E value 53 Match length 72 % identity

HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22) NCBI Description

>gi\_549887 (U09336) homeobox protein [Arabidopsis thaliana] >gi\_549888 (U09337) homeobox protein [Arabidopsis thaliana] >gi 4490724 emb CAB38927.1 (AL035709) homeobox protein

HAT22 [Arabidopsis thaliana]

31433 Seq. No.



```
242869 1.R1040
Contig ID
                  fua701038752.h1
5'-most EST
                  BLASTX
Method
                   g1279640
NCBI GI
BLAST score
                   185
                   6.0e-14
E value
                   52
Match length
                   69
% identity
                  (X92204) NAM [Petunia x hybrida]
NCBI Description
                   31434
Seq. No.
                   242884 1.R1040
Contig ID
                   dpv701100446.h1
5'-most EST
                   31435
Seq. No.
                   242928 1.R1040
Contig ID
                   jC-gmro02800039d01a1
5'-most EST
                   31436
Seq. No.
                   242932 1.R1040
Contig ID
                   dpv701100514.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1752734
                   517
BLAST score
                   2.0e-52
E value
Match length
                   166
                   63
% identity
                  (D78510) beta-glucan-elicitor receptor [Glycine max]
NCBI Description
                   31437
Seq. No.
                   242940 1.R1040
Contig ID
5'-most EST
                   uC-gmropic111e08b1
                   31438
Seq. No.
                   242961 1.R1040
Contig ID
                   dpv701100548.h1
5'-most EST
                   BLASTX
Method
                   g1255951
NCBI GI
                   612
BLAST score
                   8.0e-64
E value
                   152
Match length
                   78
% identity
                  (X96932) PS60 [Nicotiana tabacum]
NCBI Description
                   31439
Seq. No.
                   242963 1.R1040
Contig ID
5'-most EST
                   dpv701100551.h1
                   BLASTX
Method
                   q1546704
NCBI GI
                   245
BLAST score
                   4.0e-21
E value
Match length
                   95
% identity
                   (X98854) peroxidase ATP7a [Arabidopsis thaliana]
NCBI Description
```

4806

31440

242981 1.R1040

Seq. No.

Contig ID



```
dpv701100579.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1169892
BLAST score
                  177
                  3.0e-13
E value
                  65
Match length
                  54
% identity
                  PUTATIVE GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE
NCBI Description
                  (ISOMERIZING) (HEXOSEPHOSPHATE AMINOTRANSFERASE)
                  (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT)
                  >qi 1006748 emb CAA90824 (Z54140)
                  glucosamine-fructose-6-phosphate aminotransferase
                  [Schizosaccharomyces pombe] >gi 3560205_emb_CAA20758
                  (AL031536) glucosamine--fructose-6-phosphate
                  aminotransferase (isomerizing) [Schizosaccharomyces pombe]
                  31441
Seq. No.
                  243021 1.R1040
Contig ID
                  dpv701100648.h1
5'-most EST
                  31442
Seq. No.
                  243022 1.R1040
Contig ID
                  jC-gmro02800034f04a1
5'-most EST
                  BLASTX
Method
                  q2346974
NCBI GI
                  177
BLAST score
                  7.0e-13
E value
                  69
Match length
                  58
% identity
                  (AB006599) ZPT2-12 [Petunia x hybrida]
NCBI Description
Seq. No.
                  31443
                  243023_1.R1040
Contig ID
                  jC-gmro02910031d02a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1732513
BLAST score
                   431
                  1.0e-51
E value
                  125
Match length
                  79
% identity
                  (U62743) snapdragon myb protein 305 homolog [Arabidopsis
NCBI Description
                   thaliana]
                   31444
Seq. No.
                   243044 1.R1040
Contig ID
                   hrw701062605.hl
5'-most EST
                   BLASTX
Method
                   q2342682
NCBI GI
                   296
BLAST score
                   8.0e-27
E value
                   77
Match length
% identity
                   77
                  (AC000106) Contains similarity to Rattus AMP-activated
NCBI Description
                   protein kinase (gb_X95577). [Arabidopsis thaliana]
```

Contig ID 243049\_1.R1040



```
dpv701100682.h1
5'-most EST
                  31446
Seq. No.
                  243054 1.R1040
Contig ID
5'-most EST
                  dpv701100688.h1
                  31447
Seq. No.
                  243138 1.R1040
Contig ID
                  uC-gmronoir029b10b1
5'-most EST
Method
                  BLASTX
                  q3135253
NCBI GI
BLAST score
                  363
                  2.0e-34
E value
                  151
Match length
% identity
                  51
                   (AC003058) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                   31448
Seq. No.
                   243184 1.R1040
Contig ID
                   fC-gmse7000756053r1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4006914
                   206
BLAST score
                   4.0e-16
E value
                   56
Match length
% identity
                   73
                   (Z99708) serine C-palmitoyltransferase like protein
NCBI Description
                   [Arabidopsis thaliana]
                   31449
Seq. No.
                   243237_1.R1040
Contig ID
                   jC-gmle01810018a01a2
5'-most EST
                   BLASTX
Method
                   g4455334
NCBI GI
                   189
BLAST score
                   3.0e-14
E value
                   119
Match length
                   37
% identity
                  (AL035525) myosin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   31450
                   243261 1.R1040
Contig ID
5'-most EST
                   dpv701100953.h1
                   31451
Seq. No.
                   243330 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800034h07a1
                   31452
Seq. No.
                   243360 1.R1040
Contig ID
                   jC-gmro02800040f02a1
5'-most EST
```

31453

243368 1.R1040

jC-gmro02910008g11a1

Seq. No. Contig ID

5'-most EST

Contig ID 5'-most EST

31460

243662 1.R1040

uC-gmrominsoy110h12b1



```
Seq. No.
                   31454
Contig ID
                   243373 1.R1040
5'-most EST
                   uC-gmrominsoy087a03b1
Method
                  BLASTN
                   q169980
NCBI GI
BLAST score
                   438
E value
                   0.0e + 00
Match length
                   446
                   100
% identity
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                   31455
Seq. No.
Contig ID
                   243460 1.R1040
5'-most EST
                   zsg701127693.h1
                   31456
Seq. No.
                   243463 1.R1040
Contig ID
5'-most EST
                  uC-gmropic105h10b1
                   BLASTX
Method
NCBI GI
                   q4263784
BLAST score
                   265
E value
                   3.0e-23
Match length
                   67
% identity
                   70
NCBI Description
                   (AC006068) putative glycogenin-2 protein [Arabidopsis
                   thaliana]
                   31457
Seq. No.
                   243464 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy182b03b1
Seq. No.
                   31458
                   243542 1.R1040
Contig ID
                   dpv701101402.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4469009
BLAST score
                   181
E value
                   2.0e-13
Match length
                   81
% identity
                   49
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
                   31459
Seq. No.
                   243599 1.R1040
Contig ID
5'-most EST
                   dpv701103581.h1
Method
                   BLASTX
NCBI GI
                   g2879799
BLAST score
                   138
E value
                   1.0e-08
Match length
                   34
                   79
% identity
                  (AL021813) 60s ribosomal protein [Schizosaccharomyces
NCBI Description
                   pombe]
```

4809



BLASTX Method g629561 NCBI GI BLAST score 218 1.0e-17 E value Match length 108 39 % identity

SRG1 protein - Arabidopsis thaliana NCBI Description

>gi 479047\_emb\_CAA55654\_ (X79052) SRG1 [Arabidopsis

thaliana]

Seq. No. 31461

243690 1.R1040 Contig ID 5'-most EST dpv701101586.hl

Method BLASTX q1935918 NCBI GI 156 BLAST score 1.0e-10 E value 84 Match length 48 % identity

(U93559) putative serine/threonine protein kinase [Brassica NCBI Description

rapa]

31462 Seq. No.

243723 1.R1040 Contig ID dpv701101644.h1 5'-most EST

Seq. No. 31463

243760 1.R1040 Contig ID 5'-most EST uC-gmronoir049e05b1

BLASTX Method NCBI GI g629669 BLAST score 174 1.0e-12 E value Match length 87 47

% identity

NCBI Description hypothetical protein - tomato

Seq. No. 31464

243766 1.R1040 Contig ID dpv701101709.h1 5 -most EST

31465 Seq. No.

243771\_1.R1040 Contig ID dpv701101750.h1 5'-most EST

31466 Seq. No.

Contig ID 243821 1.R1040

g4291282 5'-most EST

31467 Seq. No.

243874 1.R1040 Contig ID

5'-most EST jC-gmro02910048e02a1

Seq. No. 31468

Contig ID 243912 1.R1040 5'-most EST dpv701101924.h1

Method BLASTX



```
g3850582
NCBI GI
BLAST score
                  335
                   4.0e-31
E value
                  111
Match length
% identity
                  (AC005278) F15K9.14 [Arabidopsis thaliana]
NCBI Description
                   31469
Seq. No.
                   243919 1.R1040
Contig ID
                  uC-gmropic110f08b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3550661
BLAST score
                   441
                   7.0e-44
E value
                   121
Match length
                   46
% identity
                   (AJ001310) 39 kDa EF-Hand containing protein [Solanum
NCBI Description
                   tuberosum]
                   31470
Seq. No.
                   243922 1.R1040
Contig ID
                   zsg701117757.h2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3451078
                   234
BLAST score
                   1.0e-19
E value
                   118
Match length
                   41
% identity
                  (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                   31471
Seq. No.
Contig ID
                   243958 1.R1040
5'-most EST
                   dpv701102015.h1
Method
                   BLASTX
NCBI GI
                   g3258568
BLAST score
                   218
E value
                   1.0e-17
Match length
                   114
                   46
% identity
                  (U89959) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   31472
Seq. No.
                   243969 1.R1040
Contig ID
                   jC-gmro02910069b03a1
 5'-most EST
                   BLASTX
Method
                   g3510249
NCBI GI
BLAST score
                   452
                   5.0e-45
E value
                   143
Match length
                   57
 % identity
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]
                   31473
 Seq. No.
                   244031 1.R1040
 Contig ID
                   dpv701102116.h1
 5'-most EST
```



```
244083 1.R1040
Contig ID
                  epx701104596.hl
5'-most EST
                   31475
Seq. No.
                  244118 1.R1040
Contig ID
5'-most EST
                  dpv701102217.hl
Method
                  BLASTX
                   g3127045
NCBI GI
BLAST score
                   200
                   5.0e-32
E value
Match length
                   172
% identity
                   48
                   (AF020545) bHLH transcription factor JAF13 [Petunia x
NCBI Description
                  hybrida]
                   31476
Seq. No.
                   244177 1.R1040
Contig ID
                   jC-gmro02910046g04d1
5'-most EST
                   31477
Seq. No.
                   244251 1.R1040
Contig ID
5'-most EST
                   dpv701102403.h1
Seq. No.
                   31478
Contig ID
                   244254 1.R1040
                   kl1701204911.hl
5'-most EST
Method
                   BLASTX
                   a2136107
NCBI GI
BLAST score
                   231
E value
                   6.0e-19
                   150
Match length
                   36
% identity
                   retinoblastoma protein binding protein RBQ-3 - human
NCBI Description
                   >gi_755750_emb_CAA59446_ (X85134) RB protein binding
                   protein [Homo sapiens]
Seq. No.
                   31479
                   244262 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810056d07a1
                   31480
Seq. No.
                   244302 1.R1040
Contig ID
                   fua701042796.h1
5'-most EST
                   BLASTX
Method
                   q4206210
NCBI GI
BLAST score
                   402
E value
                   3.0e-39
Match length
                   137
                   56
% identity
                   (AF071527) putative calcium channel [Arabidopsis thaliana]
NCBI Description
                   >qi 4263043 gb AAD15312 (AC005142) putative calcium
                   channel [Arabidopsis thaliana]
```

 Seq. No.
 31481

 Contig ID
 244466 1.R1040

 5'-most EST
 dpv701102676.h1

Method BLASTN



NCBI GI g2264318 BLAST score 34 E value 9.0e-10 Match length 116 % identity 87 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MUP24, complete sequence [Arabidopsis thaliana] 31482 Seq. No. 244467 1.R1040 Contig ID  $qsv701\overline{0}44845.h1$ 5'-most EST

Method BLASTX

NCBI GI q1002796 BLAST score 186 E value 3.0e-14 Match length 57 % identity 63

(U33915) Cpm10 [Craterostigma plantagineum] NCBI Description

ż.

Seq. No. 31483

Contig ID 244522 1.R1040 5'-most EST dpv701102747.h1

Method BLASTX NCBI GI g3779024 BLAST score 554 E value 4.0e-57 Match length 122 87 % identity

(AC005171) unknown protein [Arabidopsis thaliana] NCBI Description

31484 Seq. No.

Contig ID 244543 2.R1040

5'-most EST jC-gmst02400054g08a1

Seq. No. 31485

Contig ID 244603 1.R1040

5'-most EST jC-gmle01810003g02d1

31486 Seq. No.

Contig ID 244682 1.R1040 5'-most EST dpv701102942.h1

Seq. No. 31487

Contig ID 244709 1.R1040 5'-most EST dpv701102973.hl

Seq. No. 31488

Contig ID 244711 1.R1040 5'-most EST dpv701102975.h1

Method BLASTX NCBI GI q4006829 BLAST score 265 E value 3.0e-23Match length 70 % identity 73

NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]



Contig ID 244721\_1.R1040 5'-most EST asn701142469.h1

Method BLASTX
NCBI GI g2388580
BLAST score 451
E value 3.0e-45
Match length 94
% identity 87

NCBI Description (AC000098) Similar to Sequence 10 from patent 5477002

(gb\_1253956). [Arabidopsis thaliana]

Seq. No. 31490

Contig ID 244727 1.R1040

5'-most EST uC-gmrominsoy233e04b1

Seq. No. 31491

Contig ID 244791\_1.R1040 5'-most EST uC-gmropic078c12b1

Method BLASTX
NCBI GI g2569940
BLAST score 342
E value 3.0e-32
Match length 134
% identity 51

NCBI Description (Y15194) GRS protein [Arabidopsis thaliana]

Seq. No. 31492

Contig ID 244834\_1.R1040 5'-most EST dpv701103152.h1

Method BLASTX
NCBI GI g4572669
BLAST score 666
E value 4.0e-70
Match length 154
% identity 82

NCBI Description (AC006954) putative glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 31493

Contig ID 244954\_1.R1040 5'-most EST gsv701053674.h1

Seq. No. 31494

Contig ID 244974\_1.R1040 5'-most EST uC-gmropic110a11b1

Seq. No. 31495

Contig ID 245045\_1.R1040

5'-most EST jC-gmr002910059a03d1

Seq. No. 31496

Contig ID 245144\_1.R1040 5'-most EST leu701150419.h1

Method BLASTX NCBI GI g4371280 BLAST score 355



9.0e-34 E value 113 Match length % identity

(AC006260) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

31497 245173 1.R1040 Contig ID

uC-gmrominsoy248f11b1 5'-most EST

31498 Seq. No.

245240 1.R1040 Contig ID fua701037513.hl 5'-most EST

31499 Seq. No.

245253 1.R1040 Contig ID xzy700966706.hl 5'-most EST

31500 Seq. No.

245347 1.R1040 Contig ID  $xzy700\overline{9}66827.h1$ 5'-most EST

BLASTX Method g3116212 NCBI GI BLAST score 365 5.0e-35 E value 79 Match length 89 % identity

(AB004797) homeobox gene [Nicotiana tabacum] NCBI Description

31501 Seq. No.

245395 1.R1040 Contig ID xzy700966883.hl 5'-most EST

31502 Seq. No.

245399 1.R1040 Contig ID

jC-gmro02910037g11a1 5'-most EST

31503 Seq. No.

245413 1.R1040 Contig ID fua701036906.h1 5'-most EST

Seq. No.

31504

245429 1.R1040 Contig ID fua701036924.h1 5'-most EST

BLASTX Method g1946355 NCBI GI 299 BLAST score 2.0e-27 E value 93 Match length 65 % identity

(U93215) maize transposon MuDR mudrA protein isolog NCBI Description

[Arabidopsis thaliana] >gi\_2880040 (AC002340) maize

transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.

245434 1.R1040 Contig ID 5'-most EST  $jsh701\overline{0}63843.h1$ 

31505



```
31506
Seq. No.
                   245437 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220071e12a1
                  31507
Seq. No.
                  245441 1.R1040
Contig ID
5'-most EST
                  fua701036936.hl
Seq. No.
                   31508
                  245445_1.R1040
Contig ID
5'-most EST
                   jC-gmro02910036a04d1
                  BLASTX
Method
NCBI GI
                  q1654140
                  169
BLAST score
                   8.0e-12
E value
                   56
Match length
% identity
                   62
NCBI Description (U37840) lipoxygenase [Lycopersicon esculentum]
                   31509
Seq. No.
                   245447 1.R1040
Contig ID
5'-most EST
                   fua701036942.h1
Method
                  BLASTX
NCBI GI
                  g1172874
BLAST score
                  179
                  3.0e-13
E value
Match length
                   51
                   59
% identity
NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
                  >gi_479589_pir__S34823 dehydration-induced protein RD22 -
                  Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
                   [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene
                   [Arabidopsis thaliana]
Seq. No.
                   31510
                   245455 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy045d09b1
                   31511
Seq. No.
Contig ID
                   245456 1.R1040
5'-most EST
                   fC-gmst700893453d3
                   31512
Seq. No.
Contig ID
                   245483 1.R1040
5'-most EST
                   fua701036984.h1
Method
                  BLASTX
NCBI GI
                   g3941448
BLAST score
                   424
E value
                   4.0e-48
Match length
                  110
% identity
NCBI Description
                  (AF062878) putative transcription factor [Arabidopsis
                   thaliana]
```

Contig ID 245490 1.R1040 5'-most EST fua701036991.h1



```
Seq. No.
                  31514
                  245609 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910022e08a1
                  BLASTX
Method
NCBI GI
                  q3269301
                  288
BLAST score
                  3.0e-47
E value
Match length
                  148
                  63
% identity
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                  31515
Seq. No.
                  245614 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy194d08b1
Method
                  BLASTX
NCBI GI
                  g3860266
BLAST score
                  147
E value
                  2.0e-09
Match length
                  85
% identity
                  18
                  (AC005824) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  31516
Seq. No.
                  245623 1.R1040
Contig ID
5'-most EST
                  fua701037159.hl
                  BLASTX
Method
NCBI GI
                  g3941524
BLAST score
                  400
                  3.0e-39
E value
Match length
                  83
% identity
                  83
                   (AF062916) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  31517
                   245645 1.R1040
Contig ID
                   fua701037181.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3395440
BLAST score
                  295
                  9.0e-27
E value
Match length
                  95
                  57
% identity
                  (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  31518
Contig ID
                  245688 1.R1040
5'-most EST
                  jC-qmst02400027f08d1
Method
                  BLASTX
```

NCBI GI g2606077

BLAST score 261 1.0e-22 E value Match length 74

% identity

(AF030301) auxin-induced protein [Helianthus annuus] NCBI Description



```
31519
Seq. No.
                  245703 1.R1040
Contig ID
                                                                   ٠.
                   fua701\overline{0}37254.h1
5'-most EST
                  BLASTX
Method
                   g3341678
NCBI GI
BLAST score
                   161
                   5.0e-11
E value
                   71
Match length
% identity
                   48
                   (AC003672) putative zinc finger protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   31520
                   245705 1.R1040
Contig ID
                   uC-gmronoir034h07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2292907
                   579
BLAST score
                   2.0e-62
E value
                   217
Match length
% identity
                   32
                  (Y10099) P-glycoprotein homologue [Hordeum vulgare]
NCBI Description
Seq. No.
                   31521
                   245719 1.R1040
Contig ID
5'-most EST
                   uC-qmropic033a03b1
Method
                   BLASTX
NCBI GI
                   q4097522
BLAST score
                   381
                   8.0e-37
E value
Match length
                   88
% identity
                   81
NCBI Description
                   (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
                   ananassa]
                   31522
Seq. No.
                   245810 1.R1040
Contig ID
                   fua701037375.h1
5'-most EST
                   BLASTX
Method
                   g2465008
NCBI GI
BLAST score
                   618
                   4.0e-64
E value
Match length
                   162
                   73
% identity
                  (AJ001445) ripening-induced protein [Fragaria vesca]
NCBI Description
                   31523
Seq. No.
                   245841 1.R1040
Contig ID
                   fua701037419.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3068705
```

BLAST score 156 E value 2.0e-10

84 Match length 45 % identity

(AF049236) unknown [Arabidopsis thaliana] NCBI Description



Contig ID 245853 1.R1040

5'-most EST jC-gmf102220142c01a1

Seq. No. 31525

245889 1.R1040 Contig ID 5'-most EST fua701037472.h1

31526 Seq. No.

245912 1.R1040 Contig ID

5'-most EST g4276943 BLASTX Method q3080393 NCBI GI BLAST score 393 4.0e-38 E value Match length 77 90 % identity

(AL022603) NADH dehydrogenase like protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 31527

245927 1.R1040 Contig ID fua701037534.h1 5'-most EST

31528 Seq. No.

246084 1.R1040 Contig ID fua701037815.h1 5'-most EST

BLASTX Method g3785989 NCBI GI BLAST score 135 E value 6.0e-18 Match length 63 % identity 79

(AC005560) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 31529

246117 1.R1040 Contig ID 5'-most EST

jC-qmst02400058f12a1

Method BLASTX g4056421 NCBI GI BLAST score 165 3.0e-11 E value Match length 36 75 % identity

(AC005322) Similar to gb Z30094 basic transcripion factor NCBI Description

2, 44 kD subunit from Homo sapiens. EST gb W43325 comes

from this gene. [Arabidopsis thaliana]

Seq. No. 31530

Contig ID 246153 1.R1040 5'-most EST leu701152312.h1

31531 Seq. No.

Contig ID 246155 1.R1040 uC-qmropic039b08b1 5'-most EST

Method BLASTX NCBI GI g2982434



BLAST score 448
E value 3.0e-44
Match length 144
% identity 60
NCBI Description (AL022224) putative protein [Arabidopsis thaliana]
Seq. No. 31532
Contig ID 246160 1.R1040

5'-most EST leu701151955.h1
Method BLASTX
NCBI GI g4056506
BLAST score 272
E value 5.0e-24

E value 5.0 Match length 91 % identity 56

NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 31533

Contig ID 246199 1.R1040 5'-most EST hrw701062931.h1

Seq. No. 31534

Contig ID 246225\_1.R1040

5'-most EST jC-gmfl02220085b12d1

Seq. No. 31535

Contig ID 246311\_1.R1040 5'-most EST uC-gmropic112a07b1

Method BLASTX
NCBI GI g1117793
BLAST score 399
E value 5.0e-39
Match length 104
% identity 73

NCBI Description (U24232) lipoxygenase [Solanum tuberosum]

Seq. No. 31536

Contig ID 246340 1.R1040 5'-most EST fua701041137.h1

Method BLASTX
NCBI GI g1402920
BLAST score 193
E value 6.0e-15
Match length 58
% identity 60

NCBI Description (X98321) peroxidase [Arabidopsis thaliana]

Seq. No. 31537

Contig ID 246341\_1.R1040 5'-most EST fua701038152.h1

Method BLASTX
NCBI GI g2088651
BLAST score 169
E value 7.0e-12
Match length 148
% identity 39

NCBI Description (AF002109) hypersensitivity-related gene 201 isolog



## [Arabidopsis thaliana]

31538 Seq. No. 246393 1.R1040 Contig ID fua701040387.hl 5'-most EST Method BLASTX q2739008 NCBI GI BLAST score 402 E value 6.0e-39 Match length 154

% identity 53 (AF022463) CYP78A3p [Glycine max] NCBI Description

31539 Seq. No.

246404 1.R1040 Contig ID 5'-most EST asn701138624.hl

Seq. No. 31540

246414 1.R1040 Contig ID 5'-most EST jC-qmst02400046d08a1

31541 Seq. No.

246436 1.R1040 Contig ID

jC-gmf102220093a06a1 5'-most EST

BLASTX Method q119640 NCBI GI BLAST score 253 1.0e-21 E value Match length 109

44 % identity

1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN NCBI Description

E8) >qi 82109 pir S01642 ripening protein E8 - tomato >qi 19199 emb CAA31789 (X13437) E8 protein [Lycopersicon

esculentum]

31542 Seq. No.

246438 1.R1040 Contig ID fua701038275.h1 5'-most EST

31543 Seq. No.

246482 1.R1040 Contig ID fua701038350.hl 5'-most EST

31544 Seq. No.

246509 1.R1040 Contig ID

jC-gmst02400041e03a1 5'-most EST

BLASTX Method g2213602 NCBI GI BLAST score 152 7.0e-10 E value 52 Match length 62 % identity

NCBI Description (AC000348) T7N9.22 [Arabidopsis thaliana]

31545 Seq. No.

246512 1.R1040 Contig ID jC-gmst02400055d01a1 5'-most EST



```
BLASTX
Method
                  q3426039
NCBI GI
BLAST score
                  271
                  6.0e-24
E value
                  76
Match length
% identity
                  66
                  (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
                  31546
Seq. No.
                  246575 1.R1040
Contig ID
                  jC-gmle01810060e09d1
5'-most EST
                  31547
Seq. No.
                  246589 1.R1040
Contig ID
                   fua701038535.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                   g3892050
BLAST score
                   200
                   2.0e-15
E value
Match length
                   96
                   54
% identity
NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                 31548
                   246621 1.R1040
Contig ID
5'-most EST
                   uC-qmrominsoy133h11b1
                   BLASTX
Method
NCBI GI
                   q3786007
BLAST score
                   159
                   1.0e-10
E value
                   114
Match length
                   33
% identity
                  (AC005499) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   31549
Seq. No.
                   246642 1.R1040
Contig ID
                   uC-gmflminsoy044d11b1
5'-most EST
                   BLASTX
Method
                   g3953470
NCBI GI
                   146
BLAST score
                   5.0e-09
E value
Match length
                   89
                   40
% identity
                  (AC002328) F20N2.15 [Arabidopsis thaliana]
NCBI Description
                   31550
Seq. No.
                   246704_1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy236e08b1
                   31551
Seq. No.
                   246800 1.R1040
```

Contig ID

5'-most EST jC-gmro02910061b06a1

BLASTX Method g1403134 NCBI GI BLAST score 278 E value 1.0e-24 Match length 117



% identity 53
NCBI Description (X98453) peroxidase [Arabidopsis thaliana]

Seq. No. 31552

Contig ID 246807\_1.R1040 5'-most EST fua701038813.h1

Seq. No. 31553

Contig ID 246840\_1.R1040

5'-most EST uC-gmronoir0001g01b1

Method BLASTX
NCBI GI g2262178
BLAST score 388
E value 3.0e-37
Match length 141
% identity 58

NCBI Description (AC002329) putative Mlo-like protein [Arabidopsis thaliana]

Seq. No. 31554

Contig ID 246841\_1.R1040

5'-most EST jC-gmst02400060c06a1

Seq. No. 31555

Contig ID 246860\_1.R1040 5'-most EST kl1701211237.h1

Seq. No. 31556

Contig ID 246957\_1.R1040 5'-most EST fua701039013.h1

Seq. No. 31557

Contig ID 246971\_1.R1040 5'-most EST fua701039063.h1

Seq. No. 31558

Contig ID 247066\_1.R1040

5'-most EST g5753703
Method BLASTX
NCBI GI g3695019
BLAST score 599
E value 3.0e-62
Match length 173
% identity 65

NCBI Description (AF055848) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 31559

Contig ID 247068 1.R1040

5'-most EST uC-gmflminsoy053d03b1

Method BLASTX
NCBI GI g2052510
BLAST score 603
E value 9.0e-63
Match length 138
% identity 80

NCBI Description (U95758) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Arabidopsis thaliana]



Contig ID 247090\_1.R1040

5'-most EST uC-gmrominsoy229e05b1

Seq. No. 31561

Contig ID 247093 1.R1040

5'-most EST jC-gmro02910066b03a1

Method BLASTX
NCBI GI g4063751
BLAST score 152
E value 9.0e-10

Match length 60 % identity 52

NCBI Description (AC005851) putative white protein [Arabidopsis thaliana]

>gi\_4510409\_gb\_AAD21495.1\_ (AC006929) putative white

protein [Arabidopsis thaliana]

Seq. No. 31562

Contig ID 247152\_1.R1040 5'-most EST fua701039274.h1

Seq. No. 31563

Contig ID 247256\_1.R1040

5'-most EST g4296712

Seq. No. 31564

Contig ID 247259\_1.R1040 5'-most EST fua701039432.h1

Seq. No. 31565

Contig ID 247372 1.R1040 5'-most EST leu701156929.h1

Seq. No. 31566

Contig ID 247444\_1.R1040

5'-most EST jC-gmst02400054f04a1

Method BLASTX
NCBI GI g1293835
BLAST score 288
E value 2.0e-27
Match length 130
% identity 45

NCBI Description (U56965) C15H9.5 gene product [Caenorhabditis elegans]

Seq. No. 31567

Contig ID 247476\_1.R1040 5'-most EST fua701039812.h1

Seq. No. 31568

Contig ID 247488 1.R1040 5'-most EST fua701039833.h1

Method BLASTX
NCBI GI g1149556
BLAST score 152
E value 5.0e-23
Match length 92
% identity 51





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NCBI Description (X94443) pectinmethylesterase [Vigna radiata]
```

Seq. No. 31569

Contig ID 247490\_1.R1040 5'-most EST gsv701046837.h1

Seq. No. 31570

Contig ID 247523\_1.R1040 5'-most EST fua701039911.h1

Seq. No. 31571

Contig ID 247533\_1.R1040 5'-most EST fua701039923.h1

Method BLASTX
NCBI GI g4151319
BLAST score 240
E value 2.0e-20
Match length 52
% identity 90

NCBI Description (AF089084) putative auxin efflux carrier protein; AtPIN1

[Arabidopsis thaliana]

Seq. No. 31572

Contig ID 247548 1.R1040

5'-most EST jC-gmf102220080a04d1

Seq. No. 31573

Contig ID 247553\_1.R1040 5'-most EST fua701039971.h1

Method BLASTX
NCBI GI g2829910
BLAST score 147
E value 1.0e-09
Match length 84
% identity 45

NCBI Description (AC002291) Unknown protein, contains regulator of

chromosome condensation motifs [Arabidopsis thaliana]

Seq. No. 31574

Contig ID 247667 1.R1040 5'-most EST fua701040157.h1

Seq. No. 31575

Contig ID 247674\_1.R1040 5'-most EST fua701040166.h1

Method BLASTX
NCBI GI g1002800
BLAST score 629
E value 2.0e-65
Match length 139
% identity 82

NCBI Description (U33917) Cpm7 [Craterostigma plantagineum]

Seq. No. 31576

Contig ID 247708\_1.R1040 5'-most EST epx701108580.h1

Method BLASTX



NCBI GI g3746059 BLAST score 603 E value 9.0e-63 Match length 148 % identity 72

NCBI Description (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis

thaliana] >gi\_4432812\_gb\_AAD20662\_ (AC006593) putative

cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 31577

Contig ID 247717 1.R1040

5'-most EST jC-gmro02910001g08d1

Method BLASTX
NCBI GI g1708424
BLAST score 301
E value 2.0e-27
Match length 71
% identity 76

NCBI Description ISOFLAVONE REDUCTASE HOMOLOG >gi\_1230614 (U48590)

isoflavone reductase-like protein [Lupinus albus]

Seq. No. 31578

Contig ID 247727 1.R1040

5'-most EST uC-gmflminsoy076b01b1

Seq. No. 31579

Contig ID 247738\_1.R1040 5'-most EST fua701040272.h1

Seq. No. 31580

Contig ID 247759\_1.R1040 5'-most EST fua701040314.h1

Seq. No. 31581

Contig ID 247761 1.R1040 5'-most EST fua701040318.h1

Seq. No. 31582

Contig ID 247766\_1.R1040 5'-most EST fua701040324.h1

Method BLASTN
NCBI GI g166411
BLAST score 180
E value 1.0e-96
Match length 374
% identity 88

NCBI Description Medicago sativa NADH-glutamate synthase mRNA, comlete cds

Seq. No. 31583

Contig ID 247783\_1.R1040 5'-most EST fua701040345.h1

Method BLASTX
NCBI GI g3935168
BLAST score 494
E value 8.0e-50
Match length 187
% identity 59



NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No. 31584

Contig ID 247846\_1.R1040 5'-most EST fua701040528.h1

Method BLASTX
NCBI GI g3927836
BLAST score 296
E value 8.0e-27
Match length 76

% identity 79

NCBI Description (AC005727) unknown protein [Arabidopsis thaliana]

Seq. No. 31585

Contig ID 247889\_1.R1040 5'-most EST fua701040581.h1

Seq. No. 31586

Contig ID 247930\_1.R1040 5'-most EST fua701040629.h1

Seq. No. 31587

Contig ID 247936\_1.R1040 5'-most EST jC-gmst02400058h11a1

Method BLASTX
NCBI GI g2781348
BLAST score 559
E value 2.0e-57
Match length 183
% identity 59

NCBI Description (AC003113) F2401.4 [Arabidopsis thaliana]

Seq. No. 31588

Contig ID 247954\_1.R1040
5'-most FST iC-cmle01810051h

5'-most EST jC-gmle01810051h11d1 Method BLASTX

Method BLASTX
NCBI GI g4263695
BLAST score 363
E value 1.0e-34
Match length 152
% identity 8

NCBI Description (AC006223) putative myosin II heavy chain [Arabidopsis

thaliana]

Seq. No. 31589

Contig ID 247996\_1.R1040 5'-most EST asn701140715.h1

Seq. No. 31590

Contig ID 248013 1.R1040

5'-most EST uC-gmrominsoy314e11b1

Seq. No. 31591

Contig ID 248025\_1.R1040 5'-most EST leu701154384.h1

Seq. No. 31592



248028 1.R1040 Contig ID fC-gmro700835214b1 5'-most EST BLASTX Method q860676 NCBI GI BLAST score 958 1.0e-104 E value Match length 232 77 % identity (U24188) calcium/calmodulin-dependent protein kinase NCBI Description [Lilium longiflorum] >gi 1097385 prf 2113422A Ca/calmodulin-dependent protein kinase [Lilium longiflorum] 31593 Seq. No.

248031 1.R1040 Contig ID fua701040753.hl 5'-most EST

31594 Seq. No. 248079 1.R1040 Contig ID fua701040818.hl 5'-most EST

Seq. No. 31595 248089 1.R1040 Contig ID fua701040834.hl 5'-most EST

31596 Seq. No. 248102 1.R1040 Contig ID 5'-most EST leu701153459.hl

31597 Seq. No. 248164 1.R1040 Contig ID 5'-most EST uC-gmflminsoy093e01b1

31598 Seq. No. 248176 1.R1040 Contig ID fua701040948.h1 5'-most EST

Method BLASTX g3928543 NCBI GI BLAST score 206 2.0e-16 E value 85 Match length % identity

(AB016819) UDP-glucose glucosyltransferase [Arabidopsis NCBI Description

thaliana]

31599 Seq. No.

Contig ID 248413 1.R1040

5'-most EST jC-gmst02400048g08a1

Seq. No. 31600

Contig ID 248488 1.R1040 5'-most EST fua701042965.h1

Method BLASTN NCBI GI q3985955 BLAST score 33 E value 4.0e-09 Match length 87 % identity 54



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH16, complete sequence [Arabidopsis thaliana]

Seq. No. 31601

248504 1.R1040 Contig ID fua701041350.hl 5'-most EST

BLASTX Method g4522004 NCBI GI BLAST score 370 3.0e-35 E value Match length 168 56 % identity

(AC007069) putative histidine kinase, sensory transduction NCBI Description

[Arabidopsis thaliana]

31602 Seq. No.

248506 1.R1040 Contig ID fua701041354.hl 5'-most EST

31603 Seq. No.

Contig ID 248518 1.R1040

5'-most EST uC-gmrominsoy116e12b1

BLASTN Method q4138138 NCBI GI BLAST score 40 5.0e-13 E value Match length 52 94

Lycopersicon esculentum mRNA for ss-galactosidase, clone NCBI Description

tEG1B

Seq. No. 31604

% identity

248542 1.R1040 Contig ID 5'-most EST fua701041435.h1

Seq. No. 31605

248614 1.R1040 Contig ID fua701041504.h1 5'-most EST

31606 Seq. No.

Contig ID 248615 1.R1040

5'-most EST uC-gmrominsoy169a04b1

Method BLASTX q4572674 NCBI GI BLAST score 524 4.0e-53 E value Match length 157 % identity 68

(AC006954) unknown protein [Arabidopsis thaliana] NCBI Description

31607 Seq. No.

Contig ID 248633 1.R1040

5'-most EST jC-gmro02910068f04a1

Method BLASTX NCBI GI q2827637 BLAST score 238 E value 6.0e-20



Match length 133 % identity 38

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 31608

Contig ID 248655\_1.R1040 5'-most EST fua701041554.h1

Method BLASTX
NCBI GI 94510348
BLAST score 140
E value 1.0e-08
Match length 84
% identity 40

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 31609

Contig ID 248681 1.R1040 5'-most EST leu701154148.h1

Method BLASTX
NCBI GI g2497219
BLAST score 182
E value 3.0e-13
Match length 89
% identity 42

NCBI Description HYPOTHETICAL 15.4 KD PROTEIN IN HAS1-JNM1 INTERGENIC REGION

>gi\_626266\_pir\_\_S47453 probable membrane protein YMR292w yeast (Saccharomyces cerevisiae) >gi\_530349\_emb\_CAA56801\_

(X80836) len:138, CAI:0.12, potential spliced gene, hydropho bic composition [Saccharomyces cerevisiae]

Seq. No. 31610

Contig ID 248699\_1.R1040 5'-most EST fua701041608.h1

Method BLASTX
NCBI GI g4558673
BLAST score 170
E value 3.0e-12
Match length 67

% identity 58

NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31611

Contig ID 248712\_1.R1040 5'-most EST fua701041635.h1

Seq. No. 31612

Contig ID 248739 1.R1040

5'-most EST jC-gmro02910011a05d1

Seq. No. 31613

Contig ID 248746 1.R1040

5'-most EST jC-gmst02400062e06a1

Seq. No. 31614

Contig ID 248750 1.R1040 5'-most EST leu701152047.h1



Seq. No. 31615

Contig ID 248756 1.R1040

5'-most EST jC-gmst02400050h11a1

Seq. No. 31616

Contig ID 248764\_1.R1040 5'-most EST fua701041707.h1

Seq. No. 31617

Contig ID 248771\_1.R1040 5'-most EST fua701041815.h1

Method BLASTX
NCBI GI g2924509
BLAST score 403
E value 1.0e-39
Match length 88
% identity 86

NCBI Description (AL022023) subtilisin proteinase - like [Arabidopsis

thaliana]

Seq. No. 31618

Contig ID 248780\_1.R1040 5'-most EST fua701041824.h1

Seq. No. 31619

Contig ID 248805\_1.R1040 5'-most EST fua701041754.h1

Seq. No. 31620

Contig ID 248807\_1.R1040 5'-most EST fua701041856.h1

Method BLASTX
NCBI GI g100226
BLAST score 174
E value 8.0e-13
Match length 92
% identity 42

NCBI Description hypothetical protein - tomato >gi\_19275\_emb\_CAA78112\_

(Z12127) protein of unknown function [Lycopersicon esculentum] >gi 445619 prf 1909366A Leu zipper protein

[Lycopersicon esculentum]

Seq. No. 31621

Contig ID 248818\_1.R1040 5'-most EST fua701041767.h1

Method BLASTX
NCBI GI g116337
BLAST score 262
E value 4.0e-23
Match length 83
% identity 60

NCBI Description BASIC ENDOCHITINASE PRECURSOR >gi 100310\_pir\_\_S23545

chitinase (EC 3.2.1.14) III, basic - common tobacco >gi\_19803\_emb\_CAA77657\_ (Z11564) basic chitinase III

[Nicotiana tabacum]

Seq. No. 31622

% identity

43



```
248831 1.R1040
Contig ID
                   fua701041785.hl
5'-most EST
                   31623
Seq. No.
                   248833 1.R1040
Contig ID
                   fua701041888.hl
5'-most EST
                   31624
Seq. No.
                   248929 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir045e11b1
                   BLASTN
Method
                   q438248
NCBI GI
                   80
BLAST score
                   5.0e-37
E value
                   224
Match length
                   84
% identity
                   S.tuberosum mRNA for precursor of the mitochondrial
NCBI Description
                   NAD+-dependent malic enzyme (malate dehydrogenase)
                   31625
Seq. No.
                   248950 1.R1040
Contig ID
5'-most EST
                   fua701041968.hl
                   31626 - -
Seq. No.
                   248951 1.R1040
Contig ID
                   fua701041969.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g3941493
BLAST score
                   81
                   8.0e-38
E value
                   161
Match length
                   88
% identity
                   Arabidopsis thaliana putative transcription factor (MYB68)
NCBI Description
                   mRNA, complete cds
                   31627
Seq. No.
                   248983 1.R1040
Contiq ID
                   fua701042011.h1
5'-most EST
                   BLASTX
Method
                   g1396054
NCBI GI
BLAST score
                   591
                   4.0e-61
E value
                   154
Match length
                   68
% identity
                   (D86180) phosphoribosylanthranilate transferase [Pisum
NCBI Description
                   sativum]
Seq. No.
                   31628
                   249001 1.R1040
Contig ID
                   fua701042031.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2498629
                   171
BLAST score
                   4.0e-12
E value
Match length
                   82
```

NCBI Description TRANSCRIPTIONAL REPRESSOR NF-X1 >gi\_2135825\_pir\_\_I38869



NFX1 - human >gi\_563217 (U15306) NFX1 [Homo sapiens] >gi\_4505387\_ref\_NP\_002495.1\_pNFX1\_ nuclear transcription factor, X-box binding

Seq. No. 31629

Contig ID 249006 1.R1040

5'-most EST uC-gmrominsoy192a04b1

Method BLASTX
NCBI GI g2335096
BLAST score 355
E value 1.0e-33
Match length 156
% identity 48

NCBI Description (AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31630

Contig ID 249016\_1.R1040

5'-most EST jC-gmro02910051e06a1

Method BLASTX
NCBI GI g119351
BLAST score 209
E value 1.0e-16
Match length 51
% identity 82

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 84950 pir S07586

phosphopyruvate hydratase (EC 4.2.1.11) - fruit fly (Drosophila melanogaster) >gi\_7946\_emb\_CAA34895\_ (X17034)

enolase (AA 1-433) [Drosophila melanogaster]

Seq. No. 31631

Contig ID 249023\_1.R1040 5'-most EST leu701144413.h1

Seq. No. 31632

Contig ID 249058 2.R1040 5'-most EST fua701042108.h1

Method BLASTX
NCBI GI g3695392
BLAST score 160
E value 1.0e-10
Match length 35
% identity 80

NCBI Description (AF096371) No definition line found [Arabidopsis thaliana]

Seq. No. 31633

Contig ID 249119 1.R1040

5'-most EST uC-gmrominsoy044h11b1

Method BLASTX
NCBI GI g3176686
BLAST score 706
E value 1.0e-74
Match length 169
% identity 75

NCBI Description (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]



 Seq. No.
 31634

 Contig ID
 249129 1.R1040

 5'-most EST
 jsh701067681.h1

Method BLASTX
NCBI GI g4008372
BLAST score 193
E value 7.0e-15
Match length 113
% identity 37

NCBI Description (Z27079) cDNA EST CEMSF67FB comes from this gene; cDNA EST

CEMSF67R comes from this gene; cDNA EST yk195e10.3 comes from this gene; cDNA EST yk195e10.5 comes from this gene; cDNA EST yk397a5.3 comes from this gene; cDNA EST yk3

Seq. No. 31635

Contig ID 249180\_1.R1040

NCBI Description P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3'

end

Seq. No. 31636

Contig ID 249237\_1.R1040 5'-most EST jC-gmro02910073h08a1

Method BLASTX
NCBI GI g4063742
BLAST score 320
E value 2.0e-29
Match length 176
% identity 48

NCBI Description (AC005851) putative phaseolin G-box binding protein

[Arabidopsis thaliana]

Seq. No. 31637

Contig ID 249241\_1.R1040 5'-most EST uC-gmropic075e12b1

Seq. No. 31638

Contig ID 249241\_2.R1040 5'-most EST gsv701049418.h1

Seq. No. 31639

Contig ID 249275\_1.R1040 5'-most EST fua701042384.h1

Seq. No. 31640

Contig ID 249313\_1.R1040 5'-most EST fua701042540.h1

Seq. No. 31641

Contig ID 249323 1.R1040



5'-most EST asn701143432.hl 31642 Seq. No. 249329 1.R1040 Contig ID 5'-most EST fua701042561.hl Seq. No. 31643 249369 1.R1040 Contig ID 5'-most EST fua701042610.h1 Seq. No. 31644 249386 1.R1040 Contig ID 5'-most EST fua701042629.hl BLASTX Method q3924604 NCBI GI 346 BLAST score 1.0e-32 E value Match length 89 74 % identity (AF069442) putative leucine-rich repeat protein NCBI Description [Arabidopsis thaliana] Seq. No. 31645 Contig ID 249389 1.R1040 5'-most EST fua701042632.h1 31646 Seq. No. 249515 1.R1040 Contig ID 5'-most EST fua701043364.h1 Method BLASTX NCBI GI g129813 BLAST score 192 E value 6.0e-15 77 Match length % identity 49 PEROXIDASE C1A PRECURSOR >gi 2144377 pir\_OPRHC peroxidase NCBI Description (EC 1.11.1.7) C1 precursor - horseradish Seq. No. 31647 249570 1.R1040 Contig ID leu701151908.h1 5'-most EST 31648 Seq. No. 249592 1.R1040 Contig ID jC-gmro02910024h02d1 5'-most EST Seq. No. 31649 249609 1.R1040 Contig ID uC-gmflminsoy061h06b1 5'-most EST

BLASTX Method NCBI GI g2497539 BLAST score 322 4.0e-30 E value 76 Match length 79 % identity

PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi 169703 NCBI Description (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]



Seq. No. 31650

Contig ID 249705 1.R1040

5'-most EST jC-gmro02910051a02a1

Method BLASTX
NCBI GI g2492820
BLAST score 253
E value 2.0e-21
Match length 104
% identity 41

NCBI Description HYPOTHETICAL 54.0 KD PROTEIN IN NRGA-USD INTERGENIC REGION

>gi\_1684649\_emb\_CAB05378\_ (Z82987) unknown, similar to
uracil permease from Schizosaccharomyces pombe [Bacillus
subtilis] >gi\_2636172\_emb\_CAB15664.1\_ (Z99122) similar to

permease [Bacillus subtilis]

Seq. No. 31651

Contig ID 249731\_1.R1040 5'-most EST leu701150624.h1

Seq. No. 31652

Contig ID 249784\_1.R1040 5'-most EST asn701142062.h1

Seq. No. 31653

Contig ID 249811\_1.R1040 5'-most EST fua701043283.h1

Seq. No. 31654

Contig ID 249817 1.R1040 5'-most EST fua701043290.h1

Method BLASTX
NCBI GI g3540183
BLAST score 407
E value 8.0e-40
Match length 138
% identity 59

NCBI Description (AC004122) Highly Similar to branched-chain amino acid

aminotransferase [Arabidopsis thaliana]

Seq. No. 31655

Contig ID 249827\_1.R1040 5'-most EST fua701043305.h1

Method BLASTN
NCBI GI g3860320
BLAST score 92
E value 2.0e-44
Match length 258
% identity 85

NCBI Description Cicer arietinum mRNA for beta-galactosidase, clone

CanBGal-5

Seq. No. 31656

Contig ID 249832\_1.R1040 5'-most EST leu701145936.h1

Method BLASTN NCBI GI g2598574



BLAST score 114 E value 4.0e-57 Match length 358 % identity 83

NCBI Description Medicago truncatula mRNA for MtN21 gene

Seq. No. 31657

Contig ID 249838\_1.R1040

5'-most EST jC-gmf102220053e06a1

Method BLASTX
NCBI GI g3152566
BLAST score 309
E value 3.0e-28
Match length 148
% identity 45

NCBI Description (AC002986) Similar to hypothetical protein YLR002c,

gb\_Z7314 from S. cerevisiae. [Arabidopsis thaliana]

Seq. No. 31658

Contig ID 249860\_1.R1040 5'-most EST kl1701211805.h1

Seq. No. 31659

Contig ID 249915\_1.R1040 5'-most EST fua701043414.h1

Method BLASTX
NCBI GI g1791307
BLAST score 570
E value 1.0e-58
Match length 198
% identity 57

NCBI Description (U83501) permease homolog [Arabidopsis thaliana]

Seq. No. 31660

Contig ID 249980\_1.R1040 5'-most EST lus701015749.h1

Seq. No. 31661

Contig ID 249990\_1.R1040 5'-most EST asn701131156.h1

Seq. No. 31662

Contig ID 250041\_1.R1040 5'-most EST fC-gmro700564066f2

Seq. No. 31663

Contig ID 250063 1.R1040 5'-most EST fua701043589.h1

Seq. No. 31664

Contig ID 250069\_1.R1040 5'-most EST hrw701060533.h1

Seq. No. 31665

Contig ID 250074\_1.R1040 5'-most EST kl1701202347.h1

Method BLASTX



```
NCBI GI
                   q557472
BLAST score
                   234
E value
                   2.0e-19
                   148
Match length
                   39
% identity
                  (U15178) arabinosidase [Bacteroides ovatus]
NCBI Description
                   31666
Seq. No.
                   250082 1.R1040
Contig ID
                   jC-gmst02400071f09a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3281861
BLAST score
                   557
                   3.0e-57
E value
                   177
Match length
                   62
% identity
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   31667
Seq. No.
                   250112 1.R1040
Contig ID
5'-most EST
                   fua701043660.h1
                   BLASTX
Method
NCBI GI
                   q3859112
BLAST score
                   231
                   3.0e-19
E value
Match length
                   56
                   75
% identity
                  (AF031607) male sterility MS5 [Arabidopsis thaliana]
NCBI Description
                   31668
Seq. No.
                   250116 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810021d02a1
                   31669
Seq. No.
                   250117 1.R1040
Contig ID
5'-most EST
                   fua701043666.h1
Seq. No.
                   31670
                   250129 1.R1040
Contig ID
                   uC-gmflminsoy031d08b1
5'-most EST
Method
                   BLASTX
                   g3329368
NCBI GI
BLAST score
                   430
E value
                   2.0e-42
                   175
Match length
% identity
                   53
NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana]
                   31671
Seq. No.
                   250134 1.R1040
Contig ID
                   fua701043686.hl
5'-most EST
```

Seq. No. 31672

Contig ID 250144\_1.R1040 5'-most EST yz1700966904.h1

Method BLASTX NCBI GI g2765821



BLAST score 1.0e-21 E value 112 Match length

% identity 46

(Z95496) Mlo-h1 protein [Hordeum vulgare] NCBI Description

Seq. No. 31673

250152 1.R1040 Contig ID

5'-most EST uC-gmrominsoy042f08b1

Seq. No. 31674

250217 1.R1040 Contig ID leu701150261.h1 5'-most EST

Method BLASTX NCBI GI q4415918 BLAST score 211 E value 4.0e-17 Match length 91 21 % identity

(AC006282) hypothetical protein [Arabidopsis thaliana] NCBI Description

31675 Seq. No.

250219 1.R1040 Contig ID 5'-most EST yz1700966990.hl

BLASTX Method q2809264 NCBI GI BLAST score 398 1.0e-38 E value Match length 172 48 % identity

(AC002560) F21B7.33 [Arabidopsis thaliana] NCBI Description

31676 Seq. No.

250226 1.R1040 Contig ID

5'-most EST jC-gmf102220068h03a1

Method BLASTX g3096925 NCBI GI BLAST score 222 E value 1.0e-17 153 Match length % identity 42

(AL023094) putative protein [Arabidopsis thaliana] NCBI Description

31677 Seq. No.

250229 1.R1040 Contig ID gsv701055909.hl 5'-most EST

Method BLASTX q3236241 NCBI GI BLAST score 293 1.0e-26 E value 73 Match length 64 % identity

(AC004684) putative zinc finger protein [Arabidopsis NCBI Description

thaliana]

31678 Seq. No.

250237 1.R1040 Contig ID



5'-most EST uC-gmropic050e08b1

Seq. No. 31679

Contig ID 250340\_1.R1040 5'-most EST asj700967375.h1

Method BLASTX
NCBI GI g4097522
BLAST score 381
E value 7.0e-37
Match length 107
% identity 60

NCBI Description (U63534) cinnamyl alcohol dehydrogenase [Fragaria x

ananassa]

Seq. No. 31680

Contig ID 250355\_1.R1040 5'-most EST leu701152742.h1

Method BLASTX
NCBI GI g3047114
BLAST score 149
E value 8.0e-10
Match length 44
% identity 66

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 31681

Contig ID 250381\_1.R1040 5'-most EST gsv701056131.h1

Seq. No. 31682

Contig ID 250388\_1.R1040 5'-most EST asj700967463.h1

Seq. No. 31683

Contig ID 250428 1.R1040 5'-most EST leu701144353.h1

Seq. No. 31684

Contig ID 250485 1.R1040 5'-most EST leu701156763.h1

Method BLASTX
NCBI GI g3757525
BLAST score 413
E value 3.0e-40
Match length 184
% identity 51

NCBI Description (AC005167) tetracycline transporter-like protein, 3'

partial [Arabidopsis thaliana]

Seq. No. 31685

Contig ID 250497\_1.R1040 5'-most EST leu701156076.h1

Seq. No. 31686

Contig ID 250551\_1.R1040 5'-most EST uC-gmropic045d10b1

Method BLASTX



```
q4454484
NCBI GI
BLAST score
                  370
E value
                  2.0e-35
                  126
Match length
% identity
                  61
                  (AC006234) putative diacylglycerol kinase [Arabidopsis
NCBI Description
                  thaliana]
                  31687
Seq. No.
                  250569 1.R1040
Contig ID
                  g5058429
5'-most EST
Method
                  BLASTX
                  g3540182
NCBI GI
                  183
BLAST score
                  2.0e-13
E value
                  106
Match length
                  44
% identity
                  (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  31688
Seq. No.
                  250624 1.R1040
Contig ID
                  leu701154368.h1
5'-most EST
Seq. No.
                  31689
Contig ID
                  250662 1.R1040
                  leu701144823.hl
5'-most EST
                  31690
Seq. No.
                  250667 1.R1040
Contig ID
                  leu701144826.hl
5'-most EST
                  31691
Seq. No.
                  250686 1.R1040
Contig ID
5'-most EST
                  leu701150509.hl
                  BLASTX
Method
NCBI GI
                  q3075399
BLAST score
                  230
                  2.0e-19
E value
Match length
                  81
% identity
                   56
NCBI Description (AC004484) SF16-like protein [Arabidopsis thaliana]
                   31692
Seq. No.
                   250760 1.R1040
Contig ID
                  leu701145018.h1
5'-most EST
                  BLASTX
Method
                  g282964
NCBI GI
BLAST score
                   308
                  2.0e-28
E value
                   67
Match length
                  76
% identity
                  transforming protein (myb) homolog (clone myb.Ph3) - garden
NCBI Description
                   petunia >gi 20563 emb CAA78386 (Z13996) protein 1 [Petunia
```

Seq. No. 31693

Contig ID 250806\_1.R1040

x hybrida]



5'-most EST gsv701045130.h1

Method BLASTN NCBI GI g3510331

BLAST score 38

E value 3.0e-12 Match length 98 % identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K13P22, complete sequence [Arabidopsis thaliana]

Seq. No. 31694

Contig ID 250835\_1.R1040 5'-most EST leu701145151.h1

Seq. No. 31695

Contig ID 250994\_1.R1040 5'-most EST kl1701204441.h2

Seq. No. 31696

Contig ID 251026\_1.R1040 5'-most EST epx701107713.h1

Method BLASTX
NCBI GI g129021
BLAST score 149
E value 7.0e-10
Match length 74
% identity 43

NCBI Description SPOOB-ASSOCIATED GTP-BINDING PROTEIN >gi\_98326\_pir\_\_B32804

GTP-binding protein, spo0B 3'-region - Bacillus subtilis >gi\_508979 (M24537) GTP-binding protein [Bacillus subtilis]

>gi 2635257\_emb\_CAB14752\_ (Z99118) GTPase activity

[Bacillus subtilis]

Seq. No. 31697

Contig ID 251036\_1.R1040 5'-most EST leu701145455.h1

Seq. No. 31698

Contig ID 251046\_1.R1040 5'-most EST leu701145467.h1

Seq. No. 31699

Contig ID 251047\_1.R1040 5'-most EST leu701145468.h1

Seq. No. 31700

Contig ID 251066 1.R1040

5'-most EST jC-gmle01810012d06d1

Method BLASTX
NCBI GI g1652078
BLAST score 279
E value 8.0e-25
Match length 110
% identity 46

NCBI Description (D90902) hypothetical protein [Synechocystis sp.]

Seq. No. 31701



Contig ID 251070\_1.R1040 5'-most EST uC-gmropic088b04b1

Method BLASTX
NCBI GI g3892055
BLAST score 372
E value 1.0e-35
Match length 90
% identity 70

NCBI Description (AC002330) putative transport protein [Arabidopsis

thaliana]

Seq. No. 31702

Contig ID 251119\_1.R1040 5'-most EST leu701145607.h1

Seq. No. 31703

Contig ID 251159\_1.R1040 5'-most EST leu701150940.h1

Seq. No. 31704

Contig ID 251163\_1.R1040 5'-most EST leu701145667.h1

Method BLASTN
NCBI GI - - - g12979 BLAST score 99
E value 2.0e-48
Match length 113

Match length 113 % identity 97

NCBI Description Soybean mitDNA for elongator tRNA-Met and tRNA-Glu

Seq. No. 31705

Contig ID 251232\_1.R1040

5'-most EST uC-gmflminsoy036b03b1

Method BLASTX
NCBI GI 94530126
BLAST score 511
E value 5.0e-52
Match length 134
% identity 72

NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1

[Phaseolus vulgaris]

Seq. No. 31706

Contig ID 251238\_1.R1040 5'-most EST leu701149221.h1

Seq. No. 31707

Contig ID 251311 1.R1040 5'-most EST leu701157740.h1

Seq. No. 31708

Contig ID 251392 1.R1040 5'-most EST leu701145987.h1

Method BLASTX
NCBI GI g1352267
BLAST score 180
E value 1.0e-16



Match length

63 % identity NCBI Description

DEOXYHYPUSINE SYNTHASE >gi\_994715 (L39068) deoxyhypusine synthase [Homo sapiens] >gi 1710220 (U79262) deoxyhypusine

synthase [Homo sapiens] >gi\_3021398\_emb\_CAA04940\_ (AJ001701) deoxyhypusine synthase [Homo sapiens]

>gi\_4503325\_ref\_NP\_001921.1\_pDHPS\_ deoxyhypusine synthase

31709 Seq. No.

251454 1.R1040 Contig ID 5'-most EST epx701105335.h1

31710 Seq. No.

251527 1.R1040 Contig ID  $k11701\overline{2}09769.h1$ 5'-most EST

Seq. No. 31711

251535 1.R1040 Contig ID leu701146226.h1 5'-most EST

Seq. No. 31712

251596 1.R1040 Contig ID 5'-most EST leu701146322.h1

31713 Seq. No.

251656 1.R1040 Contig ID 5'-most EST leu701146466.h1

31714 Seq. No.

251672 1.R1040 Contig ID 5'-most EST  $leu701\overline{1}46441.h1$ 

Seq. No. 31715

251710 1.R1040 Contig ID  $leu701\overline{1}46504.h1$ 5'-most EST

31716 Seq. No.

251715 1.R1040 Contig ID

5'-most EST uC-qmflminsoy022q07b1

BLASTXMethod NCBI GI g2190535 BLAST score 165 1.0e-13 E value Match length 131 37 % identity

NCBI Description (U31240) luciferase [Photuris pennsylvanica]

Seq. No. 31717

251744 1.R1040 Contig ID  $leu701\overline{1}46550.h1$ 5'-most EST

BLASTX Method NCBI GI g114974 BLAST score 133 3.0e-12 E value Match length 53 % identity 51

NCBI Description NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR



>gi 67491 pir GLJY31 beta-glucosidase (EC 3.2.1.21) precursor (clone TRE361) - white clover >gi 21955 emb CAA40058.1\_ (X56734) beta-glucosidase [Trifolium repens]

31718 Seq. No. Contig ID

251809 1.R1040 jC-gmf102220062f12a1 5'-most EST

BLASTX Method NCBI GI g2062167 577 BLAST score E value 1.0e-59 137 Match length 78 % identity

(AC001645) Proline-rich protein APG isolog [Arabidopsis NCBI Description

thaliana]

31719 Seq. No.

251958\_1.R1040 Contig ID  $leu701\overline{1}46890.h1$ 5'-most EST

Seq. No. 31720

251966 1.R1040 Contig ID asn701143134.h1 5'-most EST

31721 Seq. No.

251971 1.R1040 Contig ID 5'-most EST leu701146909.h1

31722 Seq. No.

251975 1.R1040 Contig ID 5'-most EST leu701149831.h1

31723 Seq. No.

252053 1.R1040 Contig ID hrw701061054.hl 5'-most EST

BLASTX Method g2275202 NCBI GI BLAST score 488 2.0e-49 E value 132 Match length 66 % identity

(AC002337) acyl-CoA synthetase isolog [Arabidopsis NCBI Description

thaliana]

31724 Seq. No.

252069 1.R1040 Contig ID 5'-most EST  $leu701\overline{1}47048.h1$ 

Seq. No. 31725

252113 1.R1040 Contig ID 5'-most EST leu701147115.h1

31726 Seq. No.

252136 1.R1040 Contig ID 5'-most EST  $1eu701\overline{1}47236.h1$ 

BLASTX Method



```
q3912919
NCBI GI
                   594
BLAST score
                   1.0e-61
E value
                   166
Match length
% identity
                   73
NCBI Description (AF001308) hypothetical protein [Arabidopsis thaliana]
                   31727
Seq. No.
                   252139 1.R1040
Contig ID
5'-most EST
                   gsv701045770.h1
Method
                   BLASTX
NCBI GI
                   g3183617
BLAST score
                   413
                   2.0e-40
E value
Match length
                   126
% identity
                   68
                   (AJ005586) MYB-related transcription factor [Antirrhinum
NCBI Description
                   majus]
                   31728
Seq. No.
                   252141 1.R1040
Contig ID
5'-most EST
                   epx701\overline{1}09413.h1
Seq. No.
                   31729
                   252177 1.R1040
Contig ID
                   leu701147211.hl
5'-most EST
                   31730
Seq. No.
                   252196 1.R1040
Contig ID
                   leu701147232.h1
5'-most EST
Method
                   BLASTN
                   g3510539
NCBI GI
BLAST score
                   66
                   8.0e-29
E value
Match length
                   126
% identity
                   88
NCBI Description Prunus armeniaca expansin (Exp2) mRNA, complete cds
Seq. No.
                   31731
                   252424 1.R1040
Contig ID
                   leu701\overline{1}47568.h1
5'-most EST
                   BLASTX
Method
                   g629693
NCBI GI
                   171
BLAST score
                   1.0e-12
E value
Match length
                   51
                   55
% identity
                   probable integrase - common tobacco (fragment)
NCBI Description
                   >gi 530742 emb CAA56791 (X80830) integrase [Nicotiana
                   tabacum]
                   31732
Seq. No.
                   252436 1.R1040
Contig ID
5'-most EST
                   leu701147851.h1
```

31733

252449\_1.R1040

Seq. No.

Contig ID

NCBI GI

BLAST score



```
5'-most EST
                  gsv701056660.h1
Seq. No.
                  31734
                  252454 1.R1040
Contig ID
5'-most EST
                  leu701147662.h1
Method
                  BLASTX
NCBI GI
                  g2760328
BLAST score
                  151
                  4.0e-10
E value
Match length
                  86
                  37
% identity
NCBI Description
                  (AC002130) F1N21.13 [Arabidopsis thaliana]
Seq. No.
                  31735
                  252475 1.R1040
Contig ID
                  leu701150839.h1
5'-most EST
                  BLASTX
Method
                  g3292829
NCBI GI
BLAST score
                  160
                  4.0e-11
E value
Match length
                  75
% identity
                  48
NCBI Description
                  (AL031018) putative protein [Arabidopsis thaliana]
Seq. No.
                  31736
                  252492 1.R1040
Contig ID
5'-most EST
                  zsq701127494.h1
Method
                  BLASTX
NCBI GI
                  g2462825
BLAST score
                  265
                  9.0e-25
E value
Match length
                  79
                  73
% identity
                  (AF000657) contains Procite 'RNP1' putative RNA-binding
NCBI Description
                  region [Arabidopsis thaliana]
Seq. No.
                  31737
                  252606 1.R1040
Contig ID
                  leu701147908.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2244784
BLAST score
                  388
E value
                  1.0e-37
Match length
                  133
% identity
NCBI Description
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
                  31738
Seq. No.
                  252691 1.R1040
Contig ID
5'-most EST
                  leu701148059.h1
Seq. No.
                  31739
                  252811 1.R1040
Contig ID
5'-most EST
                  leu701148184.h1
Method
                  BLASTX
```

4847

q1653395



E value 2.0e-21 Match length 92 % identity 53

NCBI Description (D90913) PET112 [Synechocystis sp.]

Seq. No.
Contig ID
5'-most EST

31740 252818\_1.R1040 leu701148193.h1

Seq. No.

31741

Contig ID 5'-most EST 252826\_1.R1040 leu701148207.h1

Method BLASTX
NCBI GI g3241943
BLAST score 678
E value 2.0e-71
Match length 148
% identity 82

% identity
NCBI Description

NCBI Description (AC004625) hypothetical protein [Arabidopsis thaliana]

Seq. No.

31742

Contig ID 5'-most EST 253029\_1.R1040 uC-gmropic039d03b1

Seq. No.

31743

Contig ID

253029 2.R1040

5'-most EST

uC-gmrominsoy067a08b1

Seq. No.

31744

Contig ID 5'-most EST

253037\_1.R1040 leu701148509.h1

Seq. No.

31745

Contig ID 5'-most EST

253113\_1.R1040 leu701148606.h1

Seq. No.

31746

Contig ID

253123 1.R1040

5'-most EST

jC-gmro02910041085a1

Seq. No.

31747

Contig ID 5'-most EST

253126\_1.R1040 epx701104995.h1

Seq. No.

31748

Contig ID 5'-most EST

253162\_1.R1040 leu701155120.h1

Seq. No.

31749

Contig ID

253167\_1.R1040

5'-most EST

jC-gmro02800032f04a1

Method BLASTX
NCBI GI g3831451
BLAST score 563
E value 4.0e-58
Match length 114
% identity 64



(AC005700) putative O-GlcNAc transferase [Arabidopsis NCBI Description thaliana]

31750 Seq. No.

253173 1.R1040 Contig ID 5'-most EST leu701148706.hl

Method BLASTX NCBI GI g2190187 BLAST score 313 E value 4.0e-29 Match length 102 % identity 33

NCBI Description (D64087) nuclear matrix constituent protein 1 (NMCP1)

[Daucus carota]

Seq. No. 31751

Contig ID 253181 1.R1040 5'-most EST leu701148717.h1

Seq. No. 31752

253222 1.R1040 Contig ID 5'-most EST kl1701214281.h1

Method BLASTX NCBI GI q1706371 BLAST score 194 E value 4.0e-15 Match length 62 66 % identity

NCBI Description DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL

4-REDUCTASE) >gi\_486744\_pir\_\_S35189 dihydroflavonol-4-reductase (EC 1.-.-.) - gerbera hybrid

>gi 312777 emb CAA78930 (Z17221)

dihydroflavonol-4-reductase [Gerbera hybrida]

31753 Seq. No.

253228 1.R1040 Contig ID  $leu701\overline{1}56342.h1$ 5'-most EST

Seq. No. 31754

253304 1.R1040 Contig ID 5'-most EST leu701148887.h1

BLASTX Method g3426039 NCBI GI BLAST score 239 4.0e-20 E value 99 Match length % identity 49

NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

31755 Seq. No.

253324 1.R1040 Contig ID 5'-most EST leu701148919.h1

Seq. No. 31756

253355 1.R1040 Contig ID

5'-most EST g5126801 Method BLASTX



```
NCBI GI
                  q4376592
BLAST score
                  156
E value
                  4.0e-10
Match length
                  144
% identity
                  (AE001616) S1 Ribosomal Protein [Chlamydia pneumoniae]
NCBI Description
                  31757
Seq. No.
                  253359 1.R1040
Contig ID
5'-most EST
                  leu701156353.hl
```

31758 Seq. No. Contig ID 253515 1.R1040 leu701149235.hl 5'-most EST BLASTX Method a114974 NCBI GI

458 BLAST score E value 1.0e-45 138 Match length % identity 63

NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR NCBI Description

>gi\_67491\_pir\_\_GLJY31 beta-glucosidase (EC 3.2.1.21)

precursor (clone TRE361) - white clover >gi\_21955\_emb\_CAA40058.1\_ (X56734) beta-glucosidase

[Trifolium repens]

31759 Seq. No.

253588 1.R1040 Contig ID 5'-most EST leu701149335.h1

Seq. No. 31760

253599 1.R1040 Contig ID 5'-most EST leu701150064.h1

31761 Seq. No.

253603 1.R1040 Contig ID

5'-most EST q4395889 Method BLASTX NCBI GI q1703052 BLAST score 145 5.0e-18 E value Match length 137 % identity 40

ACTIVATOR 1 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD NCBI Description

SUBUNIT) (A1 37 KD SUBUNIT) (RF-C 37 KD SUBUNIT) (RFC37) >gi 1498256 (M87339) replication factor C, 37-kDa subunit

[Homo sapiens] >gi\_4506491\_ref\_NP\_002907.1\_pRFC4\_

replication factor C (activator 1) 4 (37kD)

Seq. No. 31762

253610 1.R1040 Contig ID qsv701045948.h1 5'-most EST

BLASTX Method NCBI GI g2132184 201 BLAST score 8.0e-16 E value Match length 49



% identity 67
NCBI Description hypothetical protein YPL093w - yeast (Saccharomyces cerevisiae) >gi\_1151233 (U43281) Lpg15p [Saccharomyces cerevisiae]

Seq. No. 31763
Contig ID 253628\_1.R1040
5'-most EST leu701150093.h1

يعانع

Seq. No. 31764
Contig ID 253645\_1.R1040
5'-most EST asn701134216.h1

Method BLASTX
NCBI GI g2335100
BLAST score 474
E value 8.0e-48
Match length 112
% identity 79

NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 31765

Contig ID 253699\_1.R1040 5'-most EST leu701151830.h1

Seq. No. 31766

Contig ID 253700\_1.R1040 5'-most EST leu701149508.h1

Method BLASTN
NCBI GI g3128136
BLAST score 39
E value 2.0e-12
Match length 51
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K1F13, complete sequence [Arabidopsis thaliana]

Seq. No. 31767

Contig ID 253791\_1.R1040 5'-most EST kl1701213583.h1

Method BLASTX
NCBI GI g2213629
BLAST score 258
E value 1.0e-22
Match length 52
% identity 88

NCBI Description (AC000103) F21J9.21 [Arabidopsis thaliana]

Seq. No. 31768

Contig ID 253867\_1.R1040 5'-most EST leu701149741.h1

Seq. No. 31769

Contig ID 253887\_1.R1040 5'-most EST leu701149768.h1

Seq. No. 31770

Contig ID 253934 1.R1040

NCBI GI

E value

BLAST score

Match length % identity

NCBI Description



```
5'-most EST
                   uC-qmflminsoy001e12b1
Method
                   BLASTX
NCBI GI
                   q3080389
                   253
BLAST score
                   1.0e-21
E value
                   58
Match length
% identity
                   86
                   (AL022603) putative membrane associated protein
NCBI Description
                   [Arabidopsis thaliana]
                   31771
Seq. No.
Contig ID
                   254085 1.R1040
5'-most EST
                   leu701150058.h1
                   31772
Seq. No.
                   254086 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810023g06d1
Seq. No.
                   31773
                   254112 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400067d03d1
                   31774
Seq. No.
Contig ID
                   254116_1.R1040
                   leu701150107.h1
5'-most EST
                   31775
Seq. No.
                   254119 1.R1040
Contig ID
5'-most EST
                   leu701150110.h1
                   31776
Seq. No.
                   254192 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400053b09d1
                   31777
Seq. No.
                   254262 1.R1040
Contig ID
5'-most EST
                   leu701150330.h1
                   31778
Seq. No.
                   254283 1.R1040
Contig ID
                   1eu701\overline{1}50359.h1
5'-most EST
Seq. No.
                   31779
Contig ID
                   254298 1.R1040
                   leu701151987.h1
5'-most EST
Seq. No.
                   31780
                   254339 1.R1040
Contig ID
                   asn701\overline{1}40117.h1
5'-most EST
Method
                   BLASTX
```

4852

(AC007087) putative copper methylamine oxidase [Arabidopsis

q4559342

2.0e-65

thaliana]

626

121



 Seq. No.
 31781

 Contig ID
 254385 1.R1040

 5'-most EST
 leu701151904.h1

Seq. No. 31782

Contig ID 254471 1.R1040

5'-most EST uC-gmrominsoy034c12b1

Seq. No. 31783

Contig ID 254488\_1.R1040 5'-most EST gsv701047738.h1

Seq. No. 31784

Contig ID 254530\_1.R1040

5'-most EST jC-gmf102220051g07a1

Seq. No. 31785

Contig ID 254541\_1.R1040 5'-most EST leu701150790.h1

Method BLASTX
NCBI GI g3402692
BLAST score 338
E value 8.0e-32
Match length 82
% identity 79

NCBI Description (AC004697) putative

CDP-diacylglycerol--glycerol-3-phosphate

3-phosphatidyltransferase [Arabidopsis thaliana]

Seq. No. 31786

Contig ID 254630\_1.R1040 5'-most EST leu701155825.h1

Seq. No.

Contig ID 254654 1.R1040

31787

5'-most EST g5606123
Method BLASTX
NCBI GI g4455202
BLAST score 671
E value 6.0e-73
Match length 210
% identity 64

NCBI Description (AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No. 31788

Contig ID 254798 1.R1040 5'-most EST leu701151278.h1

Seq. No. 31789

Contig ID 254815\_1.R1040 5'-most EST asn701139715.h1

Seq. No. 31790

Contig ID 254959\_1.R1040 5'-most EST gsv701056139.h1



```
Seq. No.
                  254975 1.R1040
Contig ID
5'-most EST
                  leu701151630.hl
                  31792
Seq. No.
                  254986 1.R1040
Contig ID
5'-most EST
                  gsv701048289.h1
                  BLASTX
Method
                  q953179
NCBI GI
                  168
BLAST score
E value
                  7.0e-12
Match length
                  45
% identity
                  69
NCBI Description (Z37980) ORF14 [Escherichia coli]
                   31793
Seq. No.
                  254990 1.R1040
Contig ID
                  leu701151649.hl
5'-most EST
                  31794
Seq. No.
                  255104 1.R1040
Contig ID
                  leu701151824.h1
5'-most EST
Seq. No.
                   31795
                   255105 1.R1040
Contig ID
                   leu701151825.hl
5'-most EST
                  BLASTX
Method
                   a2190549
NCBI GI
BLAST score
                   325
                   4.0e-30
E value
                   105
Match length
% identity
                   58
NCBI Description (AC001229) No definition line found [Arabidopsis thaliana]
                   31796
Seq. No.
                   255116 1.R1040
Contig ID
5'-most EST
                   leu701151844.hl
                   31797
Seq. No.
                   255127 1.R1040
Contig ID
                   jC-qmst02400001a02a1
5'-most EST
                   BLASTX
Method
                   g2950472
NCBI GI
BLAST score
                   200
                   2.0e-15
E value
Match length
                   86
% identity
                   49
                   (AL022070) putative autophagocytosis protein
NCBI Description
                   [Schizosaccharomyces pombe]
```

31798 Seq. No. 255147 1.R1040 Contig ID leu701151905.h1 5'-most EST BLASTX Method g2335106 NCBI GI

BLAST score 267 9.0e-24 E value



Match length 85 % identity 31

NCBI Description (AC002339) salt inducible protein-like [Arabidopsis

thaliana]

Seq. No. 31799

Contig ID 255151 1.R1040 5'-most EST leu701151909.h1

Seq. No. 31800

Contig ID 255202 1.R1040 5'-most EST leu701152071.h1

Seq. No. 31801

Contig ID 255206\_1.R1040 5'-most EST leu701151982.h1

Method BLASTN
NCBI GI g3860320
BLAST score 161
E value 1.0e-85
Match length 249
% identity 91

NCBI Description Cicer arietinum mRNA for beta-galactosidase, clone

CanBGal-5

Seq. No. 31802

Contig ID 255219 1.R1040 5'-most EST leu701152005.h1

Seq. No. 31803

Contig ID 255234 1.R1040 5'-most EST leu701152032.h1

Seq. No. 31804

Contig ID 255287\_1.R1040 5'-most EST epx701108938.h1

Method BLASTN
NCBI GI g3021354
BLAST score 131
E value 1.0e-67
Match length 299
% identity 86

NCBI Description Cyamopsis tetragonoloba mRNA for UDP-galactose 4-epimerase,

clone GEPI42

Seq. No. 31805

Contig ID 255301 1.R1040 5'-most EST leu701152137.h1

Seq. No. 31806

Contig ID 255307\_1.R1040 5'-most EST leu701152188.h1

Seq. No. 31807

Contig ID 255346\_1.R1040 5'-most EST leu701152226.h1



Seq. No. 31808 Contig ID 255355\_1.R1040 5'-most EST epx701105781.h1 Seq. No. 31809 Contig ID 255364\_1.R1040

Contig ID 255364 1.R1040 5'-most EST asn701142396.h1

Seq. No. 31810

Contig ID 255388\_1.R1040 5'-most EST asn701140536.h1

Seq. No. 31811

Contig ID 255441\_1.R1040 5'-most EST leu701152366.h1

Seq. No. 31812

Contig ID 255447\_1.R1040 5'-most EST leu701152364.h1

Seq. No. 31813

Contig ID 255550\_1.R1040 5'-most EST leu701152549.h1

Seq. No. 31814

Contig ID 255604\_1.R1040 5'-most EST leu701152607.h1

Method BLASTX
NCBI GI g3641834
BLAST score 274
E value 1.0e-24
Match length 65
% identity 78

NCBI Description (AJ007312) pyruvate dehydrogenase kinase [Arabidopsis

thaliana]

Seq. No. 31815

Contig ID 255670\_1.R1040

5'-most EST jC-gmle01810004c05d1

Seq. No. 31816

Contig ID 255705\_1.R1040 5'-most EST leu701152767.h1

Method BLASTX
NCBI GI g2135070
BLAST score 157
E value 2.0e-10
Match length 90
% identity 36

NCBI Description enoyl-CoA hydratase (EC 4.2.1.17) / AU-specific RNA-binding

protein - human >gi\_780241\_emb\_CAA56260\_ (X79888)
AU-binding protein/Enoyl-CoA hydratase [Homo sapiens]
>gi\_4502327\_ref\_NP\_001689.1\_pAUH\_ AU RNA-binding

protein/enoyl-Coenzyme A hydratase

Seq. No. 31817

Contig ID 255760 1.R1040



```
leu701152950.h1
5'-most EST
                  31818
Seq. No.
                  255786 1.R1040
Contig ID
                  leu701152986.h1
5'-most EST
Method
                  BLASTX
                  q1946366
NCBI GI
BLAST score
                  410
E value
                  2.0e-40
Match length
                  106
% identity
                  77
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
                  31819
                  255791 1.R1040
Contig ID
5'-most EST
                  leu701152993.h1
Seq. No.
                  31820
                  255798 1.R1040
Contig ID
5'-most EST
                  leu701153008.h1
Seq. No.
                  31821
                  255861 1.R1040
Contig ID
5'-most EST
                  gsv701052033.h1
Seq. No.
                  31822
                  255870 1.R1040
Contig ID
5'-most EST
                  leu701153136.h1
Seq. No.
                  31823
                  255877 1.R1040
Contig ID
                  leu701153464.h1
5'-most EST
                  31824
Seq. No.
                  255909 1.R1040
Contig ID
5'-most EST
                  q5126284
Seq. No.
                  31825
                  255958 1.R1040
Contig ID
5'-most EST
                  g4277036
                  BLASTX
Method
NCBI GI
                  g3482919
BLAST score
                  246
                  6.0e-21
E value
Match length
                  77
                  68
% identity
NCBI Description (AC003970) Putative protein kinase [Arabidopsis thaliana]
                  31826
Seq. No.
                  255964 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810048b11a1
```

Seq. No.

31827 255981 1.R1040 Contig ID 5'-most EST  $leu701\overline{1}55318.h1$ 

Seq. No. 31828



```
Contig ID
                   255989 1.R1040
5'-most EST
                   leu701153444.hl
Seq. No.
                   31829
                   255995 1.R1040
Contig ID
5'-most EST
                   leu701157044.hl
                   31830
Seq. No.
                   256053 1.R1040
Contig ID
5'-most EST
                   leu701153536.h1
Method
                   BLASTX
NCBI GI
                   q82056
BLAST score
                   346
E value
                   4.0e-33
Match length
                   81
                   84
% identity
                  protein kinase, calcium-dependent (EC 2.7.1.-) - carrot
NCBI Description
                   (fragment)
                   31831
Seq. No.
                   256065 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}54631.h1
Seq. No.
                   31832
                   256067 1.R1040
Contig ID
                   leu701157703.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4455202
BLAST score
                   198
E value
                   1.0e-15
Match length
                   49
                   73
% identity
NCBI Description
                  (AL035440) putative APG protein [Arabidopsis thaliana]
Seq. No.
                   31833
Contig ID
                   256103 1.R1040
5'-most EST
                   jC-qmst02400048h05a1
Method
                   BLASTX
NCBI GI
                   q4406778
BLAST score
                   424
                   4.0e-42
E value
Match length
                   90
% identity
                   87
NCBI Description
                   (AC006532) putative brassinosteroid insensitive protein
                   [Arabidopsis thaliana]
Seq. No.
                   31834
                   256105 1.R1040
Contig ID
5'-most EST
                   leu701153775.h1
Method
                   BLASTN
                   q3599418
NCBI GI
BLAST score
                   33
E value
                   3.0e-09
                   58
Match length
                   90
% identity
                   Glycine max alternative oxidase precursor (Aox1) gene,
NCBI Description
                   nuclear gene encoding mitochondrial protein, complete cds
```



```
31835
Seq. No.
                   256232 1.R1040
Contig ID
                   kl1701215249.h1
5'-most EST
                   BLASTX
Method
                   q2244818
NCBI GI
BLAST score
                   227
                   5.0e-19
E value
                   85
Match length
                   59
% identity
```

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31836

Contig ID 256247\_1.R1040 5'-most EST leu701156002.h1

Seq. No. 31837

Contig ID 256284\_1.R1040

5'-most EST uC-gmrominsoy250d07b1

Method BLASTX
NCBI GI g4454470
BLAST score 396
E value 9.0e-39
Match length 96
% identity 77

NCBI Description (AC006234) putative sugar transporter [Arabidopsis

thaliana]

Seq. No. 31838

Contig ID 256490\_1.R1040 5'-most EST leu701154354.h1

Method BLASTX
NCBI GI g3036795
BLAST score 188
E value 7.0e-14
Match length 100
% identity 34

NCBI Description (AL022373) putative protein [Arabidopsis thaliana] >gi 3805857 emb CAA21477\_ (AL031986) putative protein

[Arabidopsis thaliana]

Seq. No. 31839

Contig ID 256526\_1.R1040 5'-most EST leu701154409.h1

Method BLASTX
NCBI GI g1170619
BLAST score 494
E value 6.0e-50
Match length 156
% identity 66

NCBI Description KINESIN-LIKE PROTEIN A >gi\_479594\_pir\_\_S34830

kinesin-related protein katA - Arabidopsis thaliana >gi\_303502\_dbj\_BAA01972\_ (D11371) kinesin-like motor

protein heavy chain [Arabidopsis thaliana]

>gi 2911084 emb CAA17546 (AL021960) kinesin-related

protein katA [Arabidopsis thaliana]



Seq. No. 31840 Contig ID 25656

Contig ID 256562 1.R1040 5'-most EST leu701154463.h1

Seq. No. 31841

Contig ID 256640\_1.R1040 5'-most EST leu701154583.h1

Seq. No. 31842

Contig ID 256660\_1.R1040 5'-most EST leu701154616.h1

Seq. No. 31843

Contig ID 256677\_1.R1040 5'-most EST gsv701051142.h1

Seq. No. 31844

Contig ID 256686\_1.R1040 5'-most EST leu701154688.h1

Method BLASTX
NCBI GI g3892052
BLAST score 143
E value 3.0e-09
Match length 72
% identity 43

NCBI Description (AC002330) predicted protein of unknown function

14

[Arabidopsis thaliana]

Seq. No. 31845

Contig ID 256696 1.R1040 5'-most EST kl1701212105.h1

Seq. No. 31846

Contig ID 256717\_1.R1040 5'-most EST leu701154812.h1

Method BLASTX
NCBI GI g1076715
BLAST score 159
E value 4.0e-11
Match length 51
% identity 57

% identity 57
NCBI Description abscisic acid-induced protein HVA22 - barley >gi\_404589

(L19119) A22 [Hordeum vulgare]

Seq. No. 31847

Contig ID 256718\_1.R1040 5'-most EST leu701154813.h1

Seq. No. 31848

Contig ID 256780\_1.R1040 5'-most EST leu701157246.h1

Seq. No. 31849

Contig ID 256866 1.R1040 5'-most EST leu701155254.h1

Seq. No. 31850



Contig ID 256908\_1.R1040 5'-most EST leu701155323.h1

Seq. No. 31851

Contig ID 256936\_1.R1040 5'-most EST leu701156683.h1

Seq. No. 31852

Contig ID 256991\_1.R1040 5'-most EST leu701155434.h1

Seq. No. 31853

Contig ID 257028\_1.R1040 5'-most EST leu701155488.h1

Seq. No. 31854

Contig ID 257062 1.R1040 5'-most EST leu701155537.h1

Seq. No. 31855

Contig ID 257081\_1.R1040

5'-most EST  $jC-gmf\overline{1}02220070c02d1$ 

Seq. No. 31856

Contig ID 257084 1.R1040 5'-most EST leu701155563.h1

Seq. No. 31857

Contig ID 257106\_1.R1040 5'-most EST leu701155594.h1

Seq. No. 31858

Contig ID 257125\_1.R1040 5'-most EST gsv701051789.h1

Seq. No. 31859

Contig ID 257271\_1.R1040

5'-most EST jC-gmle01810089b10a1

Method BLASTX
NCBI GI g3004564
BLAST score 532
E value 1.0e-70
Match length 164
% identity 79

NCBI Description (AC003673) putative receptor Ser/Thr protein kinase

[Arabidopsis thaliana]

Seq. No. 31860

Contig ID 257340\_1.R1040 5'-most EST leu701155940.h1

Seq. No. 31861

Contig ID 257371\_1.R1040



E value 2.0e-62 Match length 166 % identity 69

NCBI Description (AF055848) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 31862

Contig ID 257379\_1.R1040 5'-most EST jC-gmro02800030a11a1

Method BLASTX
NCBI GI g3004551
BLAST score 134
E value 2.0e-12
Match length 83
% identity 48

NCBI Description (AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31863

Contig ID 257382\_1.R1040 5'-most EST leu701155988.h1

Seq. No. 31864

Contig ID 257383\_1.R1040 5'-most EST leu701156155.h1

Seq. No. 31865

Contig ID 257415\_1.R1040 5'-most EST leu701157027.h1

Seq. No. 31866

Contig ID 257420 1.R1040 5'-most EST leu701157020.h1

Seq. No. 31867

Contig ID 257427\_1.R1040 5'-most EST leu701156709.h1

Method BLASTX
NCBI GI g2129675
BLAST score 102
E value 1.0e-08
Match length 38
% identity 92

NCBI Description probable chlorophyll synthetase G4 - Arabidopsis thaliana

>gi\_972938 (U19382) putative chlorophyll synthetase
[Arabidopsis thaliana] >gi 3068709 (AF049236) putative

chlorophyll synthetase [Arabidopsis thaliana]

Seq. No. 31868

Contig ID 257432\_1.R1040 5'-most EST leu701156068.h1

Seq. No. 31869

Contig ID 257457 1.R1040 5'-most EST leu701156109.h1

Seq. No. 31870

Contig ID 257521\_1.R1040 5'-most EST jsh701069515.h1



Method BLASTX
NCBI GI g2213538
BLAST score 169
E value 4.0e-12
Match length 45
% identity 80

NCBI Description (X98740) DNA-binding protein PD2 [Pisum sativum]

Seq. No. 31871

Contig ID 257560\_1.R1040 5'-most EST leu701156284.h1

Seq. No. 31872

Contig ID 257607\_2.R1040 5'-most EST leu701156572.h1

Seq. No. 31873

Contig ID 257673 1.R1040

5'-most EST jC-gmro02800039b09d1

Seq. No. 31874

Contig ID 257682\_1.R1040 5'-most EST leu701156601.h1

Seq. No. 31875

Contig ID 257720\_1.R1040

5'-most EST jC-gmst02400057h11a1

Method BLASTX
NCBI GI g3236261
BLAST score 304
E value 1.0e-27
Match length 86
% identity 67

NCBI Description (AC004684) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 31876

Contig ID 257767\_1.R1040 5'-most EST leu701156585.h1

Seq. No.

31877

Contig ID 5'-most EST

257804\_1.R1040 jC-gmro02910061h05a1

Method BLASTX NCBI GI g3033377

BLAST score 273 E value 5.0e-24 Match length 137

% identity 43

NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis

thaliana]

Seq. No.

31878

Contig ID 5'-most EST

257824\_1.R1040 leu701156664.h1

Seq. No.



```
Contig ID
                   257831 1.R1040
5'-most EST
                   leu701156671.h1
                   31880
Seq. No.
                   257832 1.R1040
Contig ID
                   leu701\overline{1}56672.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1101770
BLAST score
                   475
E value
                   1.0e-47
Match length
                   149
                   58
% identity
NCBI Description
                  (U39448) MYB-like transcriptional factor MBF1 [Picea
                   mariana]
                   31881
Seq. No.
Contig ID
                   257834 1.R1040
5'-most EST
                   kl1701209132.h1
Method
                   BLASTX
NCBI GI
                   g2959781
BLAST score
                   316
E value
                   4.0e-29
Match length
                   145
% identity
                   35
NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]
                   31882
Seq. No.
Contig ID
                   257853 1.R1040
5'-most EST
                   epx701\overline{1}07054.h1
Seq. No.
                   31883
Contig ID
                   257856 1.R1040
5'-most EST
                   leu701156706.h1
Method
                   BLASTX
NCBI GI
                   g3646324
BLAST score
                   206
E value
                   1.0e-16
Match length
                   78
% identity
                   56
NCBI Description
                  (AJ000761) MADS-box protein [Malus domestica]
                   31884
Seq. No.
                   257863 1.R1040
Contig ID
5'-most EST
                   leu701156715.h1
Seq. No.
                   31885
                   257894 1.R1040
Contig ID
5'-most EST
                   leu701156756.h1
Method
                   BLASTX
NCBI GI
                   g2921336
BLAST score
                   581
E value
                   5.0e-60
Match length
                   119
```

% identity 87 NCBI Description (A

(AF034132) MYB-like DNA-binding domain protein [Gossypium

hirsutum]



Seq. No. 3188

Contig ID 257926\_1.R1040 5'-most EST leu701157083.h1

Seq. No. 31887

Contig ID 257973\_1.R1040 5'-most EST leu701156974.h1

Seq. No. 31888

Contig ID 257976\_1.R1040 5'-most EST leu701156988.h1

Seq. No. 31889

Contig ID 257986\_1.R1040 5'-most EST leu701156994.h1

Seq. No. 31890

Contig ID 257992\_1.R1040 5'-most EST leu701157008.h1

Method BLASTX
NCBI GI g3776559
BLAST score 436
E value 2.0e-43
Match length 106
% identity 80

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi\_3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb\_AC003970. ESTs gb\_Z35332 and gb\_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 31891

Contig ID 258018\_1.R1040 5'-most EST leu701157043.h1

Seq. No. 31892

Contig ID 258054 1.R1040 5'-most EST leu701157092.h1

Method BLASTX
NCBI GI g2623304
BLAST score 181
E value 3.0e-13
Match length 119
% identity 32

NCBI Description (AC002409) similar to Medicago nodulin N21 [Arabidopsis

thaliana]

Seq. No. 31893

Contig ID 258080\_1.R1040 5'-most EST leu701157163.h1

Seq. No. 31894

Contig ID 258095\_1.R1040 5'-most EST leu701157186.h1

Seq. No. 31895

Contig ID 258096\_1.R1040 5'-most EST leu701157204.h1



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Seq. No.
                  31896
                  258117_1.R1040
Contig ID
                  leu701157227.h1
5'-most EST
Method
                  BLASTX
                  g2689720
NCBI GI
BLAST score
                  255
                  3.0e-22
E value
Match length
                  78
                  71
% identity
                  (AF037168) DnaJ homologue [Arabidopsis thaliana]
NCBI Description
                  31897
Seq. No.
                  258219 1.R1040
Contig ID
5'-most EST
                  zsg701123070.h1
                  31898
Seq. No.
Contig ID
                  258261 1.R1040
                  hrw701061515.h1
5'-most EST
                  31899
Seq. No.
Contig ID
                  258266 1.R1040
5'-most EST
                  leu701157545.h1
Method
                  BLASTX
                  g4530126
NCBI GI
                  205
BLAST score
                   4.0e-16
E value
Match length
                  113
% identity
                   42
                  (AF078082) receptor-like protein kinase homolog RK20-1
NCBI Description
                   [Phaseolus vulgaris]
                   31900
Seq. No.
Contig ID
                   258282 1.R1040
5'-most EST
                   leu701157704.h1
Seq. No.
                   31901
                   258328 1.R1040
Contig ID
5'-most EST
                   leu701157879.hl
                   31902
Seq. No.
                   258334 1.R1040
Contig ID
5'-most EST
                   leu701157733.h1
Seq. No.
                   31903
                   258547 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400055e10a1
Method
                   BLASTX
NCBI GI
                   g2737926
BLAST score
                   641
```

E value

Match length

4.0e-67 155

% identity NCBI Description

(U77673) fimbrin-like protein AtFim2 [Arabidopsis thaliana]

Seq. No.

31904

77

Contig ID

258614 1.R1040



```
uC-gmflminsoy065a10b1
5'-most EST
                  31905
Seq. No.
                  258642 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy089c09b1
                  BLASTX
Method
NCBI GI
                  g3201627
                  181
BLAST score
                  2.0e-13
E value
Match length
                  36
% identity
                  83
NCBI Description
                  (AC004669) putative SWH1 protein [Arabidopsis thaliana]
                  31906
Seq. No.
                  258668 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy018b04b1
Method
                  BLASTX
NCBI GI
                  q2529707
BLAST score
                  400
                  5.0e-39
E value
                  127
Match length
                  57
% identity
NCBI Description (AF001434) Hpast [Homo sapiens]
Seq. No.
                   31907
Contig ID
                  258676 1.R1040
5'-most EST
                  gsv701043806.hl
Method
                  BLASTX
NCBI GI
                  q4309698
BLAST score
                   420
                   1.0e-41
E value
                   99
Match length
                   78
% identity
NCBI Description
                   (AC006266) putative glucosyltransferase [Arabidopsis
                  thaliana]
Seq. No.
                   31908
Contig ID
                   258684 1.R1040
5'-most EST
                  gsv701046676.hl
                   31909
Seq. No.
Contig ID
                   258714 1.R1040
5'-most EST
                   jC-gmst02400078g05d1
Method
                   BLASTX
NCBI GI
                   q4056482
BLAST score
                   353
E value
                   2.0e-33
Match length
                   99
% identity
                   41
NCBI Description
                  (AC005896) putative ABC transporter [Arabidopsis thaliana]
                   31910
Seq. No.
```

Contig ID 258740 1.R1040 5'-most EST gsv701043922.h1

Seq. No. 31911

Contig ID 258760 1.R1040



```
5'-most EST
                  qsv701051971.h1
Method
                  BLASTX
NCBI GI
                  q1362091
BLAST score
                  369
E value
                  9.0e-36
Match length
                  83
% identity
                  cellulase (EC 3.2.1.4) precursor - tomato >gi_924622
NCBI Description
                   (U20590) endo-1,4-beta-glucanase precursor [Solanum
                  lycopersicum]
Seq. No.
                  31912
Contig ID
                  258866 1.R1040
                  gsv701050088.hl
5'-most EST
Method
                  BLASTX
                  a2288988
NCBI GI
BLAST score
                   370
E value
                  8.0e-36
                  88
Match length
                  77
% identity
                  (AC002335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   31913
Seq. No.
Contig ID
                   258870 1.R1040
5'-most EST
                  uC-qmflminsoy082q05b1
                   31914
Seq. No.
                   258890 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220108h02a1
                  BLASTX
Method
NCBI GI
                   q4432814
BLAST score
                   703
E value
                   3.0e-74
Match length
                   158
                   84
% identity
                  (AC006593) unknown protein [Arabidopsis thaliana]
NCBI Description
                   31915
Seq. No.
                   258910 1.R1040
Contig ID
5'-most EST
                   q5058417
Method
                   BLASTX
                   g4220480
NCBI GI
BLAST score
                   229
E value
                   3.0e-23
Match length
                   133
                   19
% identity
                  (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                   31916
Seq. No.
                   258928 1.R1040
Contig ID
                   asn701142720.h1
5'-most EST
```

31917 Seq. No.

258930 1.R1040 Contig ID 5'-most EST  $jsh701\overline{0}67648.h1$ 

BLASTN Method NCBI GI g1669590



BLAST score 1.0e-34 . E value Match length 249 % identity 82 NCBI Description Glycyrrhiza echinata mRNA for O-methyltransferase, complete Seq. No. 31918 Contig ID 258936 1.R1040 5'-most EST uC-gmrominsoy193a01b1 Method BLASTX NCBI GI g2258469 BLAST score 348

E value 3.0e-33 Match length 98 69 % identity

NCBI Description (AF009179) replication protein Al [Oryza sativa]

31919 Seq. No.

Contig ID 258990 1.R1040

5'-most EST  $g43134\overline{0}1$ Method BLASTX NCBI GI g2781359 BLAST score 326 -

E value 3.0e-30 Match length 137 % identity 53

NCBI Description (AC003113) F2501.15 [Arabidopsis thaliana]

Seq. No. 31920

259028 1.R1040 Contig ID 5'-most EST  $gsv701\overline{0}44331.h1$ 

Seq. No. 31921

Contig ID 259298 1.R1040 5'-most EST qsv701044745.h1

Method BLASTX NCBI GI q3687654 BLAST score 148 1.0e-18 E value Match length 78 % identity 56

(AF047975) putative ethylene receptor; ETR2 [Arabidopsis NCBI Description

thaliana]

Seq. No. 31922

259331 1.R1040 Contig ID 5'-most EST gsv701044741.h1

Seq. No. 31923

259484 1.R1040 Contig ID 5'-most EST gsv701044930.h1

Method BLASTX NCBI GI g1237250 BLAST score 387 2.0e-37 E value Match length 163



% identity NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum] 31924 Seq. No. 259525 1.R1040 Contig ID 5'-most EST gsv701044982.hl Method BLASTN NCBI GI q3832511 BLAST score 114 2.0e-57 E value Match length 246 % identity 87 NCBI Description Astragalus membranaceus granule-bound glycogen (starch) synthase mRNA, complete cds 31925 Seq. No. 259544 1.R1040 Contig ID 5'-most EST gsv701045212.h1 31926 Seq. No. 259549 1.R1040 Contig ID zsg701118809.h1 5'-most EST Method BLASTX NCBI GI g2623298 BLAST score 485 3.0e-49E value 87 Match length 97 % identity NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana] 31927 Seq. No. Contig ID 259627 1.R1040  $gsv701\overline{0}45149.h1$ 5'-most EST Seq. No. 31928 259727 1.R1040 Contig ID 5'-most EST gsv701045381.h1 Seq. No. 31929 259798 1.R1040 Contig ID 5'-most EST gsv701045392.hl Seq. No. 31930 259853 1.R1040 Contig ID 5'-most EST jC-gmst02400045g10a1 Seq. No. 31931

Contig ID 259914\_1.R1040 5'-most EST gsv701045560.h1

Seq. No. 31932

Contig ID 260018\_1.R1040 5'-most EST ekl700968110.h1

Seq. No. 31933

Contig ID 260105\_1.R1040



5'-most EST gsv701045809.h1

Method BLASTX
NCBI GI g2258469
BLAST score 288
E value 7.0e-26
Match length 115
% identity 54

NCBI Description (AF009179) replication protein A1 [Oryza sativa]

Seq. No. 31934

Contig ID 260369\_1.R1040 5'-most EST gsv701053741.h1

Seq. No. 31935

Contig ID 260459\_1.R1040 5'-most EST gsv701051136.h1

Seq. No. 31936

Contig ID 260476\_1.R1040 5'-most EST gsv701046270.h1

Method BLASTX
NCBI GI g2832408
BLAST score 404
E value 1.0e-39
Match length 75
% identity 96

NCBI Description (Y14209) R2R3-MYB transcription factor [Arabidopsis

thaliana]

Seq. No. 31937

Contig ID 260526\_1.R1040 5'-most EST uC-gmropic107e05b1

Seq. No. 31938

Contig ID 260533\_1.R1040 5'-most EST gsv701046344.h1

Seq. No. 31939

Contig ID 260661\_1.R1040 5'-most EST kl1701215484.h1

Seq. No. 31940

Contig ID 260664 1.R1040 5'-most EST gsv701048389.h1

Seq. No. 31941

Contig ID 260713\_1.R1040

5'-most EST jC-gmle01810014d09d1

Method BLASTX
NCBI GI g2911058
BLAST score 266
E value 3.0e-23
Match length 72
% identity 58

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 31942



```
260849 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}46733.h1
                   31943
Seq. No.
                   260881 1.R1040
Contig ID
                  jC-gmst02400005d09d1
5'-most EST
                   31944
Seq. No.
                   261125 1.R1040
Contig ID
                   gsv701047135.hl
5'-most EST
                   BLASTX
Method
                   g1619300
NCBI GI
BLAST score
                   254
E value
                   8.0e-22
                   108
Match length
                   47
% identity
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
                   31945
Seq. No.
                   261385 1.R1040
Contig ID
                   gsv701047665.hl
5'-most EST
Method
                   BLASTX
                   g3080452
NCBI GI
BLAST score
                   624
                   5.0e-65
E value
                   166
Match length
                   66
% identity
                   (AL022605) putative L-ascorbate oxidase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   31946
                   261488 1.R1040
Contig ID
                   gsv701047785.hl
5'-most EST
                   31947
Seq. No.
                   261495_1.R1040
Contig ID
5'-most EST
                   gsv701047792.hl
Method
                   BLASTX
NCBI GI
                   g4559355
BLAST score
                   268
                   9.0e-24
E value
Match length
                   73
                   64
% identity
                   (AC006585) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   31948
                   261508 1.R1040
Contig ID
                   gsv701\overline{0}47811.h1
5'-most EST
Seq. No.
                   31949
Contig ID
                   261596 1.R1040
```

Contig ID 261596 1.R1040 5'-most EST gsv701047921.h1

Method BLASTX
NCBI GI g2119719
BLAST score 418
E value 2.0e-41
Match length 94



% identity 84

NCBI Description heat-shock cognate protein 70-3 - tomato >gi\_762844

(L41253) Hsc70 [Lycopersicon esculentum]

Seq. No. 31950

Contig ID 261665\_1.R1040

5'-most EST g5753145

Seq. No. 31951

Contig ID 261707\_1.R1040

5'-most EST jC-gmro02910062a07d1

Method BLASTX
NCBI GI g2435522
BLAST score 198
E value 2.0e-15
Match length 62
% identity 61

NCBI Description (AF024504) contains similarity to other AMP-binding enzymes

[Arabidopsis thaliana]

Seq. No. 31952

Contig ID 261714\_1.R1040 5'-most EST gsv701048715.h1

Seq. No. 31953

Contig ID 261746\_1.R1040 5'-most EST gsv701048116.h1

Seq. No. 31954

Contig ID 261752\_1.R1040

5'-most EST uC-gmrominsoy169b08b1

Method BLASTX
NCBI GI g2443329
BLAST score 193
E value 3.0e-14
Match length 135
% identity 39

NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No. 31955

Contig ID 261790\_1.R1040 5'-most EST uC-gmropic040b10b1

Seq. No. 31956

Contig ID 261819\_1.R1040 5'-most EST gsv701048211.h1

Seq. No. 31957

Contig ID 261868\_1.R1040 5'-most EST gsv701048270.h1

Seq. No. 31958

Contig ID 261886\_1.R1040 5'-most EST hrw701061252.h1

Seq. No. 31959

Contig ID 261965\_1.R1040



```
jC-gmst02400063c04a1
5'-most EST
                  BLASTX
Method
                  q2827709
NCBI GI
                  459
BLAST score
                  1.0e-45
E value
                  246
Match length
% identity
                  (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                  31960
Seq. No.
                  261982 1.R1040
Contig ID
                  gsv701048432.hl
5'-most EST
Seq. No.
                  31961
Contig ID
                  261984 1.R1040
                  gsv701048434.hl
5'-most EST
                   31962
Seq. No.
                   262103 1.R1040
Contig ID
                   gsv701048573.hl
5'-most EST
Method
                   BLASTX
                   g2497542
NCBI GI
BLAST score
                   467
                   5.0e-47
E value
                   110
Match length
% identity
                   85
                   PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR
NCBI Description
                   >gi_629696_pir__S44287 pyruvate kinase, plastid - common
                   tobacco >gi_482938_emb_CAA82223_ (Z28374) Pyruvate kinase;
                   plastid isozyme [Nicotiana tabacum]
                   31963
Seq. No.
                   262173 1.R1040
Contig ID
                   gsv701048667.hl
5'-most EST
                   31964
Seq. No.
                   262199 1.R1040
Contig ID
                   g5752535
5'-most EST
                   31965
Seq. No.
                   262223 1.R1040
Contig ID
                   gsv701048741.hl
5'-most EST
                   31966
Seq. No.
                   262260 1.R1040
Contig ID
                   jC-gmf\overline{1}02220138b03a1
5'-most EST
                   BLASTX
Method
                   g4376203
NCBI GI
BLAST score
                   204
                   6.0e-16
E value
                   114
```

Match length % identity 36

(U35226) putative cytochrome P-450 [Nicotiana NCBI Description

plumbaginifolia]

31967 Seq. No.

262304 1.R1040 Contig ID



5'-most EST gsv701048838.h1

Method BLASTX
NCBI GI g3834307
BLAST score 260
E value 2.0e-22
Match length 113

Match length 113 % identity 61

NCBI Description (AC005679) Strong similarity to gene T10I14.120 gi\_2832679

putative protein from Arabidopsis thaliana BAC gb\_AL021712.

ESTs gb\_N65887 and gb\_N65627 come from this gene.

[Arabidopsis thaliana]

Seq. No. 31968

Contig ID 262337\_1.R1040 5'-most EST zsg701127365.h1

Method BLASTX
NCBI GI g2462835
BLAST score 476
E value 7.0e-48
Match length 124
% identity 72

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31969

Contig ID 262392\_1.R1040 5'-most EST asn701140958.h1

Seq. No. 31970

Contig ID 262400\_1.R1040 5'-most EST uC-gmropic110f02b1

Seq. No. 31971

Contig ID 262402\_1.R1040 5'-most EST uC-gmropic016f02b1

Seq. No. 31972

Contig ID 262444\_1.R1040

5'-most EST uC-gmrominsoy319b10b1

Seq. No. 31973

Contig ID 262463\_1.R1040 5'-most EST gsv701049036.h1

Seq. No. 31974

Contig ID 262480\_1.R1040 5'-most EST asn701138395.h1

Method BLASTX
NCBI GI g1168609
BLAST score 353
E value 8.0e-34
Match length 90
% identity 74

NCBI Description AUXIN-RESISTANCE PROTEIN AXR1 >gi\_479664\_pir\_S35071 auxin-resistance protein AXR1 - Arabidopsis thaliana >gi\_304104 (L13922) ubiquitin-activating enzyme E1 [Arabidopsis thaliana] >gi\_2388579 (AC000098) Match to Arabidopsis AXR1 (gb ATHAXR1122). [Arabidopsis thaliana]



>gi\_448755\_prf\_\_1917337A ubiquitin-activating enzyme E1
[Arabidopsis thaliana]

Seq. No. 31975

Contig ID 262521\_1.R1040 5'-most EST gsv701049112.h1

Seq. No. 31976

Contig ID 262529\_1.R1040 5'-most EST gsv701049122.h1

Seq. No. 31977

Contig ID 262551\_1.R1040 5'-most EST gsv701049144.h1

Seq. No. 31978

Contig ID 262639 1.R1040 5'-most EST kl1701213755.h1

Method BLASTX
NCBI GI g3059122
BLAST score 499
E value 1.0e-50
Match length 121
% identity 80

NCBI Description (AJ003783) glyeraldehyde-3-phosphate dehydrogenase

[Marsilea quadrifolia]

Seq. No. 31979

Contig ID 262640 1.R1040

5'-most EST jC-gmro02910004c12a1

Seq. No. 31980

Contig ID 262673 1.R1040

5'-most EST g5605938
Method BLASTX
NCBI GI g2739279
BLAST score 447
E value 2.0e-44
Match length 165
% identity 54

NCBI Description (AJ223177) short chain alcohol dehydrogenase [Nicotiana

tabacum] >gi\_2791348\_emb\_CAA11154\_ (AJ223178) short chain

alcohol dehydrogenase [Nicotiana tabacum]

Seq. No. 31981

Contig ID 262742\_1.R1040

5'-most EST uC-gmrominsoy096e06b1

Method BLASTX
NCBI GI g2832304
BLAST score 466
E value 1.0e-46
Match length 149
% identity 59

NCBI Description (AF044489) receptor-like protein kinase [Oryza sativa]

Seq. No. 31982

Contig ID 262772\_1.R1040



```
g5175517
5'-most EST
                  BLASTX
Method
                  g2529677
NCBI GI
BLAST score
                  148
                  1.0e-09
E value
                   37
Match length
                  73
% identity
                   (AC002535) kinesin-like protein, heavy chain [Arabidopsis
NCBI Description
                   thaliana]
                   31983
Seq. No.
                   262777 1.R1040
Contig ID
                   jC-gmro02800027d11d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2739378
BLAST score
                   141
                   8.0e-09
E value
Match length
                   63
% identity
                   48
NCBI Description (AC002505) AR781 [Arabidopsis thaliana]
Seq. No.
                   31984
Contig ID
                   262855 1.R1040
                   jC-gmro02910007b01a1
5'-most EST
                   31985
Seq. No.
                   262865_1.R1040
Contig ID
                   gsv701049586.hl
5'-most EST
                   31986
Seq. No.
                   262925 1.R1040
Contig ID
                   jC-gmf102220103e08a1
5'-most EST
                   31987
Seq. No.
                   262932 1.R1040
Contig ID
                   uC-gmrominsoy178c11b1
5'-most EST
                   31988
Seq. No.
                   262946 1.R1040
Contig ID
                   gsv701049693.h1
5'-most EST
                   BLASTX
Method
                   g1946368
NCBI GI
                   258
BLAST score
                   2.0e-22
E value
                   119
Match length
                   48
% identity
                   (U93215) unknown protein [Arabidopsis thaliana]
NCBI Description
                   31989
Seq. No.
                   263020 1.R1040
Contig ID
5'-most EST
                   g57533\overline{2}5
Method
                   BLASTX
                   g3367531
NCBI GI
BLAST score
                   131
                   7.0e-12
E value
Match length
                   148
```

4877

36

% identity



NCBI Description (AC004392) Strong similarity to gi\_2160138 F19K23.6 gene product from A. thaliana BAC gb\_AC000375. [Arabidopsis

thaliana]

Seq. No. 31990

Contig ID 263102 1.R1040 5'-most EST gsv701049942.h1

Method BLASTN
NCBI GI g169980
BLAST score 188
E value 1.0e-101
Match length 282
% identity 92

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No. 31991

Contig ID 263175\_1.R1040 5'-most EST gsv701051306.h1

Seq. No. 31992

Contig ID 263203\_1.R1040 5'-most EST gsv701050068.h1

Method BLASTX
NCBI GI g2827621
BLAST score 194
E value 4.0e-15
Match length 38
% identity 82

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 31993

Contig ID 263309\_1.R1040

5'-most EST g5753498
Method BLASTX
NCBI GI g2191168
BLAST score 147
E value 7.0e-21
Match length 91
% identity 60

NCBI Description (AF007270) contains similarity to myosin heavy chain

[Arabidopsis thaliana]

Seq. No. 31994

Contig ID 263364 1.R1040 5'-most EST zsg701124991.h1

Seq. No. 31995

Contig ID 263422\_1.R1040 5'-most EST gsv701050367.h1

Seq. No. 31996

Contig ID 263439\_1.R1040

5'-most EST g5058204 Method BLASTX NCBI GI g4038044 BLAST score 235 E value 2.0e-19



83 Match length % identity

(AC005936) unknown protein [Arabidopsis thaliana] NCBI Description

>qi 4406788 gb AAD20098\_ (AC006532) unknown protein

[Arabidopsis thaliana]

31997 Seq. No.

263481 1.R1040 Contig ID

uC-gmflminsoy071c11b2 5'-most EST

31998 Seq. No.

263483 1.R1040 Contig ID  $gsv701\overline{0}55252.h1$ 5'-most EST

Seq. No. 31999

263544 1.R1040 Contig ID gsv701050526.h1 5'-most EST

32000 Seq. No.

263548 1.R1040 Contig ID

5'-most EST jC-gmst02400055e04a1

32001 Seq. No.

263611 1.R1040 Contig ID

 $g53427\overline{2}1$ 5'-most EST Method BLASTX g1234900 NCBI GI BLAST score 313 E value 6.0e-59 Match length 168

% identity 73

(X92489) homeobox-leucine zipper protein [Glycine max] NCBI Description

32002 Seq. No.

263694 1.R1040 Contig ID 5'-most EST uC-gmropic034f11b1

32003 Seq. No.

263724 1.R1040 Contig ID uC-gmropic047c06b1 5'-most EST

BLASTX Method g1871187 NCBI GI 357 BLAST score 1.0e-33 E value 149 Match length 51 % identity

(U90439) unknown protein [Arabidopsis thaliana] NCBI Description

32004 Seq. No.

263731 1.R1040 Contig ID 5'-most EST jC-gmst02400004c05d1

32005 Seq. No.

263731 2.R1040 Contig ID

q5688425 5'-most EST

32006 Seq. No.

BLAST score

Match length

% identity

E value

262

185

51

1.0e-42



```
Contig ID
                   263747 1.R1040
                   k11701\overline{2}13958.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2335100
BLAST score
                   470
E value
                   2.0e-47
Match length
                   108
% identity
                   81
                  (AC002339) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32007
Contig ID
                   263777 1.R1040
5'-most EST
                   gsv701050836.h1
Method
                   BLASTX
NCBI GI
                   q3482920
BLAST score
                   251
E value
                   2.0e-21
Match length
                   63
% identity
                   73
                  (AC003970) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   32008
Seq. No.
                   263822 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220080c07a1
Seq. No.
                   32009
                   263837 1.R1040
Contig ID
5'-most EST
                   gsv701050960.hl
Method
                   BLASTX
NCBI GI
                   q1800223
BLAST score
                   150
E value
                   7.0e-10
Match length
                   57
% identity
                   53
NCBI Description
                  (U65018) mannosyltransferase [Dictyostelium discoideum]
                   32010
Seq. No.
                   263995 1.R1040
Contig ID
5'-most EST
                   qsv701\overline{0}51161.h1
Method
                   BLASTX
NCBI GI
                   g3668171
BLAST score
                   422
E value
                   3.0e-41
Match length
                   190
% identity
                   (AB006052) RNA polymerase I second-largest subunit
NCBI Description
                   [Neurospora crassa]
Seq. No.
                   32011
Contig ID
                   264077 1.R1040
5'-most EST
                   uC-gmflminsoy018b08b1
Method
                   BLASTX
NCBI GI
                   g4455171
```



NCBI Description (AL035521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32012

Contig ID 264119\_1.R1040 5'-most EST gsv701054444.h1

Seq. No. 32013

Contig ID 264223\_1.R1040 5'-most EST fC-gmle700554943d3

Method BLASTX
NCBI GI g2982301
BLAST score 165
E value 2.0e-11
Match length 44
% identity 66

NCBI Description (AF051235) YGL010w-like protein [Picea mariana]

Seq. No. 32014

Contig ID 264286\_1.R1040 5'-most EST gsv701051519.h1

Seq. No. 32015

Contig ID 264324\_1.R1040 5'-most EST gsv701051566.h1

Seq. No. 32016

Contig ID 264429\_1.R1040 5'-most EST gsv701051722.h1

Method BLASTX
NCBI GI g2961346
BLAST score 167
E value 5.0e-12
Match length 37
% identity 76

NCBI Description (AL022140) pectinesterase like protein [Arabidopsis

thaliana]

Seq. No. 32017

Contig ID 264454\_1.R1040 5'-most EST gsv701056174.h1

Seq. No. 32018

Contig ID 264536\_1.R1040 5'-most EST gsv701054288.h1

Seq. No. 32019

Contig ID 264565 1.R1040 5'-most EST gsv701054339.h1

Seq. No. 32020

Contig ID 264566\_1.R1040 5'-most EST gsv701051941.h1

Seq. No. 32021

Contig ID 264617\_1.R1040 5'-most EST zsg701125604.h1

Method BLASTX



q4220519 NCBI GI BLAST score 161 E value 5.0e-11 Match length 61 57 % identity

NCBI Description (AL035356) putative protein binding protein [Arabidopsis

thaliana]

Seq. No. Contig ID 5'-most EST

32022 264667 1.R1040 gsv701052072.h1

Seq. No. Contig ID 5'-most EST 32023 264775 1.R1040 gsv701052304.h1

Seq. No. Contig ID

32024 264818 1.R1040 gsv701052381.hl

5'-most EST Method BLASTX NCBI GI q2262115 BLAST score 449 2.0e-44E value Match length 261 % identity 36

(AC002343) cellulose synthase isolog [Arabidopsis thaliana] NCBI Description

Seq. No.

32025 264961 1.R1040 Contig ID 5'-most EST gsv701052605.hl

Seq. No. 32026

Contig ID 264986 1.R1040 5'-most EST uC-gmronoir000g05b1

32027 Seq. No.

264998 1.R1040 Contig ID 5'-most EST gsv701052745.h1

32028 Seq. No.

265158 1.R1040 Contig ID 5'-most EST gsv701052877.hl

Seq. No. 32029

Contig ID 265180\_1.R1040 5'-most EST uC-gmropic109h08b1

32030 Seq. No.

265232 1.R1040 Contig ID 5'-most EST jC-gmf102220063c04d1

Method BLASTX NCBI GI g2281085 BLAST score 315 7.0e-29 E value Match length 70 74 % identity

NCBI Description (AC002333) CTR1 protein kinase isolog [Arabidopsis



## thaliana]

 Seq. No.
 32031

 Contig ID
 265232\_2.R1040

 5'-most EST
 fC-gmse700658724d3

 Method
 BLASTX

 NCBI GI
 g2281085

 BLAST score
 203

BLAST score 203 E value 7.0e-16 Match length 42 % identity 76

NCBI Description (AC002333) CTR1 protein kinase isolog [Arabidopsis

thaliana]

32032

Seq. No.

Contig ID 265252\_1.R1040 5'-most EST gsv701053004.h1

Method BLASTX
NCBI GI g1172633
BLAST score 179
E value 2.0e-13
Match length 91
% identity 53

NCBI Description PROLIFERA PROTEIN >gi 675491 (L39954) contains MCM2/3/5

family signature; PROSITE; PS00847; disruption leads to early lethal phenotype; similar to MCM2/3/5 family, most

similar to YBR1441 [Arabidopsis thaliana]

Seq. No. 32033

Contig ID 265256\_1.R1040 5'-most EST uC-gmropic102g10b1

Method BLASTX
NCBI GI g1083160
BLAST score 468
E value 8.0e-47
Match length 176
% identity 51

NCBI Description mannosyl-oligosaccharide 1,2-alpha-mannosidase (EC

3.2.1.113) - rabbit (fragment)

Seq. No. 32034

Contig ID 265317 1.R1040

5'-most EST g5677973

Seq. No.

32035

Contig ID 265389\_1.R1040

5'-most EST uC-gmrominsoy258f09b1

Method BLASTX
NCBI GI g3600039
BLAST score 374
E value 5.0e-46
Match length 201
% identity 53

NCBI Description (AF080119) similar to Schizosaccharomyces pombe isp4

protein (GB:D14061) [Arabidopsis thaliana]

Seq. No. 32036



Contig ID 265550\_1.R1040 5'-most EST kl1701204243.h2

Method BLASTN
NCBI GI g3449326
BLAST score 33
E value 4.0e-09
Match length 77
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19M22, complete sequence [Arabidopsis thaliana]

Seq. No. 32037

Contig ID 265600\_1.R1040 5'-most EST uC-gmronoir026h07b1

Seq. No. 32038

Contig ID 265673\_1.R1040 5'-most EST gsv701053601.h1

Seq. No. 32039

Contig ID 265696\_1.R1040 5'-most EST gsv701056138.h1

Method BLASTX
NCBI GI g2245020
BLAST score 299
E value 3.0e-27
Match length 67
% identity 75

NCBI Description (Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No. 32040

Contig ID 265724\_1.R1040 5'-most EST gsv701053686.h1

Seq. No. 32041

Contig ID 265776\_1.R1040 5'-most EST jsh701063921.h1

Seq. No. 32042

Contig ID 265779\_1.R1040 5'-most EST gsv701053759.h1

Seq. No. 32043

Contig ID 265788\_1.R1040 5'-most EST gsv701053763.h1

Seq. No. 32044

Contig ID 265802\_1.R1040 5'-most EST gsv701053880.h1

Method BLASTX
NCBI GI g2191136
BLAST score 234
E value 7.0e-20
Match length 91
% identity 55

NCBI Description (AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A.



thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

Seq. No. 32045

Contig ID 265881\_1.R1040

5'-most EST jC-gmro02910024a09d1

Seq. No. 32046

Contig ID 265900\_1.R1040 5'-most EST gsv701053916.h1

Seq. No. 32047

Contig ID 265938\_1.R1040 5'-most EST gsv701053964.h1

Seq. No. 32048

Contig ID 265959\_1.R1040

5'-most EST jC-gmf102220090g07a1

Seq. No. 32049

Contig ID 265975\_1.R1040 5'-most EST asn701139792.h1

Seq. No. 32050

Contig ID 265983\_1.R1040 5'-most EST gsv701054023.h1

Seq. No. 32051

Contig ID 265995\_1.R1040 5'-most EST uC-gmropic113c02b1

Seq. No. 32052

Contig ID 266077\_1.R1040 5'-most EST gsv701054136.h1

Seq. No. 32053

Contig ID 266080\_1.R1040 5'-most EST jsh701064056.h1

Seq. No. 32054

Contig ID 266090\_1.R1040 5'-most EST asn701131030.h1

Method BLASTX
NCBI GI g2833378
BLAST score 319
E value 3.0e-29
Match length 172
% identity 41

NCBI Description HEXOKINASE >gi\_619928 (U18754) hexokinase [Arabidopsis

thaliana] >gi\_1582383\_prf\_\_2118367A hexokinase [Arabidopsis

thaliana]

Seq. No. 32055

Contig ID 266111\_1.R1040

5'-most EST  $g43078\overline{2}9$  Method BLASTN g3116019



BLAST score 38 E value 6.0e-12 Match length 90 % identity 86

NCBI Description Pisum sativum mRNA for ftsZ gene

Seq. No.
Contig ID
5'-most EST

32056 266143 1.R1040 gsv701054229.h1

Seq. No.

32057

Contig ID 5'-most EST 266229\_1.R1040 uC-gmropic056g11b1

Method BLASTX
NCBI GI g629561
BLAST score 248
E value 4.0e-21
Match length 121
% identity 44

NCBI Description SRG1 protein - Arabidopsis thaliana

>gi\_479047\_emb\_CAA55654\_ (X79052) SRG1 [Arabidopsis

thaliana]

Seq. No.

32058

Contig ID 5'-most EST

266238 1.R1040 zsg701119112.h1

Seq. No.

32059

Contig ID 5'-most EST

266276\_1.R1040 gsv701054413.h1

Seq. No.

32060

Contig ID 5'-most EST

266280 1.R1040 gsv701056418.h1

Method BLASTX
NCBI GI g3411152
BLAST score 191
E value 8.0e-15
Match length 54
% identity 69

NCBI Description (AF066050) thymidine kinase [Oryza sativa]

Seq. No.

32061

Contig ID

266337\_1.R1040

5'-most EST

uC-gmrominsoy310d10b1

Method BLASTX
NCBI GI g3335373
BLAST score 284
E value 2.0e-25
Match length 72
% identity 71

NCBI Description (AC003028) putative GTL1 protein [Arabidopsis thaliana]

Seq. No.

32062

Contig ID

266337 2.R1040

5'-most EST

uC-gmrominsoy125a08b1

Method

BLASTX



```
g3335373
NCBI GI
BLAST score
                  385
                  3.0e - 37
E value
Match length
                  93
% identity
                 (AC003028) putative GTL1 protein [Arabidopsis thaliana]
NCBI Description
                  32063
Seq. No.
                  266356 1.R1040
Contig ID
                  uC-gmropic012d12b1
5'-most EST
Method
                  BLASTX
                  g1663541
NCBI GI
BLAST score
                  224
                   2.0e-18
E value
                  91
Match length
% identity
                  58
NCBI Description (U55805) disease resistance protein homolog [Glycine max]
                   32064
Seq. No.
                   266428 1.R1040
Contig ID
                  gsv701054626.hl
5'-most EST
                   32065
Seq. No.
                   266487 1.R1040
Contig ID
                   jC-gmle01810018c01a2
5'-most EST
                   32066
Seq. No.
                   266605 1.R1040
Contig ID
                   epx701109042.h1
5'-most EST
Method
                   BLASTX
                   q3242071
NCBI GI
BLAST score
                   285
E value
                   3.0e-25
                   163
Match length
% identity
                  (AJ007289) myb-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32067
                   266624 1.R1040
Contig ID
                   gsv701055903.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2827709
BLAST score
                   446
                   2.0e-44
E value
                   114
Match length
                   73
% identity
                   (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                   32068
Seq. No.
```

Contig ID 5'-most EST 266713 1.R1040 gsv701055205.h1

Seq. No.

32069

Contig ID 5'-most EST 266809 1.R1040 gsv701055203.h1

Method NCBI GI BLASTN g28589



315 BLAST score 1.0e-177 E value Match length 315 100 % identity NCBI Description Human messenger RNA for serum albumin (HSA) 32070 Seq. No. 266881 1.R1040 Contig ID uC-gmrominsoy219f09b1 5'-most EST Seq. No. 32071 266882 1.R1040 Contig ID jC-gmle01810082f09a1 5'-most EST BLASTX Method q4490316 NCBI GI BLAST score 242 E value 2.0e-20 Match length 123 % identity 43 NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana] 32072 Seq. No. 266933 1.R1040 Contig ID gsv701055343.h1 5'-most EST BLASTX Method g3551954 NCBI GI BLAST score 176 1.0e-12 E value 78 Match length % identity (AF082030) senescence-associated protein 5 [Hemerocallis NCBI Description hybrid cultivar] 32073 Seq. No. 267126 1.R1040 Contig ID 5'-most EST gsv701055586.h1 Seq. No. 32074 267154 1.R1040 Contig ID jC-gmf102220103a08a1 5'-most EST Method BLASTX g3510254 NCBI GI BLAST score 148 2.0e-09 E value Match length 41 78 % identity (AC005310) putative zinc transporter [Arabidopsis thaliana] NCBI Description

Seq. No.

267155 1.R1040 Contig ID gsv701055657.hl 5'-most EST

Seq. No. 32076

267175 1.R1040 Contig ID

uC-gmrominsoy072e01b1 5'-most EST

32075

BLASTX Method NCBI GI g3334142



BLAST score 579
E value 6.0e-60
Match length 148
% identity 76

NCBI Description CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5

(CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5) >gi\_2737892 (U59150) nucleolar protein AfCbf5p [Sartorya

fumigata]

Seq. No. 32077

Contig ID 267306\_1.R1040 5'-most EST fC-gmro700763939d3

Method BLASTX
NCBI GI g3201554
BLAST score 328
E value 2.0e-30
Match length 62
% identity 95

NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No.

Contig ID 267411\_1.R1040 5'-most EST gsv701055941.h1

32078

Method BLASTX
NCBI GI g3688284
BLAST score 595
E value 8.0e-62
Match length 146
% identity 73

NCBI Description (AJ011567) lanatoside 15'-O-acetylesterase [Digitalis

lanata]

Seq. No. 32079

Contig ID 267480\_1.R1040

5'-most EST jC-gmro02910003g06a1

Seq. No. 32080

Contig ID 267608\_1.R1040

5'-most EST jC-gmro02910061c08a1

Method BLASTX
NCBI GI g1857447
BLAST score 251
E value 1.0e-21
Match length 110
% identity 47

NCBI Description (U82367) UDP-glucose glucosyltransferase [Solanum

tuberosum]

Seq. No. 32081

Contig ID 267784 1.R1040 5'-most EST zsg701126354.h1

Method BLASTX
NCBI GI 94388832
BLAST score 514
E value 2.0e-52
Match length 119
% identity 85



(AC006528) putative DNA replication licensing factor with NCBI Description an MCM family domain (prosite:PDOC00662) [Arabidopsis thaliana]

32082 Seq. No.

267856 1.R1040 Contig ID 5'-most EST epx701108984.hl

32083 Seq. No.

267885 1.R1040 Contig ID 5'-most EST gsv701056530.h1

Method BLASTX g3176671 NCBI GI 227 BLAST score 7.0e-19 E value 69 Match length

% identity

(AC004393) Contains similarity to hypothetical gene B0495.7 NCBI Description

gb\_687822 from C. elegans cosmid gb\_U21317. [Arabidopsis

thaliana]

32084 Seq. No.

267894 1.R1040 Contig ID qsv701056543.hl 5'-most EST

32085 Seq. No.

267922 1.R1040 Contig ID epx701107501.hl 5'-most EST

32086 Seq. No.

267929 1.R1040 Contig ID

jC-gmro02910048c01a1 5'-most EST

BLASTX Method g1346396 NCBI GI 150 BLAST score 1.0e-09 E value 85 Match length % identity

PUTATIVE RECEPTOR PROTEIN KINASE ZMPK1 PRECURSOR NCBI Description

>gi 100913\_pir\_\_S10930 probable receptor protein kinase (EC 2.7.1.-) precursor - maize >gi\_22432\_emb\_CAA36611\_ (X52384)

precursor protein (AA -26 to 791) [Zea mays]

>gi 22436\_emb\_CAA47962\_ (X67733) receptor-like protein kinase [Zea mays] >gi\_226927\_prf\_\_1611404A receptor protein

kinase [Zea mays]

32087 Seq. No.

267936 1.R1040 Contig ID gsv701056591.h1 5'-most EST

32088 Seq. No.

267989 1.R1040 Contig ID 5'-most EST gsv701056662.hl

32089 Seq. No.

268024 1.R1040 Contig ID qsv701056810.hl 5'-most EST



```
32090
Seq. No.
                   268048 1.R1040
Contig ID
5'-most EST
                   qsv701056739.h1
                   32091
Seq. No.
                   268093 1.R1040
Contig ID
                   qsv701056795.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2809251
                   650
BLAST score
                   8.0e-81
E value
                   179
Match length
% identity
                   80
                   (AC002560) F21B7.20 [Arabidopsis thaliana]
NCBI Description
                   32092
Seq. No.
                   268099 1.R1040
Contig ID
                   jC-gmr002910070f02a1
5'-most EST
                   32093
Seq. No.
                   268146 1.R1040
Contig ID
                   epx701106688.h1
5'-most EST
Method
                   BLASTX
                   g4455301
NCBI GI
BLAST score
                   219
                                                           ٠,
                   4.0e-18
E value
Match length
                   59
% identity
                   (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
                   32094
Seq. No.
                   268209 1.R1040
Contig ID
                   asn701141115.h1
5'-most EST
                   BLASTX
Method
                   g2245034
NCBI GI
                   409
BLAST score
                   4.0e-40
E value
                   119
Match length
% identity
                   67
                   (Z97342) enoyl-CoA hydratase [Arabidopsis thaliana]
NCBI Description
                   32095
Seq. No.
                   268296 1.R1040
Contig ID
5'-most EST
                   cle700\overline{9}67859.h1
Method
                   BLASTX
NCBI GI
                   g2262178
                   140
BLAST score
                   6.0e-09
E value
Match length
                   59
% identity
                   54
                   (AC002329) putative Mlo-like protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 32096

Contig ID 268350\_1.R1040 5'-most EST hrw701056925.h1

Method BLASTX



```
q2911276
NCBI GI
                  138
BLAST score
                  1.0e-08
E value
                  64
Match length
% identity
                  (U63631) LMW heat shock protein [Fragaria x ananassa]
NCBI Description
                  32097
Seq. No.
                  268351 1.R1040
Contig ID
                  uC-gmrominsoy136g04b1
5'-most EST
                   32098
Seq. No.
                   268417 1.R1040
Contig ID
                  hrw701057018.h2
5'-most EST
                   32099
Seq. No.
                   268438 1.R1040
Contig ID
                   hrw701057058.h2
5'-most EST
                   32100
Seq. No.
                   268504 1.R1040
Contig ID
                   hrw701057302.hl
5'-most EST
                   BLASTN
Method
                   g1620016
NCBI GI
                   189
BLAST score
                   1.0e-102
E value
                   205
Match length
                   98
% identity
NCBI Description Human heart mRNA for heat shock protein 90, partial cds
Seq. No.
                   32101
                   268521 1.R1040
Contig ID
                   hrw701057327.h1
5'-most EST
                   BLASTN
Method
                   g34200
NCBI GI
BLAST score
                   252
                   1.0e-140
E value
Match length
                   272
                   98
 % identity
                   Human mRNA for ribosomal protein L35a
NCBI Description
                   >gi_4506638_ref_NM_000996.1_RPL35A_ Homo sapiens ribosomal
                   protein L35a (RPL35A) mRNA
                    32102
 Seq. No.
                   268533 1.R1040
 Contig ID
                   hrw701057518.hl
 5'-most EST
                   BLASTN
Method
                    g28338
 NCBI GI
                    446
 BLAST score
                    0.0e + 00
 E value
```

545 Match length 96 % identity

Human mRNA for cytoskeletal gamma-actin NCBI Description

>gi\_4501886\_ref\_NM\_001614.1\_ACTG1\_ Homo sapiens actin,

gamma 1 (ACTG1) mRNA

32103 Seq. No.



Contig ID 268549\_1.R1040 5'-most EST hrw701057561.h1

Method BLASTN
NCBI GI g1702923
BLAST score 194
E value 1.0e-105
Match length 268
% identity 99

NCBI Description H.sapiens mRNA for p0071 protein

>gi 4505842\_ref\_NM\_003628.1\_PKP4\_ Homo sapiens plakophilin

4 (PKP4) mRNA

Seq. No. 32104

Contig ID 268568\_1.R1040 5'-most EST zsg701129207.h1

Method BLASTN
NCBI GI g4506742
BLAST score 429
E value 0.0e+00
Match length 429
% identity 100

NCBI Description Homo sapiens ribosomal protein S8 (RPS8) mRNA

Seq. No. 32105

Contig ID 268570\_1.R1040 5'-most EST hrw701057416.h1

Method BLASTN
NCBI GI g31101
BLAST score 287
E value 1.0e-160
Match length 287
% identity 100

NCBI Description H.sapiens mRNA for protein homologous to elongation factor 1-gamma from A.salina >gi\_4503480\_ref\_NM\_001404.1\_EEF1G\_

Homo sapiens eukaryotic translation elongation factor 1

gamma (EEF1G) mRNA

Seq. No. 32106

Contig ID 268615\_1.R1040 5'-most EST hrw701057504.h1

Method BLASTN
NCBI GI g598714
BLAST score 254
E value 1.0e-141
Match length 274
% identity 98

NCBI Description Human HepG2 3' region cDNA, clone hmd3b09

Seq. No. 32107

Contig ID 268619\_1.R1040 5'-most EST hrw701057510.h1

Method BLASTN
NCBI GI g188855
BLAST score 257
E value 1.0e-143
Match length 277
% identity 98



NCBI Description Human mitochondrial specific single stranded DNA binding

protein mRNA, complete cds.

>qi 4507230 ref\_NM 003143.1\_SSBP\_ Homo sapiens

single-stranded DNA-binding protein (SSBP), nuclear gene

encoding mitochondrial protein, mRNA

Seq. No. 32108

Contig ID 268642\_1.R1040

5'-most EST jC-gmle01810072a01d1

Method BLASTN
NCBI GI g1857236
BLAST score 393
E value 0.0e+00
Match length 505
% identity 94

NCBI Description Human p97 mRNA, complete cds

>gi\_4503538\_ref\_NM\_001418.1\_EIF4G2\_ Homo sapiens eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2) mRNA

Seq. No. 32109

Contig ID 268644 1.R1040 5'-most EST hrw701057542.h1

Method BLASTN
NCBI GI g4500180
BLAST score 248
E value 1.0e-137
Match length 264

Match length 264 % identity 98

NCBI Description Homo sapiens mRNA; cDNA DKFZp586N0318 (from clone

DKFZp586N0318)

Seq. No. 32110

Contig ID 268682 1.R1040 5'-most EST zsg701129177.h1

Method BLASTN
NCBI GI g23690
BLAST score 339
E value 0.0e+00
Match length 339
% identity 100

NCBI Description H.sapiens mRNA for 23 kD highly basic protein

Seq. No. 32111

Contig ID 268684\_1.R1040 5'-most EST hrw701057604.h1

Seq. No. 32112

Contig ID 268692 1.R1040 5'-most EST jC-gmfl02220073e01a1

Seq. No. 32113

Contig ID 268708\_1.R1040 5'-most EST kl1701212504.h1

Method BLASTX
NCBI GI g1076315
BLAST score 361
E value 1.0e-34



Match length 113 % identity

NCBI Description cytochrome P450 - Arabidopsis thaliana

>gi\_853719\_emb\_CAA60793\_ (X87367) CYP90 protein

[Arabidopsis thaliana] >gi\_871988\_emb\_CAA60794\_ (X87368)

CYP90 protein [Arabidopsis thaliana]

Seq. No. 32114

268869 1.R1040 Contig ID hrw701057915.h1 5'-most EST

Method BLASTX NCBI GI q2245006 BLAST score 155 E value 1.0e-10 Match length 83 % identity 45

(Z97341) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

32115

268870 1.R1040 Contig ID

5'-most EST uC-gmrominsoy276d09b1

Seq. No. 32116

268950 1.R1040 Contig ID 5'-most EST hrw701058033.h1

Seq. No. 32117

268983 1.R1040 Contig ID 5'-most EST hrw701058092,h1

Method BLASTN NCBI GI q1370187 BLAST score 230 E value 1.0e-126 Match length 354

% identity 92

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB7D

Seq. No. 32118

269005 1.R1040 Contig ID hrw701058205.h1 5'-most EST

Method BLASTX NCBI GI q2618684 BLAST score 183 E value 8.0e-14 Match length 61 % identity 57

NCBI Description (AC002510) putative

UDP-N-acetylglucosamine--dolichyl-phosphate

N-acetylglucosaminephosphotransferase [Arabidopsis

thaliana] >gi 3241947 (AC004625) putative UDP-N-acetylglucosamine--dolichyl-phosphate

N-acetylglucosaminephosphotransferase [Arabidopsis

thaliana]

Seq. No.

32119

269092 1.R1040 Contig ID hrw701058318,h1 5'-most EST



```
BLASTX
Method
                   g2342719
NCBI GI
BLAST score
                   141
                   6.0e-09
E value
Match length
                   87
% identity
                   39
NCBI Description (AC002341) SF16 protein isolog [Arabidopsis thaliana]
                   32120
Seq. No.
                   269096 1.R1040
Contig ID
                   hrw701058333.h1
5'-most EST
                   32121
Seq. No.
                   269119 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}68477.h1
Seq. No.
                   32122
                   269197 1.R1040
Contig ID
                   hrw701058652.h1
5'-most EST
                   32123
Seq. No.
Contig ID
                   269250 1.R1040
                   jC-gmro02910051e04d1
5'-most EST
                   BLASTX
Method
                   q3549660
NCBI GI
                   332
BLAST score
E value
                   9.0e-31
                   108
Match length
                   55
% identity
                   (AL031394) carbonate dehydratase - like protein
NCBI Description
                    [Arabidopsis thaliana]
                    32124
Seq. No.
                   269268 1.R1040
Contig ID
                   g5057717
5'-most EST
Seq. No.
                    32125
                    269308 1.R1040
Contig ID
                   hrw701\overline{0}58718.h1
 5'-most EST
                    BLASTX
Method
                    g3135269
NCBI GI
BLAST score
                    252
                    2.0e-21
E value
                    159
Match length
                    45
 % identity
                    (AC003058) unknown protein [Arabidopsis thaliana]
 NCBI Description
                    32126
 Seq. No.
                    269373 1.R1040
 Contig ID
                    hrw701061721.h1
 5'-most EST
                    BLASTX
 Method
                    g1769556
 NCBI GI
 BLAST score
                    415
```

4896

6.0e-41

NCBI Description (U81158) Forsythia x intermedia

101

81

E value

Match length

% identity



(+)-pinoresinol/(+)-lariciresinol reductase (PLR) protein, complete sequence [Forsythia x intermedia]

 Seq. No.
 32127

 Contig ID
 269382\_1.R1040

 5'-most EST
 hrw701058832.h1

 Method
 BLASTN

 NCBI GI
 g530206

 BLAST score
 40

 E value
 3.0e-13

E value 3.0e-1
Match length 112
% identity 84

NCBI Description Glycine max heat shock protein (SB100) mRNA, complete cds

Seq. No. 32128

Contig ID 269384\_1.R1040 5'-most EST hrw701058872.h1

Seq. No. 32129

Contig ID 269412\_1.R1040 5'-most EST jC-gmle01810059g06d1

Seq. No. 32130

Contig ID 269432\_1.R1040 5'-most EST hrw701059664.h1

Seq. No. Contig ID 5'-most EST 32131 269534 1.R1040 hrw701059062.h1

Seq. No.
Contig ID
5'-most EST

32132 269565\_1.R1040 epx701108592.h1

Seq. No.
Contig ID
5'-most EST

32133 269571 1.R1040 hrw701059110.h1

Seq. No.
Contig ID
5'-most EST

32134 269620\_1.R1040 zsq701120003.h1

Seq. No.
Contig ID
5'-most EST

32135 269627\_1.R1040 hrw701059195.h1

Seq. No.
Contig ID
5'-most EST

32136 269658\_1.R1040 zsg701117393.h1

Seq. No.
Contig ID
5'-most EST

32137 269674\_1.R1040 hrw701059296.h1

Seq. No.
Contig ID
5'-most EST

32138 269687 1.R1040 epx701105776.h1

4897

Contig ID

5'-most EST



```
Method
                  q4220515
NCBI GI
                  451
BLAST score
                  6.0e-45
E value
                  153
Match length
                  57
% identity
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                  32139
Seq. No.
                  269695 1.R1040
Contig ID
                  uC-gmflminsoy080h10b1
5'-most EST
                  BLASTX
Method
                   q2832629
NCBI GI
                   349
BLAST score
                   2.0e-32
E value
                   251
Match length
% identity
NCBI Description (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis
                   thaliana]
                   32140
Seq. No.
                   269751 1.R1040
Contig ID
                   jsh701\overline{0}69189.h1
5'-most EST
                   BLASTX
Method
                   g2244910
NCBI GI
                   144
BLAST score
                   1.0e-09
E value
                   52
Match length
% identity
NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]
                   32141
Seq. No.
                   269824 1.R1040
Contig ID
                   ish701064879.hl
5'-most EST
                   BLASTX
Method
                   g101065
NCBI GI
                   139
BLAST score
                   1.0e-08
E value
                   95
Match length
 % identity
NCBI Description rad4 protein - fission yeast (Schizosaccharomyces pombe)
 Seq. No.
                   32142
 Contig ID
                   269837 1.R1040
                   hrw701059564.h1
 5'-most EST
                   BLASTX
Method
                   q4249385
 NCBI GI
                    247
 BLAST score
 E value
                    2.0e-21
 Match length
                    67
 % identity
                   (AC005966) T2K10.11 [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    32143
```

269879 1.R1040

hrw701059615.hl



```
Seq. No. 32144
Contig ID 269899_1.R1040
5'-most EST jC-gmro02910046g05d1
Seq. No. 32145
Contig ID 270055 1.R1040
```

5'-most EST g5753406

Method BLASTN

NCBI GI g347456

BLAST score 73

E value 1.0e-32

Match length 250

% identity 17

NCBI Description Soybean hydroxyproline-rich glycoprotein (sbHRGP1) mRNA,

partial cds

270136 1.R1040

Seq. No. 32146

Contig ID

5'-most EST asn701133623.h2
Method BLASTX
NCBI GI g2281647
BLAST score 216
E value 1.0e-17
Match length 83

Match length 83 % identity 52

NCBI Description (AF003104) AP2 domain containing protein RAP2.11

[Arabidopsis thaliana]

Seq. No. 32147

Contig ID 270183\_1.R1040

NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein

[Nicotiana tabacum]

Seq. No. 32148

Contig ID 270203 1.R1040

5'-most EST uC-gmflminsoy036g08b1

Seq. No. 32149

Contig ID 270224\_1.R1040 5'-most EST jC-gmle01810028d01d1

Method BLASTX
NCBI GI g3047118
BLAST score 170
E value 5.0e-12
Match length 47
% identity 72

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 32150

Contig ID 270250 1.R1040

4899



```
5'-most EST
                  hrw701060156.hl
                  BLASTX
Method
                  g3269301
NCBI GI
BLAST score
                  216
E value
                  1.0e-34
Match length
                  125
% identity
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                  32151
Seq. No.
Contig ID
                  270270 1.R1040
                  jC-gmf102220138d06d1
5'-most EST
                  BLASTN
Method
                  q170059
NCBI GI
BLAST score
                  200
E value
                  1.0e-108
Match length
                  290
% identity
                  95
                  Soybean (G.max L.) beta-tubulin (S-beta-1) gene, complete
NCBI Description
                  32152
Seq. No.
                  270275 1.R1040
Contig ID
                  epx701104266.hl
5'-most EST
                  BLASTX
Method
                  g4006868
NCBI GI
BLAST score
                  187
                   4.0e-14
E value
                  43
Match length
% identity
                  (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32153
Contig ID
                   270319 1.R1040
5'-most EST
                  hrw701060263.hl
Method
                  BLASTX
NCBI GI
                   g3242077
BLAST score
                   275
                   1.0e-24
E value
Match length
                   77
% identity
                   (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]
NCBI Description
                   32154
Seq. No.
                   270589 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910071e12a1
Seq. No.
                   32155
                   270613 1.R1040
Contig ID
                   uC-gmropic050e07b1
5'-most EST
Seq. No.
                   32156
```

Contig ID 270712 1.R1040 5'-most EST hrw701063328.h1

Seq. No. 32157

Contig ID 270784 1.R1040



5'-most EST hrw701060856.h1

Method BLASTX
NCBI GI g3128210
BLAST score 183
E value 7.0e-14
Match length 56
% identity 68

NCBI Description (AC004077) putative cytochrome P450 protein [Arabidopsis

thaliana] >gi\_3337378 (AC004481) putative cytochrome P450

protein [Arabidopsis thaliana]

Seq. No. 32158

Contig ID 270990 1.R1040

5'-most EST uC-gmrominsoy0001b04a1

Seq. No. 32159

Contig ID 271051\_1.R1040 5'-most EST asn701137356.h1

Method BLASTX
NCBI GI g4522004
BLAST score 190
E value 1.0e-14
Match length 53
% identity 70

NCBI Description (AC007069) putative histidine kinase, sensory transduction

[Arabidopsis thaliana]

Seq. No. 32160

Contig ID 271120 1.R1040 5'-most EST hrw701061322.h1

Seq. No. 32161

Contig ID 271141\_1.R1040 5'-most EST hrw701061352.h1

Seq. No. 32162

Contig ID 271153 1.R1040 5'-most EST hrw701061372.h1

Method BLASTX
NCBI GI g3068704
BLAST score 414
E value 9.0e-41
Match length 118
% identity 66

NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 32163

Contig ID 271235\_1.R1040 5'-most EST hrw701061486.h1

Seq. No. 32164

Contig ID 271286\_1.R1040 5'-most EST kl1701202348.h1

Method BLASTX
NCBI GI g119095
BLAST score 187
E value 2.0e-14



Match length 67 % identity 57

NCBI Description EMBRYONIC ABUNDANT PROTEIN PRECURSOR (CLONE USP LAMBDA VF30.1) >gi\_82003\_pir\_\_S05471 embryonic abundant protein

precursor (clone USP Vf30.1) - tick bean

Seq. No. 32165

Contig ID 271305\_1.R1040 5'-most EST hrw701061582.h1

Seq. No. 32166

Contig ID 271365 1.R1040

5'-most EST jC-gmro02910043q10d1

Method BLASTX
NCBI GI 94249409
BLAST score 251
E value 2.0e-21
Match length 91
% identity 52

NCBI Description (AC006072) putative sugar transporter [Arabidopsis

thaliana]

Seq. No. 32167

Contig ID 271380\_1.R1040 5'-most EST kl1701210123.h1

Method BLASTX
NCBI GI g3746063
BLAST score 170
E value 6.0e-12
Match length 54
% identity 57

NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 32168

Contig ID 271465\_1.R1040 5'-most EST asn701136564.h1

Seq. No. 32169

Contig ID 271592 1.R1040 5'-most EST hrw701062573.h1

Seq. No. 32170

Contig ID 271607 1.R1040 5'-most EST hrw701062009.h1

Seq. No. 32171

Contig ID 271697 1.R1040

5'-most EST uC-gmrominsoy027f11b1

Seq. No. 32172

Contig ID 271757 1.R1040 5'-most EST jC-gmst02400072g10d1

Method BLASTX

NCBI GI g3935173 BLAST score 271 E value 3.0e-24 Match length 74



% identity 64

NCBI Description (AC004557) F17L21.16 [Arabidopsis thaliana]

Seq. No. 32173

Contig ID 271773 1.R1040 5'-most EST hrw701062261.h1

Method BLASTN
NCBI GI g408793
BLAST score 270
E value 1.0e-150
Match length 278

Match length 278 % identity 99

NCBI Description Glycine soja chloroplast 3-omega faty acid desaturase

(Fad3) mRNA, complete cds

Seq. No. 32174

Contig ID 271883 1.R1040 5'-most EST hrw701062821.h1

Method BLASTX
NCBI GI g4262176
BLAST score 159
E value 3.0e-14
Match length 53
% identity 75

NCBI Description (AC005508) 18857 [Arabidopsis thaliana]

Seq. No. 32175

Contig ID 271990\_1.R1040 5'-most EST hrw701062572.h1

Method BLASTX
NCBI GI g4510385
BLAST score 337
E value 1.0e-31
Match length 96
% identity 67

NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 32176

Contig ID 272015\_1.R1040 5'-most EST hrw701062609.h1

Seq. No. 32177

Contig ID 272032\_1.R1040

5'-most EST jC-gmro02800032f03a1

Seq. No. 32178

Contig ID 272062 1.R1040 5'-most EST jsh701066162.h1

Seq. No. 32179

Contig ID 272086\_1.R1040 5'-most EST hrw701062718.h1

Method BLASTX
NCBI GI g3355484
BLAST score 206
E value 1.0e-29
Match length 134



% identity 56

NCBI Description (AC004218) putative geranylgeranyl transferase type I beta subunit [Arabidopsis thaliana]

Seq. No. 32180

Contig ID 272092\_1.R1040 5'-most EST hrw701062734.h1

Method BLASTX
NCBI GI g1931654
BLAST score 338
E value 6.0e-38
Match length 134
% identity 61

NCBI Description (U95973) BRCA1-associated RING domain protein isolog

[Arabidopsis thaliana]

Seq. No. 32181

Contig ID 272131\_1.R1040 5'-most EST hrw701062820.h1

Seq. No. 32182

Contig ID 272154\_1.R1040 5'-most EST uC-gmropic038a06b1

Seq. No. 32183

Contig ID 272196\_1.R1040 5'-most EST hrw701062910.h1

Method BLASTX
NCBI GI g2373405
BLAST score 223
E value 3.0e-18
Match length 124
% identity 10

NCBI Description (D85194) no known genes showing a high homology to 4B-1

clone sequence were found in the EMBL database. Orf was 640 amino acid long and contained a proline and alanine repeat

[Arabidopsis thaliana]

Seq. No. 32184

Contig ID 272212\_1.R1040 5'-most EST asn701140314.h1

Seq. No.

32185

Contig ID 272247 1.R1040 5'-most EST kl1701207262.h1

Seq. No.

32186

Contig ID 272272\_1.R1040 5'-most EST asn701134541.h1

Method BLASTX
NCBI GI g3559816
BLAST score 297
E value 6.0e-27
Match length 78
% identity 72

NCBI Description (Y15782) transketolase 2 [Capsicum annuum]



```
Seq. No.
                   32187
Contig ID
                   272325 1.R1040
5'-most EST
                   hrw701063082.h1
Method
                   BLASTX
NCBI GI
                   q3047096
BLAST score
                   585
E value
                   1.0e-60
Match length
                   143
% identity
                   77
                   (AF058826) similar to eukaryotic protein kinase domains
NCBI Description
                   (Pfam: pkinase.hmm, score: 189.74) [Arabidopsis thaliana]
Seq. No.
                   32188
Contig ID
                   272377 1.R1040
5'-most EST
                   jC-gmro02910065c08d1
Method
                   BLASTX
NCBI GI
                   q1370174
BLAST score
                   271
E value
                   9.0e-24
Match length
                   63
% identity
                   79
NCBI Description (Z73936) RAB1Y [Lotus japonicus]
Seq. No.
                   32189
Contig ID
                   272394_1.R1040
5'-most EST
                   jC-gmst02400077h05d1
Method
                   BLASTX
NCBI GI
                   q3395432
BLAST score
                   286
E value
                   1.0e-25
Match length
                   63
% identity
                   83
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                   32190
Contig ID
                   272486 1.R1040
5'-most EST
                  hrw701063284.h1
Seq. No.
                   32191
Contig ID
                  272534 2.R1040
5'-most EST
                  kl1701211827.h1
Method
                  BLASTX
NCBI GI
                  g3337367
BLAST score
                  128
E value
                  6.0e-17
Match length
                  77
% identity
NCBI Description
                  (AC004481) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  32192
Contig ID
                  272641 1.R1040
```

Contig ID 272641\_1.R1040 5'-most EST jsh701065193.h1

Seq. No. 32193

Contig ID 272710 1.R1040 5'-most EST hrw701063586.h1 BLASTX



NCBI GI g4262183 BLAST score 246 E value 7.0e-38 Match length 111 % identity 70

NCBI Description (AC005508) 51434 [Arabidopsis thaliana]

Seq. No. 32194

Contig ID 272812\_1.R1040 5'-most EST jC-gmro02910020g11d1

Seq. No. 32195

Contig ID 272814\_1.R1040 5'-most EST dkc700967938.h1

Method BLASTX
NCBI GI g2435395
BLAST score 423
E value 2.0e-41
Match length 146
% identity 62

NCBI Description (U63550) pectate lyase [Fragaria x ananassa]

Seq. No. 32196

Contig ID 272818 1.R1040

5'-most EST uC-gmflminsoy070c11b1

Method BLASTX
NCBI GI g3687248
BLAST score 307
E value 5.0e-28
Match length 90
% identity 59

NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32197

Contig ID 272830\_1.R1040

5'-most EST jC-gmst02400077d05a1

Seq. No. 32198

Contig ID 273000 1.R1040 5'-most EST jsh701063793.h1

Seq. No. 32199

Contig ID 273098\_1.R1040 5'-most EST kl1701202633.h1

Seq. No. 32200

Contig ID 273108\_1.R1040 5'-most EST jsh701063934.h1

Method BLASTX
NCBI GI g2829925
BLAST score 458
E value 8.0e-46
Match length 131
% identity 66

NCBI Description (AC002291) Similar to dnaj-like protein, gp\_Y11969\_2230757

[Arabidopsis thaliana]



```
Seq. No.
                    273183 1.R1040
Contig ID
5'-most EST
                    jsh701\overline{0}64044.h1
Method
                    BLASTX
NCBI GI
                    q571484
BLAST score
                    359
E value
                    1.0e-34
Match length
                    84
% identity
                    85
NCBI Description
                   (U16727) peroxidase precursor [Medicago truncatula]
Seq. No.
                    32202
Contig ID
                    273229 1.R1040
5'-most EST
                    jsh701\overline{0}64102.h1
Method
                   BLASTX
NCBI GI
                   q3201541
BLAST score
                   148
E value
                    9.0e-10
Match length
                   31
% identity
                   77
NCBI Description (AJ005077) TCTR2 protein [Lycopersicon esculentum]
Seq. No.
                   32203
Contig ID
                   273375 1.R1040
                   jsh701\overline{0}65331.h1
5'-most EST
Seq. No.
                   32204
Contig ID
                   273443 1.R1040
5'-most EST
                   uC-gmflminsoy010c03b1
Seq. No.
                   32205
Contig ID
                   273451 2.R1040
5'-most EST
                   jsh701065694.h1
Method
                   BLASTX
NCBI GI
                   g4262173
BLAST score
                   211
E value
                   3.0e-17
Match length
                   82
% identity
                   59
NCBI Description (AC005508) 3975 [Arabidopsis thaliana]
Seq. No.
                   32206
Contig ID
                   273492 1.R1040
5'-most EST
                   jC-gmf102220068d02a1
Seq. No.
                   32207
Contig ID
                   273547 1.R1040
5'-most EST
                   jC-gmf102220050f07d1
```

Seq. No. 32208

Contig ID 273621 1.R1040 5'-most EST zsq701125691.h1

Seq. No. 32209

Contig ID 273637 1.R1040

5'-most EST g5508930

```
Seq. No.
                   32210
Contiq ID
                   273793 1.R1040
5'-most EST
                   uC-gmrominsoy261e02b1
Seq. No.
                   32211
Contig ID
                   273816 1.R1040
5'-most EST
                   g4437099
Seq. No.
                   32212
Contig ID
                   273847 1.R1040
5'-most EST
                   q4396069
Seq. No.
                   32213
Contig ID
                   273853 1.R1040
5'-most EST
                   jsh701065028.h1
Seq. No.
                   32214
Contig ID
                   273854 1.R1040
5'-most EST
                   g5688430
Method
                   BLASTX
NCBI GI
                   g625241
BLAST score
                   147
E value
                   2.0e-15
Match length
                   72
% identity
                   56
NCBI Description
                   inorganic pyrophosphatase (EC 3.6.1.1) - yeast
                   (Saccharomyces cerevisiae) >gi_536206_emb_CAA84949
                   (Z35880) ORF YBR011c [Saccharomyces cerevisiae]
Seq. No.
                   32215
                   273935 1.R1040
Contig ID
5'-most EST
                   jsh701065338.h1
Seq. No.
                   32216
Contig ID
                   273947 1.R1040
5'-most EST
                  jC-gmro02910037b11a1
Seq. No.
                  32217
Contig ID
                  273950 1.R1040
5'-most EST
                  jC-gmro02910049c05d1
Seq. No.
                  32218
Contig ID
                  274011 1.R1040
                  g5508929
                  BLASTN
                  g255580
                  378
```

5'-most EST Method NCBI GI BLAST score E value 0.0e+00Match length 398 % identity 99

NCBI Description small auxin up RNA gene cluster: orf 10A5 [Glycine max=soybeans, cv. Wayne, Genomic, 646 nt]

Seq. No. 32219 Contig ID

274061 1.R1040 5'-most EST  $jsh701\overline{0}65493.h1$ 

Method BLASTX



```
NCBI GI
                   q3540207
BLAST score
                   243
E value
                   6.0e-21
Match length
                   73
                   60
% identity
NCBI Description
                  (AC004260) Putative protein kinase [Arabidopsis thaliana]
                   32220
Seq. No.
Contig ID
                   274108 1.R1040
5'-most EST
                   jsh701\overline{0}65431.h1
Method
                   BLASTN
NCBI GI
                   g348719
BLAST score
                   83
                   1.0e-38
E value
Match length
                   211
% identity
                   85
NCBI Description
                  MtNMedicago truncatula protochlorophyllide reductase
                   homolgue mRNA, complete cds
Seq. No.
                   32221
                   274322 1.R1040
Contig ID
5'-most EST
                   zsg701121638.hl
Seq. No.
                   32222
Contig ID
                   274338 1.R1040
5'-most EST
                   jsh701065764.h1
                   32223
Seq. No.
Contig ID
                   274344 1.R1040
5'-most EST
                   jsh701\overline{0}65774.h1
Method
                   BLASTX
NCBI GI
                   q730832
BLAST score
                   142
E value
                   1.0e-08
Match length
                   51
% identity
                   59
NCBI Description 8.4 KD SULFUR-RICH PROTEIN PRECURSOR (SE60 PROTEIN)
                   (PROBABLE PROTEINASE INHIBITOR P322) >gi_99949_pir__S24965
                   probable proteinase inhibitor (Bowman-Birk) p322 - soybean
                   >gi 18748 emb CAA78359 (Z13956) a protein similar to
                   potato tuber protein p322 homolgous to Bowman-Birk
                   Proteinase Inhibitor [Glycine max]
Seq. No.
                   32224
                   274361 1.R1040
Contig ID
5'-most EST
                   jsh701065804.h1
Method
                   BLASTX
NCBI GI
                   q3834306
BLAST score
                   152
                   8.0e-10
E value
Match length
                   36
```

69 % identity

(AC005679) EST gb\_R65024 comes from this gene. [Arabidopsis NCBI Description

thaliana]

32225 Seq. No.

274433\_1.R1040 Contig ID



```
jC-gmle01810044b10a1
5'-most EST
Seq. No.
                  32226
Contig ID
                  274480 1.R1040
5'-most EST
                  jsh701065988.hl
Method
                  BLASTX
NCBI GI
                  q3184285
BLAST score
                  178
E value
                  9.0e-13
Match length
                  78
% identity
NCBI Description (AC004136) hypothetical protein [Arabidopsis thaliana]
                  32227
Seq. No.
Contig ID
                  274535 1.R1040
5'-most EST
                  kwa701015687.hl
Seq. No.
                  32228
                  274623 1.R1040
Contig ID
5'-most EST
                  jsh701066228.h1
                  BLASTX
Method
NCBI GI
                  g2244732
BLAST score
                  185
                  9.0e-14
E value
Match length
                  69
                  48
% identity
NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
                  32229
Seq. No.
Contig ID
                  274653 1.R1040
5'-most EST
                  jsh701066272.hl
Seq. No.
                  32230
                  274795 1.R1040
Contiq ID
5'-most EST
                  jC-gmro02910072c05a1
                  32231
Seq. No.
                  274810 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910070b12a1
                  32232
Seq. No.
                  274867_1.R1040
Contig ID
5'-most EST
                  jsh701066587.h1
                   32233
Seq. No.
                  274955 1.R1040
Contig ID
5'-most EST
                  zsg701118382.hl
                  BLASTX
Method
                   g2252632
NCBI GI
BLAST score
                   339
E value
                   6.0e-32
                  92
Match length
% identity
                   64
```

Seq. No. 32234

Contig ID 274968 1.R1040

NCBI Description (U95973) Barley Mlo protein isolog [Arabidopsis thaliana]



```
jC-gmle01810091f09a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2864618
BLAST score
                  231
                  3.0e-19
E value
Match length
                  85
% identity
                  53
                  (AL021811) putative protein [Arabidopsis thaliana]
NCBI Description
                  32235
Seq. No.
                  275067 1.R1040
Contig ID
                  jsh701066875.hl
5'-most EST
Seq. No.
                  32236
Contig ID
                  275072 1.R1040
                  jC-qmle01810043a10a1
5'-most EST
                  BLASTX
Method
                  q3096947
NCBI GI
                  186
BLAST score
                  8.0e-14
E value
Match length
                  83
                  54
% identity
                  (Y16327) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
                  32237
Seq. No.
                  275094 1.R1040
Contig ID
                  jsh701\overline{0}66921.h1
5'-most EST
                  32238
Seq. No.
                  275196 1.R1040
Contig ID
5'-most EST
                  jsh701067139.hl
                   32239
Seq. No.
Contig ID
                   275270 1.R1040
5'-most EST
                  zsg701122675.h1
Method
                  BLASTX
                  q3281868
NCBI GI
                   216
BLAST score
E value
                   9.0e-18
Match length
                   48
                   92
% identity
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
Seq. No.
                   32240
                   275366 1.R1040
Contig ID
5'-most EST
                   fC-qmse700754068d2
                   BLASTX
Method
NCBI GI
                   q3785996
BLAST score
                   334
E value
                   1.0e-35
Match length
                   125
% identity
                  (AC005499) putative annexin [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 32241

Contig ID 275367\_1.R1040



uC-qmflminsoy072f04b1 5'-most EST BLASTX Method q3367571 NCBI GI BLAST score 360 3.0e-34 E value 116 Match length % identity 61 (AL031135) putative protein [Arabidopsis thaliana] NCBI Description 32242 Seq. No. 275435 1.R1040 Contig ID 5'-most EST jsh701067638.h1 Seq. No. 32243 Contig ID 275456 1.R1040 5'-most EST jsh701067739.h1 Seq. No. 32244 Contig ID 275490 1.R1040 5'-most EST jsh701068418.hl Seq. No. 32245 Contig ID 275579 1.R1040 jC-gmf102220054f05d1 5'-most EST Method BLASTX NCBI GI g1946355 BLAST score 171 E value 4.0e-12 Match length 88 % identity 42 (U93215) maize transposon MuDR mudrA protein isolog NCBI Description [Arabidopsis thaliana] >gi 2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana] 32246 Seq. No. 275588\_1.R1040 Contig ID 5'-most EST uC-gmflminsoy064g11b1 BLASTX Method g3452263 NCBI GI 734 BLAST score 4.0e-78 E value 150 Match length % identity (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis NCBI Description thaliana] Seq. No. 32247 275600 1.R1040 Contig ID 5'-most EST jC-gmro02910023f06d1 Method BLASTX NCBI GI q4240122

Method BLASTX
NCBI GI g4240122
BLAST score 291
E value 2.0e-26
Match length 89
% identity 53

NCBI Description (AB007802) cytochrome b5 [Arabidopsis thaliana]



```
Seq. No.
                   32248
                   275623 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910064c02a1
                   BLASTX
Method
                   g1082054
NCBI GI
BLAST score
                   179
                   4.0e-13
E value
Match length
                   87
% identity
                   37
                  (Z49859) copper transporter protein [Arabidopsis thaliana]
NCBI Description
                   32249
Seq. No.
                   275677 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910019d06d1
                   32250
Seq. No.
Contig ID
                   275689 1.R1040
5'-most EST
                   jsh701068243.h1
Method
                   BLASTX
NCBI GI
                   q1575699
BLAST score
                   541
                   1.0e-55
E value
Match length
                   125
                   82
% identity
NCBI Description
                  (U70478) putative leucoanthocyanidin dioxygenase
                   [Arabidopsis thaliana] >gi_3292813_emb_CAA19803_ (AL031018)
                   putative leucoanthocyanidin dioxygenase (LDOX) [Arabidopsis
                   thaliana]
                   32251
Seq. No.
                   275701 1.R1040
Contig ID
                   jsh701\overline{0}68263.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2129854
                   178
BLAST score
E value
                   2.0e-14
Match length
                   63
% identity
                   57
NCBI Description early nodulin 8 precursor - alfalfa >gi_304037 (L18899)
                   early nodulin [Medicago sativa]
Seq. No.
                   32252
                   275895 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}68541.h1
                   32253
Seq. No.
Contig ID
                   275898 1.R1040
5'-most EST
                   zsq701121326.h1
Method
                   BLASTN
NCBI GI
                   q2618600
```

Method BLASTN
NCBI GI g2618600
BLAST score 37
E value 2.0e-11
Match length 41
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDC12, complete sequence [Arabidopsis thaliana]



Seq. No. 32254 Contig ID

276134·1.R1040 jsh701068942.h1 5'-most EST

BLASTX Method q2435406 NCBI GI BLAST score 284 2.0e-25 E value Match length 123 53 % identity

(U83490) thaumatin-like protein [Arabidopsis thaliana] NCBI Description

32255 Seq. No.

276694 1.R1040 Contig ID 5'-most EST jsh701069816.hl

BLASTX Method NCBI GI q4218120 326 BLAST score 4.0e-30 E value Match length 75 % identity 77

(AL035353) Proline-rich APG-like protein [Arabidopsis NCBI Description

thaliana]

32256 Seq. No.

Contig ID 276694 2.R1040 jC-gmst02400006g10d1 5'-most EST

Method BLASTX g4218120 NCBI GI BLAST score 371 E value 1.0e-35 92 Match length 72 % identity

(AL035353) Proline-rich APG-like protein [Arabidopsis NCBI Description

thaliana]

32257 Seq. No.

Contig ID 276713 1.R1040

g5605703 5'-most EST Method BLASTX NCBI GI q3341694 244 BLAST score 2.0e-20 E value Match length 116 % identity 44

NCBI Description (AC003672) PREG-like protein [Arabidopsis thaliana]

32258 Seq. No.

Contig ID 276867 1.R1040 5'-most EST jsh701070084.h2 Method BLASTX

NCBI GI q746487 BLAST score 185 E value 8.0e-14 Match length 76

% identity 45

(U23514) No definition line found [Caenorhabditis elegans] NCBI Description



Seq. No. 32259

Contig ID 276986\_1.R1040 5'-most EST jC-gmst02400004d04d1

Method BLASTX
NCBI GI g1354849
BLAST score 281
E value 5.0e-25
Match length 77
% identity 66

NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No. 32260

Contig ID 277132\_1.R1040 5'-most EST jsh701070426.h1

Method BLASTX
NCBI GI g4218144
BLAST score 287
E value 2.0e-25
Match length 88
% identity 60

NCBI Description (AJ132398) glutathione transferase, GST 10b [Arabidopsis

thaliana]

Seq. No. 32261

Contig ID 277244\_1.R1040 5'-most EST ekl700968205.h1

Method BLASTX
NCBI GI g4539394
BLAST score 139
E value 8.0e-09
Match length 78
% identity 12

NCBI Description (AL035526) putative protein [Arabidopsis thaliana]

Seq. No. 32262

Contig ID 277333\_1.R1040 5'-most EST kl1701202324.h1

Seq. No. 32263

Contig ID 277349 1.R1040 5'-most EST kll701202346.h1

Method BLASTX
NCBI GI g542058
BLAST score 186
E value 2.0e-14
Match length 47
% identity 68

NCBI Description HSR203J protein - common tobacco >gi 444002 emb CAA54393\_

(X77136) HSR203J [Nicotiana tabacum]

Seq. No. 32264

Contig ID 277354\_1.R1040 5'-most EST kl1701202353.h1

Seq. No. 32265

Contig ID 277441 1.R1040

5'-most EST jC-gmf102220142g03a1

```
32266
Seq. No.
                   277447 1.R1040
Contig ID
                   kl1701213720.hl
5'-most EST
Method
                   BLASTX
                   g3859592
NCBI GI
BLAST score
                   267
                   1.0e-23
E value
Match length
                   73
                   73
% identity
                   (AF104919) contains similarity to expansins [Arabidopsis
NCBI Description
                   thaliana]
                   32267
Seq. No.
Contig ID
                   277568 1.R1040
5'-most EST
                   kl1701207518.h1
Method
                   BLASTX
                   g4056506
NCBI GI
BLAST score
                   140
E value
                   9.0e-09
Match length
                   75
% identity
                   36
                  (AC005896) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32268
Contig ID
                   277591 1.R1040
                   kl1701202657.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1076274
                   183
BLAST score
                   7.0e-14
E value
Match length
                   53
                   62
% identity
                   cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)
NCBI Description
Seq. No.
                   32269
                   277674 1.R1040
Contig ID
5'-most EST
                   kl1701202770.h1
                   32270
Seq. No.
Contig ID
                   277677 1.R1040
                   k11701\overline{2}02774.h1
5'-most EST
                   32271
Seq. No.
                   277743 1.R1040
Contig ID
                   k11701202883.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2191137
BLAST score
                   290
E value
                   2.0e-26
Match length
                   77
```

% identity NCBI Description

(AF007269) similar to the GDSL family of lipolytic enzymes

[Arabidopsis thaliana]

Seq. No.

Contig ID 277750 1.R1040

69

32272

Seq. No. Contig ID



```
kl1701202993.h1
5'-most EST
Seq. No.
                   32273
                   277767 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}02917.h1
                   BLASTX
Method
                   g1669591
NCBI GI
BLAST score
                   361
                   9.0e-35
E value
Match length
                   90
% identity
                   73
                  (D88742) O-methyltransferase [Glycyrrhiza echinata]
NCBI Description
                   32274
Seq. No.
                   277777_1.R1040
Contig ID
                   kl1701202933.h1
5'-most EST
                   BLASTX
Method
                   q3688284
NCBI GI
                   232
BLAST score
                   1.0e-19
E value
Match length
                   89
                   51
% identity
                  (AJ011567) lanatoside 15'-O-acetylesterase [Digitalis
NCBI Description
                   lanata]
                   32275
Seq. No.
                   277801 1.R1040
Contig ID
                   g5753444
5'-most EST
Method
                   BLASTX
                   g2832625
NCBI GI
BLAST score
                   152
                   1.0e-12
E value
                   91
Match length
% identity
                   56
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                   32276
Seq. No.
                   277804 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}05008.h1
                   32277
Seq. No.
                   277817 1.R1040
Contig ID
5'-most EST
                   kl1701209742.h1
                   BLASTX
Method
NCBI GI
                   g4056403
BLAST score
                   343
                   3.0e-32
E value
Match length
                   124
% identity
                   56
NCBI Description
                  (AD001673) lipoxygenase [Persea americana]
Seq. No.
                   32278
                   277844 1.R1040
Contig ID
5'-most EST
                   zsg701130384.hl
```

32279 277877 1.R1040

4917



```
kl1701203134.h1
5'-most EST
Seq. No.
                   32280
Contig ID
                   277878 1.R1040
5'-most EST
                  kl1701203123.h1
                   32281
Seq. No.
Contig ID
                   277893 1.R1040
5'-most EST
                  kl1701214961.h1
Seq. No.
                   32282
Contig ID
                   278003 1.R1040
5'-most EST
                  k11701\overline{2}12941.h1
Seq. No.
                   32283
Contig ID
                   278011 1.R1040
                   uC-gmrominsoy066a05b1
5'-most EST
Method
                   BLASTX
                  q2262177
NCBI GI
BLAST score
                   485
                   1.0e-48
E value
Match length
                   214
% identity
                  (AC002329) hypothetical protein similar to T18A10.3
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   32284
Contig ID
                   278018 1.R1040
5'-most EST
                   kl1701203338.h1
Method
                   BLASTX
NCBI GI
                   q4204277
BLAST score
                   409
E value
                   3.0e-40
Match length
                   98
% identity
NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]
                   32285
Seq. No.
                   278040 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800043a11a1
Method
                   BLASTX
                   g2655098
NCBI GI
BLAST score
                   360
E value
                   3.0e-34
Match length
                   108
% identity
                   63
                  (AF023472) peptide transporter [Hordeum vulgare]
NCBI Description
```

Seq. No. 32286

Contig ID 278093 1.R1040 5'-most EST kl1701212102.h1

Method BLASTX
NCBI GI g4538930
BLAST score 306
E value 4.0e-28
Match length 99
% identity 63



```
(ALO49483) putative peroxidase [Arabidopsis thaliana]
NCBI Description
                  32287
Seq. No.
                  278112 1.R1040
Contig ID
5'-most EST
                  uC-gmropic093g12b1
Method
                  BLASTX
NCBI GI
                  q3548806
                  379
BLAST score
                  2.0e-36
E value
Match length
                  148
                   47
% identity
                  (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                   32288
Seq. No.
                   278116 1.R1040
Contig ID
                   jC-gmro02910071a12a1
5'-most EST
                   BLASTX
Method
                   g2262111
NCBI GI
BLAST score
                   528
                   8.0e-54
E value
                   178
Match length
                   59
% identity
                  (AC002343) ribitol dehydrogenase isolog [Arabidopsis
NCBI Description
                   thaliana]
                   32289
Seq. No.
                   278120 1.R1040
Contig ID
                   k11701212133.h1
5'-most EST
                   32290
Seq. No.
                   278124 1.R1040
Contig ID
                   kl1701203501.h2
5'-most EST
Seq. No.
                   32291
                   278157 1.R1040
Contig ID
                   uC-qmflminsoy057f04b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3201617
                   281
BLAST score
                   6.0e-25
E value
                   82
Match length
% identity
NCBI Description
                   (AC004669) hypothetical protein [Arabidopsis thaliana]
                   32292
Seq. No.
                   278162 1.R1040
Contig ID
                   k11701204108.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2443890
BLAST score
                   221
                   2.0e-18
E value
```

NCBI Description

Match length

% identity

Seq. No.

32293

52

73

(AC002294) similar to NAM (gp\_X92205\_1321924) and CUC2

(gp\_AB002560\_1944132) proteins [Arabidopsis thaliana]



```
278178 1.R1040
Contig ID
5'-most EST
                  kl1701203571.h2
Method
                  BLASTX
NCBI GI
                  q1421741
BLAST score
                   330
E value
                   4.0e-31
                  86
Match length
                  74
% identity
                  (U54770) cytochrome P450 homolog [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   32294
Contig ID
                   278242 1.R1040
5'-most EST
                  jC-gmro02910036e04d1
                  BLASTX
Method
                  g2506139
NCBI GI
BLAST score
                   217
                  1.0e-17
E value
Match length
                   61
                   67
% identity
                  COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
NCBI Description
                   (ARCHAIN) >gi 1314049 emb CAA91901 (Z67962)
                  archain/delta-COP [Oryza sativa]
                   32295
Seq. No.
                   278295 1.R1040
Contig ID
5'-most EST
                   q5058190
Method
                  BLASTX
NCBI GI
                   q4262226
BLAST score
                   268
E value
                   2.0e-23
Match length
                   140
% identity
NCBI Description
                  (AC006200) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   32296
Contig ID
                   278332 1.R1040
5'-most EST
                   kl1701203793.h2
Method
                   BLASTX
NCBI GI
                   g3641865
BLAST score
                   493
E value
                   6.0e-50
Match length
                   131
% identity
                   70
                  (AJ011010) beta-galactosidase [Cicer arietinum]
NCBI Description
Seq. No.
                   32297
                   278335 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}03881.h1
                   32298
Seq. No.
Contig ID
                   278394 1.R1040
```

Method BLASTX
NCBI GI g3249103
BLAST score 347
E value 8.0e-33
Match length 134



% identity NCBI Description (AC003114) Contains similarity to membrane-associated salt-inducible protein homolog TM021B04.10 gb 2191192 from A. thaliana BAC gb AF007271. [Arabidopsis thaliana] 32299 Seq. No. 278470 1.R1040 Contig ID jC-qmro02910005a11d1 5'-most EST Method BLASTX NCBI GI g3193284 BLAST score 285 2.0e-25 E value 70 Match length % identity 76 (AF069298) No definition line found [Arabidopsis thaliana] NCBI Description Seq. No. 32300 Contig ID 278512 1.R1040 5'-most EST kl1701204057.hl Seq. No. 32301 Contia ID 278535 1.R1040 5'-most EST kl1701204114.h1 Method BLASTX NCBI GI q867691 BLAST score 210 E value 5.0e-17 Match length 84 % identity 49 (M19735) beta-hexosaminidase beta-subunit [Homo sapiens] NCBI Description Seq. No. 32302 278571 1.R1040 Contig ID 5'-most EST zsq701121108.hl Seq. No. 32303 Contig ID 278574 1.R1040 5'-most EST kl1701204184.h1 Method BLASTX NCBI GI g3360289 BLAST score 429 E value 3.0e-42 Match length 164 52 % identity (AF023164) leucine-rich repeat transmembrane protein kinase NCBI Description 1 [Zea mays] 32304 Seq. No. 278627 1.R1040 Contig ID epx701108916.h1

5'-most EST

Method BLASTX NCBI GI g4098647 BLAST score 346 E value 1.0e-32 Match length 86 74 % identity

(U80668) homogentisate 1,2-dioxygenase [Arabidopsis NCBI Description



## thaliana]

Seq. No. 32305 Contig ID 278652 1.R1040 5'-most EST kl1701204312.h2

32306 Seq. No.

278697 1.R1040 Contig ID 5'-most EST  $k11701\overline{2}04367.h2$ 

32307 Seq. No.

278737 1.R1040 Contig ID kl1701212025.h1 5'-most EST

Seq. No. 32308

Contig ID 278744 1.R1040 5'-most EST  $k11701\overline{2}04431.h2$ 

Seq. No. 32309

278746 2.R1040 Contig ID 5'-most EST  $k11701\overline{2}12792.h1$ 

Seq. No. 32310

Contig ID 278751 1.R1040 kl1701204438.h2 5'-most EST

Method BLASTX NCBI GI g4454467 BLAST score 999 E value 1.0e-109 Match length 250

% identity 77

(AC006234) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 32311

278761 1.R1040 Contig ID 5'-most EST  $epx701\overline{1}05670.h1$ 

Method BLASTX q544250 NCBI GI BLAST score 258 2.0e-22 E value Match length 61

77 % identity

ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR) NCBI Description

>qi 541860 pir A49677 endoplasmic reticulum retention

receptor Erd2 - Arabidopsis thaliana

32312 Seq. No.

Contig ID 278764 1.R1040  $k11701\overline{2}11424.h1$ 5'-most EST

Seq. No. 32313

Contig ID 278808 1.R1040 5'-most EST  $k11701\overline{2}04518.h2$ 

Seq. No. 32314

Contig ID 278811 1.R1040 5'-most EST kl1701204522.h2



Method BLASTX
NCBI GI 94371292
BLAST score 167
E value 5.0e-12
Match length 69
% identity 54

NCBI Description (AC006260) unknown protein [Arabidopsis thaliana]

Seq. No. 32315

Contig ID 278862\_1.R1040 5'-most EST jC-gmro02910062f07d1

Seq. No. 32316

Contig ID 278940\_1.R1040 5'-most EST kl1701204694.h1

Method BLASTX
NCBI GI g3269287
BLAST score 147
E value 3.0e-09
Match length 113
% identity 34

NCBI Description (AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No. 32317

Contig ID 278965\_1.R1040 5'-most EST uC-gmropic110c12b1

Seq. No. 32318

Contig ID 278999\_1.R1040 5'-most EST kl1701204795.h1

Seq. No. 32319

Contig ID 279082\_1.R1040 5'-most EST kl1701207154.h1

Method BLASTX
NCBI GI g529353
BLAST score 419
E value 8.0e-49
Match length 159
% identity 56

NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No. 32320

Contig ID 279116\_1.R1040 5'-most EST kl1701204975.h1

Method BLASTX
NCBI GI g3426038
BLAST score 597
E value 6.0e-62
Match length 176
% identity 66

NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 32321

Contig ID 279440 1.R1040 5'-most EST kl1701205461.h1



Seq. No. 32322

Contig ID 279480\_1.R1040 5'-most EST uC-gmropic108a02b1

Seq. No. 32323

Contig ID 279503\_1.R1040 5'-most EST zsg701125331.h1

Method BLASTX
NCBI GI g4538980
BLAST score 155
E value 4.0e-10
Match length 74
% identity 38

NCBI Description (AL049487) putative protein [Arabidopsis thaliana]

Seq. No. 32324

Contig ID 279593\_1.R1040 5'-most EST kl1701205651.h1

Seq. No. 32325

Contig ID 279910\_1.R1040 5'-most EST kl1701206114.h1

Seq. No. 32326

Contig ID 279992 1.R1040 5'-most EST kl1701206234.h1

Seq. No. 32327

Contig ID 279994\_1.R1040

5'-most EST g5509328

Seq. No. 32328

Contig ID 280031\_1.R1040 5'-most EST jC-qmro02910012f01a1

Method BLASTX
NCBI GI g3643608
BLAST score 230
E value 6.0e-19
Match length 71
% identity 62

NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32329

Contig ID 280049 1.R1040

5'-most EST g5509307

Seq. No. 32330

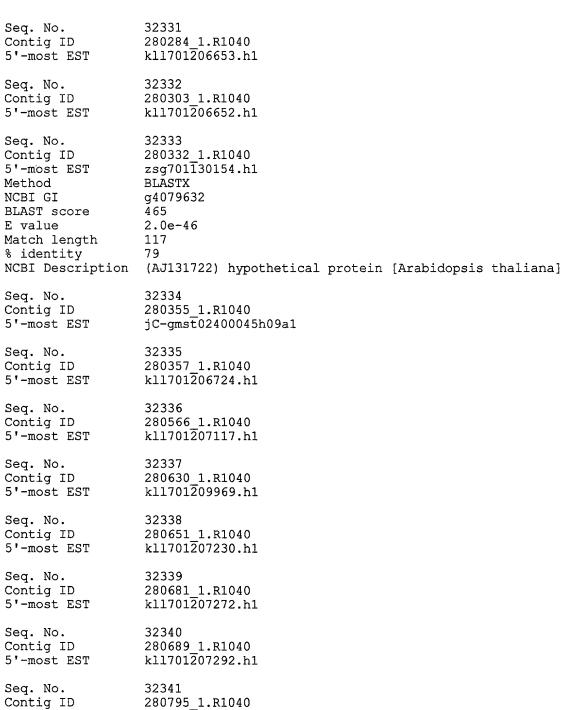
Contig ID 280088\_1.R1040

5'-most EST jC-gmro02910003b06a1

Method BLASTX
NCBI GI g2344901
BLAST score 444
E value 3.0e-44
Match length 133
% identity 68

NCBI Description (AC002388) serine/threonine protein kinase isolog

[Arabidopsis thaliana]



5'-most EST

jC-gmf102220126g09a1

Seq. No. Contig ID 32342

280812 1.R1040

5'-most EST uC-gmrominsoy120e10b1

Seq. No. 32343



Contig ID 280837 1.R1040

5'-most EST uC-gmflminsoy003c12b1

Method BLASTX
NCBI GI g4218011
BLAST score 770
E value 4.0e-82
Match length 200
% identity 72

NCBI Description (AC006135) putative protein kinase [Arabidopsis thaliana]

>gi 4309721 gb AAD15491 (AC006439) putative

serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 32344

Contig ID 280906 1.R1040

5'-most EST uC-gmflminsoy109b08b1

Method BLASTX
NCBI GI g2133437
BLAST score 219
E value 7.0e-18
Match length 100
% identity 47

NCBI Description RNA polymerase II second largest chain RPB2 - Euplotes octocarinatus (SGC9) >qi 2654279 emb CAA47069 (X66453)

DNA-directed RNA polymerase [Euplotes octocarinatus]

Seq. No. 32345

Contig ID 280913\_1.R1040 5'-most EST kl1701207655.h1

Method BLASTX
NCBI GI g3776559
BLAST score 409
E value 3.0e-40
Match length 97
% identity 77

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi\_3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb AC003970. ESTs gb Z35332 and gb F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 32346

Contig ID 280934 1.R1040 5'-most EST epx701109379.h1

Seq. No. 32347

Contig ID 280949\_1.R1040 5'-most EST kl1701207867.h1

Seq. No. 32348

Contig ID 280958\_1.R1040 5'-most EST kl1701209323.h1

Method BLASTX
NCBI GI g3924597
BLAST score 138
E value 1.0e-08
Match length 87
% identity 37

NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]



```
32349
Seq. No.
Contig ID
                   281016 1.R1040
5'-most EST
                   jC-gmro02910004a10d1
Method
                   BLASTX
NCBI GI
                   q2244973
BLAST score
                   413
                   3.0e-40
E value
                   193
Match length
                   40
% identity
                  (Z97340) similarity to extensin class 1 protein
NCBI Description
                   [Arabidopsis thaliana]
                   32350
Seq. No.
                   281054 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}08323.h1
Method
                   BLASTX
NCBI GI
                   g2342735
BLAST score
                   162
                   2.0e-11
E value
                   49
Match length
                   67
% identity
                  (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
                   32351
Seq. No.
                   281129 1.R1040
Contig ID
5'-most EST
                   k11701207975.h1
                   32352
Seq. No.
Contig ID
                   281132 1.R1040
                   jC-qmle01810018a08a2
5'-most EST
Seq. No.
                   32353
Contig ID
                   281150 1.R1040
5'-most EST
                   kl1701208002.hl
                   32354
Seq. No.
Contig ID
                   281183 1.R1040
5'-most EST
                   k11701208043.h1
Method
                   BLASTX
NCBI GI
                   q4204297
BLAST score
                   519
E value
                   6.0e-53
Match length
                   106
% identity
                  (AC003027) ADK1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32355
                   281226 1.R1040
Contig ID
                   kl1701208104.h1
5'-most EST
Method
                   BLASTX
                   g3150412
NCBI GI
BLAST score
                   231
                   2.0e-19
E value
```

NCBI Description (AC004165) putative Fe(II) transport protein [Arabidopsis

67

66

Match length

% identity

4927



thaliana] >gi\_3420044 (AC004680) putative Fe(II) transport protein [Arabidopsis thaliana]

Seq. No. 32356

Contig ID 281256\_1.R1040 5'-most EST kl1701208136.h1

Seq. No. 32357

Contig ID 281280\_1.R1040 5'-most EST kl1701208165.h1

Seq. No. 32358

Contig ID 281382 1.R1040

5'-most EST uC-gmrominsoy154a05b1

Seq. No. 32359

Contig ID 281409\_1.R1040 5'-most EST kl1701208332.h1

Seq. No. 32360

Contig ID 281441\_1.R1040 5'-most EST kl1701208373.h1

Seq. No. 32361

Contig ID 281462\_1.R1040 5'-most EST kl1701215446.h1

Seq. No. 32362

Contig ID 281545\_1.R1040 5'-most EST uC-gmronoir030e01b1

Seq. No. 32363

Contig ID 281681\_1.R1040 5'-most EST kl1701208708.h1

Seq. No. 32364

Contig ID 281683 1.R1040 5'-most EST kl1701212911.h1

Method BLASTX
NCBI GI g1619602
BLAST score 235
E value 7.0e-20
Match length 53
% identity 87

NCBI Description (Y08726) MtN3 [Medicago truncatula]

Seq. No. 32365

Contig ID 281705 1.R1040 5'-most EST kl1701208747.h1

Method BLASTX
NCBI GI g3115374
BLAST score 483
E value 1.0e-48
Match length 106
% identity 86

NCBI Description (AF002016) acyl CoA oxidase homolog [Cucurbita sp.]

32366 Seq. No. 281719 1.R1040 Contig ID  $k11701\overline{2}09188.h1$ 5'-most EST Seq. No. 32367 281749 1.R1040 Contig ID epx701104434.hl 5'-most EST 32368 Seq. No. Contig ID 281796 1.R1040 kl1701209567.hl 5'-most EST 32369 Seq. No. 281813 1.R1040 Contig ID 5'-most EST  $k11701\overline{2}08908.h1$ Method BLASTX q3077640 NCBI GI 228 BLAST score 3.0e-19 E value Match length 79 % identity 59 NCBI Description (AJ223151) O-methyltransferase [Prunus dulcis] Seq. No. 32370 281891 1.R1040 Contig ID 5'-most EST  $k11701\overline{2}09045.h1$ Seq. No. 32371 Contig ID 281920 1.R1040  $k11701\overline{2}09102.h1$ 5'-most EST BLASTX Method

Method BLASTX
NCBI GI g1685005
BLAST score 199
E value 9.0e-16
Match length 51
% identity 73

NCBI Description (U32644) immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]

Seq. No. 32372

Contig ID 281921\_1.R1040 5'-most EST kl1701209103.h1

Seq. No. 32373

Contig ID 281959\_1.R1040 5'-most EST epx701103727.h1

Method BLASTX
NCBI GI g1076331
BLAST score 306
E value 5.0e-34
Match length 96
% identity 74

NCBI Description histidine transport protein - Arabidopsis thaliana

>gi\_510238\_emb\_CAA54634\_ (X77503) oligopeptide transporter
1-1 [Arabidopsis thaliana] >gi\_744157\_prf\_\_2014244A His

transporter [Arabidopsis thaliana]



32374 Seq. No. 281977 1.R1040 Contig ID kll701209177.hl 5'-most EST Seq. No. 32375 282020 1.R1040 Contig ID  $k11701\overline{2}09233.h1$ 5'-most EST 32376 Seq. No. 282027 1.R1040 Contig ID  $k11701\overline{2}12080.h1$ 5'-most EST

 Seq. No.
 32379

 Contig ID
 282326\_1.R1040

 5'-most EST
 g4293821

 Method
 BLASTX

 NCBI GI
 g2981463

 BLAST score
 118

 E value
 5.0e-09

E value 5.0e
Match length 93
% identity 34

NCBI Description (AF052663) gamma-tubulin interacting protein [Xenopus

laevis]

Seq. No. 32380

Contig ID 282347\_1.R1040 5'-most EST asn701140632.h1

Method BLASTX
NCBI GI g4235430
BLAST score 239
E value 3.0e-20
Match length 69
% identity 68

NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No. 32381

Contig ID 282379\_1.R1040 5'-most EST kl1701214478.h1

Seq. No. 32382

Contig ID 282402 1.R1040 5'-most EST kl1701213719.h1

Seq. No. 32383

Contig ID 282420\_1.R1040 5'-most EST kl1701213504.h1

Method BLASTX
NCBI GI g4220491
BLAST score 202



7.0e-16 E value Match length 103 % identity 42

(AC006069) hypothetical protein [Arabidopsis thaliana] NCBI Description

32384 Seq. No.

282442 1.R1040 Contig ID  $k11701\overline{2}09829.h1$ 5'-most EST

32385 Seq. No.

Contig ID 282521 1.R1040  $k11701\overline{2}11385.h1$ 5'-most EST

32386 Seq. No.

Contig ID 282528 1.R1040 5'-most EST  $k11701\overline{2}09951.h1$ 

Method BLASTX NCBI GI q3128186 BLAST score 164 E value 8.0e-12 56 Match length % identity 54

NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

32387 Seq. No.

Contig ID 282552 1.R1040 5'-most EST kl1701211063.hl

Seq. No. 32388

Contig ID 282554 1.R1040  $k11701\overline{2}09976.h1$ 5'-most EST

Method BLASTX NCBI GI q1351303 BLAST score 334 3.0e-31 E value 92 Match length

% identity 70

INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE PRECURSOR (IGPS) NCBI Description >gi 619732 (U18770) indole-3-glycerol phosphate synthase

[Arabidopsis thaliana]

32389 Seq. No.

Contig ID 282616 1.R1040 kl1701210061.h1 5'-most EST

BLASTX Method g4454012 NCBI GI BLAST score 212 E value 6.0e-17 Match length 86 52 % identity

(AL035396) Pollen-specific protein precursor like NCBI Description

[Arabidopsis thaliana]

Seq. No. 32390

Contig ID 282630 1.R1040 5'-most EST  $k11701\overline{2}10079.h1$ 

Method BLASTX



NCBI GI g3024871 BLAST score 223 E value 2.0e-18 Match length 83 % identity 55

NCBI Description HYPOTHETICAL 77.3 KD PROTEIN SLL0005

>gi\_1001579\_dbj\_BAA10206\_ (D64000) ABC1-like [Synechocystis

sp.]

Seq. No. 32391

Contig ID 282712\_1.R1040 5'-most EST kl1701210189.h1

Method BLASTX
NCBI GI 94490297
BLAST score 188
E value 7.0e-14
Match length 113
% identity 42

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 32392

Contig ID 282735\_1.R1040 5'-most EST kll701210560.h1

Seq. No. Contig ID

32393 282742\_1.R1040

5'-most EST kl1701210229.h1
Method BLASTX
NCBI GI g3128199
BLAST score 207
E value 9.0e-17
Match length 57

% identity 68

NCBI Description (AC004521) putative proteinase [Arabidopsis thaliana]

Seq. No. 32394

Contig ID 282755\_1.R1040 5'-most EST kl1701210252.h1

Seq. No. 32395

Contig ID 282926\_1.R1040

5'-most EST uC-gmrominsoy164d02b1

Method BLASTX
NCBI GI g1708863
BLAST score 145
E value 5.0e-09
Match length 53
% identity 51

NCBI Description ACYL-[ACYL-CARRIER-PROTEIN] -- UDP-N-ACETYLGLUCOSAMINE

O-ACYLTRANSFERASE (UDP-N-ACETYLGLUCOSAMINE ACYLTRANSFERASE)

>gi\_1262294 (U51683) LpxA [Brucella abortus]

Seq. No. 32396

Contig ID 283013 1.R1040

5'-most EST uC-gmrominsoy158g11b1

Method BLASTX NCBI GI g2827141



BLAST score 394 E value 5.0e-38 Match length 86 % identity 83

NCBI Description (AF027173) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 32397

Contig ID 283040 1.R1040 5'-most EST kl1701210762.h1

Seq. No. 32398

Contig ID 283158\_1.R1040

5'-most EST jC-gmst02400051e11d1

Seq. No. 32399

Contig ID 283287\_1.R1040 5'-most EST kll701211109.h1

Method BLASTX
NCBI GI g3928150
BLAST score 433
E value 6.0e-43
Match length 103
% identity 75

NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 32400

Contig ID 283386 1.R1040 5'-most EST kl1701211250.h1

Seq. No. 32401

Contig ID 283461\_1.R1040 5'-most EST kll701211360.h1

Seq. No. 32402

Contig ID 283489 1.R1040

NCBI Description (Z81038) Similarity to Bovine NADH-ubiquinone

oxidoreducatse B8 subunit (SW:Q02370) [Caenorhabditis

elegans]

Seq. No. 32403

Contig ID 283563\_1.R1040

5'-most EST g4300673
Method BLASTX
NCBI GI g4099092
BLAST score 426
E value 6.0e-42
Match length 140
% identity 60

NCBI Description (U83179) unknown [Arabidopsis thaliana]



283571 1.R1040 Contig ID

jC-gmle01810006e04a1 5'-most EST

BLASTX Method g2809251 NCBI GI 916 BLAST score E value 7.0e-99 305 Match length % identity 56

(AC002560) F21B7.20 [Arabidopsis thaliana] NCBI Description

32405 Seq. No.

Contig ID 283700 1.R1040 5'-most EST jC-gmle01810089a12a1

Method BLASTX g3819699 NCBI GI BLAST score 373 E value 1.0e-41 197 Match length % identity 51

NCBI Description (AJ009609) BnMAP4K alpha2 [Brassica napus]

32406 Seq. No.

Contig ID 283704\_1.R1040

5'-most EST g5126825

32407 Seq. No.

283729 1.R1040 Contig ID 5'-most EST  $k11701\overline{2}11749.h1$ 

32408 Seq. No.

Contig ID 283838 1.R1040

5'-most EST jC-gmf102220080a01a1

32409 Seq. No.

Contig ID 283930 1.R1040 5'-most EST kl1701212503.hl

Seq. No. 32410

283964 1.R1040 Contig ID

5'-most EST uC-gmrominsoy162e03b1

32411 Seq. No.

283988 1.R1040 Contig ID 5'-most EST  $k11701\overline{2}12094.h1$ 

Seq. No. 32412

Contig ID 284071 1.R1040 5'-most EST  $k11701\overline{2}12210.h1$ 

Method BLASTX NCBI GI q2346966 BLAST score 220 E value 7.0e-18 Match length 56 % identity 68

NCBI Description (AB004871) CPC [Arabidopsis thaliana]



>gi\_4559383\_gb\_AAD23043.1\_AC006526\_8 (AC006526) putative DNA binding protein CPC [Arabidopsis thaliana]

Seq. No. 32413

Contig ID 284077\_1.R1040

5'-most EST jC-gmle01810050a05a1

Method BLASTX
NCBI GI g3355486
BLAST score 193
E value 6.0e-15
Match length 51

Match length 51 % identity 63

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 32414

Contig ID 284124\_1.R1040 5'-most EST kl1701212277.h1

Seq. No. 32415

Contig ID 284193 1.R1040

5'-most EST uC-gmrominsoy046e07b1

32417

Seq. No. 32416

Contig ID 284214\_1.R1040 5'-most EST kl1701212403.h1

Seq. No.

Contig ID 284244\_1.R1040 5'-most EST kl1701212684.h1

Method BLASTX
NCBI GI g3885329
BLAST score 339
E value 3.0e-32
Match length 78

% identity 82

NCBI Description (AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No. 32418

Contig ID 284423\_1.R1040

5'-most EST uC-gmflminsoy071a07b2

Seq. No. 32419

Contig ID 284428\_1.R1040 5'-most EST asn701143228.h1

Seq. No. 32420

Contig ID 284450\_1.R1040

5'-most EST jC-gmle01810054a10a1

Seq. No. 32421

Contig ID 284511\_1.R1040 5'-most EST epx701107757.h1

Seq. No. 32422

Contig ID 284560 1.R1040

5'-most EST uC-gmflminsoy025c12b1

Method BLASTX



NCBI GI g2352492 BLAST score 520 E value 7.0e-53 Match length 125 % identity 75

NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis

thaliana] >gi\_2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

Seq. No. 32423

Contig ID 284660\_1.R1040 5'-most EST epx701108257.h1

Seq. No. 32424

Contig ID 284705\_1.R1040 5'-most EST epx701109068.h1

Seq. No. 32425

Contig ID 284768 1.R1040

5'-most EST uC-gmflminsoy007b12b1

Seq. No. 32426

Contig ID 284798\_1.R1040

5'-most EST jC-gmro02910039h06a1

Seq. No. 32427

Contig ID 284824\_1.R1040 5'-most EST kll701213216.h1

Seq. No. 32428

Contig ID 284855\_1.R1040 5'-most EST zsg701121725.h1

Seq. No. 32429

Contig ID 284880 1.R1040

5'-most EST jC-gmr002910050e09d1

Seq. No. 32430

Contig ID 284889 1.R1040

5'-most EST jC-gmf\(\bar{1}\)02220092d01a1

Seq. No. 32431

Contig ID 285001 1.R1040

5'-most EST uC-gmrominsoy033d10b1

Method BLASTX
NCBI GI g2459412
BLAST score 172
E value 6.0e-12
Match length 103
% identity 43

NCBI Description (AC002332) putative G9a protein [Arabidopsis thaliana]

Seq. No. 32432

Contig ID 285042 1.R1040

5'-most EST jC-gmro02910002a07a1

Seq. No. 32433



Contig ID 285049\_1.R1040

5'-most EST g5509313

Method BLASTX

NCBI GI g2864625

BLAST score 320

E value 2.0e-29

Match length 92

% identity 67

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 32434

Contig ID 285172 1.R1040 5'-most EST kl1701213667.h1

Seq. No. 32435

Contig ID 285185 2.R1040

5'-most EST jC-gmst02400066b03d1

Seq. No. 32436

Contig ID 285304\_1.R1040 5'-most EST uC-gmropic015d09b1

Method BLASTN
NCBI GI g3869068
BLAST score 64
E value 3.0e-27
Match length 300
% identity 80

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC16, complete sequence [Arabidopsis thaliana]

Seq. No. 32437

Contig ID 285340\_1.R1040 5'-most EST kl1701213890.h1

Method BLASTX
NCBI GI g2569940
BLAST score 264
E value 1.0e-27
Match length 136
% identity 50

NCBI Description (Y15194) GRS protein [Arabidopsis thaliana]

Seq. No. 32438

Contig ID 285365\_1.R1040 5'-most EST zsg701122787.h1

Seq. No. 32439

Contig ID 285400 1.R1040 5'-most EST zsg701125845.h1

Seq. No. 32440

Contig ID 285447\_1.R1040 5'-most EST kll701214043.h1

Method BLASTX
NCBI GI g2160166
BLAST score 288
E value 4.0e-26
Match length 94



% identity NCBI Description (AC000132) No definition line found [Arabidopsis thaliana] 32441 Seq. No. 285508 1.R1040 Contig ID 5'-most EST jC-qmf102220112g07d1 BLASTX Method NCBI GI g2583123 BLAST score 470 4.0e-47 E value 115 Match length 78 % identity (AC002387) putative nucleotide sugar epimerase [Arabidopsis NCBI Description thaliana] 32442 Seq. No.

285606 1.R1040 Contig ID  $k11701\overline{2}14241.h1$ 5'-most EST

Seq. No. 32443

285676 1.R1040 Contig ID 5'-most EST kl1701214344.h1

BLASTX Method g2894600 NCBI GI BLAST score 215 E value 1.0e-17 Match length 51 % identity 67

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

32444 Seq. No.

285699 1.R1040 Contig ID 5'-most EST  $k11701\overline{2}14351.h1$ 

Method BLASTX NCBI GI g1711382 BLAST score 176 E value 5.0e-13 Match length 55 % identity 51

NCBI Description SET PROTEIN >gi\_940889 (U30470) SET [Drosophila

melanogaster]

32445 Seq. No.

285750 1.R1040 Contig ID

5'-most EST jC-gmle01810084h09a1

Method BLASTX NCBI GI g4185507 BLAST score 866 E value 2.0e-93 Match length 216 % identity 70

NCBI Description (AF100163) EZA1 [Arabidopsis thaliana]

Seq. No. 32446

Contig ID 285774 1.R1040 5'-most EST asn701140406.hl



Contig ID 285827\_1.R1040 5'-most EST uC-gmropic017h02b1

Method BLASTX
NCBI GI g1076758
BLAST score 528
E value 6.0e-54
Match length 131
% identity 76

NCBI Description heat-shock protein precursor - rye >gi\_2130093\_pir\_\_\_S65776

heat-shock protein, 82K, precursor - rye

>gi 556673 emb CAA82945 (Z30243) heat-shock protein

[Secale cereale]

Seq. No. 32448

Contig ID 285852\_1.R1040 5'-most EST kl1701214562.h1

Method BLASTX
NCBI GI g4151319
BLAST score 147
E value 1.0e-09
Match length 30
% identity 93

NCBI Description (AF089084) putative auxin efflux carrier protein; AtPIN1

[Arabidopsis thaliana]

Seq. No. 32449

Contig ID 285872\_1.R1040 5'-most EST kll701214554.h1

Seq. No. 32450

Contig ID 285905 1.R1040

5'-most EST uC-gmflminsoy072d01b1

Method BLASTX
NCBI GI g3763934
BLAST score 230
E value 4.0e-19
Match length 109
% identity 47

NCBI Description (AC004450) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32451

Contig ID 285926 1.R1040 5'-most EST kl1701214620.h1

Method BLASTX
NCBI GI g2827637
BLAST score 200
E value 3.0e-15
Match length 185
% identity 30

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 32452

Contig ID 285927 1.R1040 5'-most EST kl1701215491.h1

Seq. No. 32453



Contig ID 285962\_1.R1040 5'-most EST jC-qmfl02220050g02a1

Method BLASTX
NCBI GI g3786000
BLAST score 262
E value 1.0e-22
Match length 108
% identity 45

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32454

Contig ID 286210\_1.R1040 5'-most EST kl1701214989.h1

Method BLASTX
NCBI GI g3142303
BLAST score 161
E value 3.0e-11
Match length 88
% identity 39

NCBI Description (AC002411) Strong similarity to MRP-like ABC transporter

gb\_U92650 from A. thaliana and canalicular multi-drug resistance protein gb\_L49379 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No. 32455

Contig ID 286282\_1.R1040 5'-most EST kll701215347.h1

Seq. No. 32456

Contig ID 286323\_1.R1040 5'-most EST kll701215149.h1

Seq. No.

Contig ID 286343\_1.R1040 5'-most EST kl1701215175.h1

32457

Seq. No. 32458

Contig ID 286388\_1.R1040 5'-most EST kl1701215237.h1

Method BLASTX
NCBI GI g3738324
BLAST score 237
E value 3.0e-20
Match length 88
% identity 50

NCBI Description (AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No. 32459

Contig ID 286478 1.R1040 5'-most EST g5605942

Seq. No.

Contig ID 286527\_1.R1040 5'-most EST asn701139270.h1

32460

Seq. No. 32461

Contig ID 286548\_1.R1040



5'-most EST kl1701215463.h1

Method BLASTX
NCBI GI g4544473
BLAST score 263
E value 3.0e-23
Match length 71
% identity 39

NCBI Description (AC006580) putative mei2 protein [Arabidopsis thaliana]

Seq. No. 32462

Contig ID 286554\_1.R1040 5'-most EST kl1701215470.h1

Method BLASTX
NCBI GI g1174718
BLAST score 381
E value 2.0e-36
Match length 93
% identity 78

NCBI Description PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR

>gi\_322579\_pir\_\_JQ1674 receptor protein kinase TMK1 (EC
2.7.1.-) precursor - Arabidopsis thaliana >gi 166888

(L00670) protein kinase [Arabidopsis thaliana]

Seq. No. 32463

Contig ID 286584\_1.R1040 5'-most EST epx701108777.h1

Seq. No. 32464

Contig ID 286651\_1.R1040 5'-most EST epx701103856.h1

Seq. No. 32465

Contig ID 286661 1.R1040 5'-most EST epx701105166.h1

Seq. No. 32466

Contig ID 286670\_1.R1040 5'-most EST asn701137942.h1

Method BLASTX
NCBI GI g2979558
BLAST score 148
E value 8.0e-10
Match length 38
% identity 74

NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32467

Contig ID 286690 1.R1040 5'-most EST epx701103939.h1

Seq. No. 32468

Contig ID 286748 1.R1040 5'-most EST epx701104058.h1

Method BLASTX
NCBI GI g4049350
BLAST score 217
E value 2.0e-17

```
73
Match length
                   56
% identity
                   (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32469
                   286798 1.R1040
Contig ID
                  uC-qmflminsoy023h11b1
5'-most EST
Method
                  BLASTN
NCBI GI
                   q3046855
BLAST score
                   70
                   4.0e-31
E value
Match length
                   266
                   82
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MSL1, complete sequence [Arabidopsis thaliana]
                   32470
Seq. No.
Contig ID
                   286902 1.R1040
5'-most EST
                   epx701105832.hl
                   32471
Seq. No.
                   286902 2.R1040
Contig ID
5'-most EST
                   epx701104610.hl
                   32472
Seq. No.
                   286981 1.R1040
Contig ID
5'-most EST
                   epx701104381.h1
                   BLASTX
Method
NCBI GI
                   g2558938
BLAST score
                   569
E value
                   2.0e-58
Match length
                   228
% identity
                   54
                  (AF024625) arm repeat containing protein [Brassica napus]
NCBI Description
                   32473
Seq. No.
                   287162 1.R1040
Contig ID
                   jC-gmf\overline{1}02220089c10a1
5'-most EST
                   32474
Seq. No.
                   287311 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy213h02b1
Method
                   BLASTX
                   g2252840
NCBI GI
BLAST score
                   179
```

Method BLASTX
NCBI GI g2252840
BLAST score 179
E value 3.0e-13
Match length 80
% identity 47

NCBI Description (AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No. 32475

Contig ID 287456\_1.R1040 5'-most EST asn701136070.h1

Method BLASTX NCBI GI g3286691 BLAST score 279



E value 8.0e-25
Match length 87
% identity 57

NCBI Description (AJ007450) auxilin-like protein [Arabidopsis thaliana]

Seq. No. 32476

Contig ID 287634 1.R1040

5'-most EST jC-gmst02400067h03a1

Seq. No. 32477

Contig ID 287636\_1.R1040 5'-most EST zsg701118226.h1

Seq. No. 32478

Contig ID 287730\_1.R1040 5'-most EST zsg701118519.h1

Method BLASTX
NCBI GI g3805765
BLAST score 564
E value 6.0e-58
Match length 156
% identity 69

NCBI Description (AC005693) putative protein kinase [Arabidopsis thaliana]

Seq. No. 32479

Contig ID 287766\_1.R1040 5'-most EST epx701105492.h1

Seq. No. 32480

Contig ID 287772\_1.R1040

5'-most EST jC-gmro02910059a04d1

Seq. No. 32481

Contig ID 287868\_1.R1040 5'-most EST epx701105637.h1

Method BLASTX
NCBI GI g4454459
BLAST score 605
E value 5.0e-63
Match length 147
% identity 79

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 32482

Contig ID 287932 1.R1040

5'-most EST jC-gmro02910009d05a1

Method BLASTX
NCBI GI g4544451
BLAST score 622
E value 5.0e-65
Match length 147
% identity 78

NCBI Description (AC006592) unknown protein [Arabidopsis thaliana]

Seq. No. 32483

Contig ID 287960\_1.R1040

5'-most EST uC-gmrominsoy028d03b1

Contig ID

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Seq. No.
                  32484
                  288006 1.R1040
Contig ID
5'-most EST
                  zsg701121033.hl
                  32485
Seq. No.
                  288048 1.R1040
Contig ID
                  epx701105890.h1
5'-most EST
Seq. No.
                  32486
                  288051 1.R1040
Contig ID
                  epx701105893.h1
5'-most EST
                  BLASTX
Method
                  g4432814
NCBI GI
BLAST score
                  397
E value
                  7.0e-39
Match length
                  103
% identity
                  73
                  (AC006593) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  32487
                  288190 1.R1040
Contig ID
                  epx701106079.h1
5'-most EST
Seq. No.
                  32488
Contig ID
                  288200 1.R1040
                  jC-gmf102220079a03a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2244753
BLAST score
                  450
                  8.0e-45
E value
Match length
                  118
% identity
                  69
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  32489
Seq. No.
                  288218 1.R1040
Contig ID
5'-most EST
                  g5676843
                   32490
Seq. No.
Contig ID
                  288258 1.R1040
5'-most EST
                  jC-gmf102220081b07d1
Seq. No.
                   32491
Contig ID
                   288325 1.R1040
5'-most EST
                  epx701106274.h1
                  BLASTX
Method
                  g3914621
NCBI GI
BLAST score
                  151
E value
                   8.0e-10
Match length
                  129
% identity
                  12
NCBI Description RAN GTPASE ACTIVATING PROTEIN 1 >gi 2062660 (U88155)
```

4944

32492

288425\_1.R1040

RanGTPase activating protein [Xenopus laevis]

```
jC-gmle01810078c08a1
5'-most EST
Method
                  BLASTN
                  q169036
NCBI GI
BLAST score
                  46
E value
                  7.0e-17
Match length
                  70
% identity
                  91
NCBI Description Pisum sativum L. aldolase gene, 3' end cds
Seq. No.
                  32493
                  288482 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910002a06d1
```

Contig ID 288502 1.R1040 5'-most EST epx701106518.h1

Method BLASTX
NCBI GI g585084
BLAST score 153
E value 6.0e-10
Match length 56
% identity 57

NCBI Description ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G) >gi\_543383\_pir\_\_S40780 translation elongation factor G, mitochondrial - rat >gi\_310102 (L14684) elongation factor G

[Rattus norvegicus]

Seq. No. 32495

Contig ID 288655\_1.R1040 5'-most EST epx701106718.h1

Method BLASTX
NCBI GI 94559371
BLAST score 160
E value 8.0e-11
Match length 58
% identity 53

NCBI Description (AC006585) putative peroxidase [Arabidopsis thaliana]

Seq. No. 32496

Contig ID 288657\_1.R1040 5'-most EST epx701106822.h1

Method BLASTX
NCBI GI g3114573
BLAST score 314
E value 3.0e-29
Match length 92
% identity 66

NCBI Description (AF019383) 1-deoxyxylulose-5-phosphate synthase [Mentha x

piperita]

Seq. No. 32497

Contig ID 288876\_1.R1040 5'-most EST epx701107014.h1

Seq. No. 32498

Contig ID 289043\_1.R1040 5'-most EST uC-gmropic037d09b1



Method BLASTX
NCBI GI g2191151
BLAST score 509
E value 1.0e-51
Match length 125
% identity 77

NCBI Description (AF007269) contains similarity to membrane associated

salt-inducible protein [Arabidopsis thaliana]

Seq. No. 32499

Contig ID 289209\_1.R1040

5'-most EST uC-gmrominsoy235h10b1

Seq. No. 32500

Contig ID 289209 2.R1040

5'-most EST uC-gmrominsoy265a01b1

Seq. No. 32501

Contig ID 289273 1.R1040

5'-most EST jC-gmle01810009h03a1

Seq. No. 32502

Contig ID 289320\_1.R1040 5'-most EST zsg701125287.h1

Method BLASTX
NCBI GI g1706885
BLAST score 146
E value 2.0e-09
Match length 78
% identity 45

NCBI Description FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR

(FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS) >gi\_1345106

(U33557) folylpolyglutamate synthetase precursor  $\overline{\text{[Mus]}}$ 

musculus]

Seq. No. 32503

Contig ID 289429\_1.R1040 5'-most EST epx701107838.h1

Seq. No. 32504

Contig ID 289501 1.R1040

5'-most EST  $g56062\overline{14}$ 

Seq. No. 32505

Contig ID 289548\_1.R1040 5'-most EST epx701108027.h1

Seq. No. 32506

Contig ID 289662 1.R1040

5'-most EST uC-gmrominsoy029a12b1

Seq. No. 32507

Contig ID 289665 1.R1040 5'-most EST epx701108193.h1

Seq. No. 32508

Contig ID 289680\_1.R1040



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5'-most EST epx701108215.h1
```

Contig ID 289746\_1.R1040

5'-most EST uC-gmflminsoy018a03b1

Seq. No. 32510

Contig ID 289836\_1.R1040 5'-most EST epx701108410.h1

Seq. No. 32511

Contig ID 290042\_1.R1040 5'-most EST epx701\overline{10}8718.h1

Seq. No. 32512

Contig ID 290092\_1.R1040 5'-most EST epx701108782.h1

Seq. No. 32513

Contig ID 290127\_1.R1040 5'-most EST epx701108896.h1

Seq. No. 32514

Contig ID 290151\_1.R1040 5'-most EST epx701108876.h1

Seq. No. 32515

Contig ID 290182 1.R1040

5'-most EST uC-gmrominsoy0001h07a1

Seq. No. 32516

Contig ID 290193\_1.R1040 5'-most EST zsg701118973.h1

Method BLASTX
NCBI GI g3420801
BLAST score 211
E value 7.0e-17
Match length 67
% identity 61

NCBI Description (AF081066) IAA-amino acid hydrolase homolog ILL3

[Arabidopsis thaliana]

Seq. No. 32517

Contig ID 290213 1.R1040

5'-most EST uC-gmflminsoy021g01b1

Method BLASTX
NCBI GI g3914020
BLAST score 282
E value 4.0e-25
Match length 111
% identity 50

NCBI Description (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR

(HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)

>gi\_1561641\_emb\_CAA69388\_ (Y08211) mandelonitrile lyase

[Prunus dulcis]

Seq. No. 32518



290367 1.R1040 Contig ID 5'-most EST epx701109171.hl 32519 Seq. No. 290387 1.R1040 Contig ID uC-gmflminsoy081h06b1 5'-most EST 32520 Seq. No. 290399 1.R1040 Contig ID epx701109213.h1 5'-most EST 32521 Seq. No. 290538\_1.R1040 Contig ID epx701109416.h1 5'-most EST Method BLASTX q4164145 NCBI GI 306 BLAST score 7.0e-28 E value 114 Match length % identity 48 (AB012205) gibberelin 3beta-hydroxylase [Lactuca sativa] NCBI Description Seq. No. 32522 290570 1.R1040 Contig ID  $epx701\overline{1}09489.h1$ 5'-most EST Method BLASTX q2289003 NCBI GI BLAST score 699 E value 7.0e-74179 Match length 76 % identity (ACO02335) membrane transporter D1 isolog [Arabidopsis NCBI Description thaliana] 32523 Seq. No. 290580 1.R1040 Contig ID jC-gmle01810025a06a1 5'-most EST BLASTX Method g2961352 NCBI GI 250 BLAST score 3.0e-21E value 58 Match length 74 % identity (AL022140) putative protein [Arabidopsis thaliana] NCBI Description 32524

Seq. No.

290699 1.R1040 Contig ID 5'-most EST epx701110431.hl

Seq. No. 32525

Contig ID 290758 1.R1040 5'-most EST epx701109965.hl

Seq. No. 32526

290812 1.R1040 Contig ID 5'-most EST uC-gmropic042c05b1



Contig ID 290842\_1.R1040

5'-most EST jC-gmf\(\bar{1}\)02220054f08d1

Method BLASTX
NCBI GI g2129755
BLAST score 433
E value 7.0e-43
Match length 103
% identity 83

NCBI Description tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis

thaliana >gi\_619753 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] >gi\_1585768\_prf\_\_2201482A Trp

synthase:SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No. 32528

Contig ID 290888 1.R1040

5'-most EST jC-gmle01810030g01a2

Method BLASTX
NCBI GI g2062173
BLAST score 502
E value 3.0e-51
Match length 103
% identity 95

NCBI Description (AC001645) cell division protein FtsH isolog [Arabidopsis

thaliana]

Seq. No. 32529

Contig ID 290900\_1.R1040

5'-most EST uC-gmrominsoy047c01b1

Seq. No. 32530

Contig ID 291084 1.R1040

5'-most EST q5058010

Seq. No. 32531

Contig ID 291208\_1.R1040

5'-most EST jC-gmro02910041017a1

Method BLASTX
NCBI GI g4314358
BLAST score 527
E value 2.0e-53
Match length 318
% identity 42

NCBI Description (AC006340) putative kinesin heavy chain protein

[Arabidopsis thaliana]

Seq. No. 32532

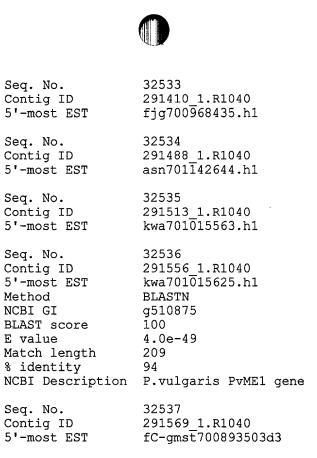
Contig ID 291237\_1.R1040

5'-most EST uC-gmrominsoy167h04b1

Method BLASTX
NCBI GI g2827549
BLAST score 691
E value 7.0e-73
Match length 146
% identity 89

NCBI Description (AL021635) glycoprotein endopeptidase - like protein

[Arabidopsis thaliana]



Seq. No. 32538 291651\_1.R1040 Contig ID 5'-most EST zsq701117506.h2

Method BLASTX NCBI GI g3220021 BLAST score 98 E value 2.0e-10 Match length 85 41

% identity

NCBI Description (U57828) lipase homolog [Arabidopsis thaliana]

32539 Seq. No.

Contig ID 291661 1.R1040 5'-most EST uC-gmropic047e09b1

32540 Seq. No.

Contig ID 291667 1.R1040 5'-most EST zsg701117441.h1

Method BLASTX g2984333 NCBI GI BLAST score 193 E value 1.0e-14 Match length 58 % identity 62

(AE000774) Na(+) dependent transporter (Sbf family) NCBI Description

[Aquifex aeolicus]

Seq. No. 32541

Contig ID 291833\_1.R1040



5'-most EST jC-gmro02910022b05a1 Method BLASTX NCBI GI g586021 BLAST score 134 1.0e-09 E value Match length 64 55 % identity PROBABLE PEPTIDYL-TRNA HYDROLASE (PTH) (STAGE V SPORULATION NCBI Description PROTEIN C) >gi 2127242 pir S66083 stage V sporulation protein - Bacillus subtilis >gi 467442 dbj BAA05288\_ (D26185) stage V sporulation [Bacillus subtilis] >gi 2632320 emb CAB11829 (Z99104) thermosensitive mutant blocks spore coat formation (stage V sporulation) [Bacillus subtilis] 32542 Seq. No. 291866 1.R1040 Contig ID 5'-most EST zsg701125639.h1 Method BLASTX NCBI GI q1055161 BLAST score 159 E value 1.0e-10 134 Match length % identity 34 NCBI Description (U40029) similar to human 100 kDa coactivator (U22055) [Caenorhabditis elegans] 32543 Seq. No. 291952 1.R1040 Contig ID 5'-most EST uC-gmrominsoy030a06b1 32544 Seq. No. 292089 1.R1040 Contig ID 5'-most EST g4396380 Seq. No. 32545 292298\_1.R1040 Contig ID 5'-most EST zsg701118524.h1 BLASTX Method NCBI GI g2959781 BLAST score 490 E value 9.0e-60

Match length 159 75 % identity

NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No. 32546

Contig ID 292303 1.R1040 5'-most EST zsg701126941.hl

Method BLASTX NCBI GI q3152559 BLAST score 504 E value 3.0e-51 Match length 127 70 % identity

NCBI Description (AC002986) Similarity to A. thaliana gene product

F21M12.20, gb\_AC000132. EST gb\_Z25651 comes from this gene.



## [Arabidopsis thaliana]

Seq. No. 32548

Contig ID 292454 1.R1040 5'-most EST zsg701118744.h1

Seq. No. 32549

Contig ID 292499\_1.R1040 5'-most EST zsg701118805.h1

Method BLASTX
NCBI GI g2384671
BLAST score 664
E value 8.0e-70
Match length 166
% identity 77

NCBI Description (AF012657) putative potassium transporter AtKT2p

[Arabidopsis thaliana]

Seq. No. 32550

Contig ID 292509\_1.R1040 5'-most EST zsg701118818.h1

Method BLASTX
NCBI GI g1777312
BLAST score 393
E value 4.0e-38
Match length 100
% identity 75

NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No. 32551

Contig ID 292534 1.R1040 5'-most EST asn701135674.h1

Seq. No. 32552

Contig ID 292677\_1.R1040 5'-most EST zsg701119045.h1

Method BLASTN
NCBI GI g3702736
BLAST score 34
E value 2.0e-09
Match length 42
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRI1, complete sequence [Arabidopsis thaliana]

Seq. No. 32553

Contig ID 292690 1.R1040

5'-most EST uC-qmflminsoy064g10b1

Seq. No. 32554

Contig ID 292737\_1.R1040 5'-most EST zsg701119132.h1



Method BLASTX
NCBI GI g4337192
BLAST score 273
E value 8.0e-24
Match length 54
% identity 89

NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32555

Contig ID 292857\_1.R1040 5'-most EST zsg701119308.h1

Seq. No. 32556

Contig ID 292873\_1.R1040 5'-most EST zsg701119326.h1

Method BLASTX
NCBI GI g2244755
BLAST score 354
E value 6.0e-34
Match length 89
% identity 70

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32557

Contig ID 292889 1.R1040 5'-most EST zsg701119350.h1

Method BLASTX
NCBI GI g2191139
BLAST score 143
E value 9.0e-09
Match length 52
% identity 50

NCBI Description (AF007269) A IG002N01.19 gene product [Arabidopsis

thaliana]

Seq. No. 32558

Contig ID 293078\_1.R1040 5'-most EST jC-gmle01810072a02a1

Method BLASTX
NCBI GI g4038592
BLAST score 555
E value 8.0e-57
Match length 162
% identity 64

NCBI Description (Y10403) RNA-directed RNA polymerase [Lycopersicon

esculentum]

Seq. No. 32559

Contig ID 293232\_1.R1040

5'-most EST uC-gmrominsoy031f07b1

Seq. No. 32560

Contig ID 293252\_1.R1040 5'-most EST jC-gmro02910070b07a1

Seq. No. 32561

Contig ID 293291\_1.R1040



5'-most EST zsg701119966.h1

Method BLASTX
NCBI GI g544075
BLAST score 542
E value 1.0e-55
Match length 148
% identity 68

NCBI Description COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)

(P102) >gi\_486768\_pir\_\_S35312 coatomer complex chain beta' - bovine >gi 312732 emb\_CAA51285\_ (X72756) beta prime cop

[Bos taurus]

Seq. No. 32562

Contig ID 293335\_1.R1040 5'-most EST zsg701120037.h1

Method BLASTX
NCBI GI g1171429
BLAST score 668
E value 2.0e-70
Match length 138
% identity 57

NCBI Description (U44028) CKC [Arabidopsis thaliana]

Seq. No. 32563

Contig ID 293394\_1.R1040

5'-most EST g5057754
Method BLASTX
NCBI GI g2959324
BLAST score 245
E value 1.0e-20
Match length 61
% identity 79

NCBI Description (Y15224) Importin alpha-like protein [Arabidopsis thaliana]

Seq. No. 32564

Contig ID 293453\_1.R1040 5'-most EST zsg701120212.h1

Method BLASTX
NCBI GI g3176723
BLAST score 188
E value 6.0e-17
Match length 104
% identity 46

NCBI Description (AC002392) putative protein kinase [Arabidopsis thaliana]

Seq. No. 32565

Contig ID 293526 1.R1040

5'-most EST jC-gmst02400055h08a1

Seq. No. 32566

Contig ID 293613 1.R1040

5'-most EST jC-gmst02400058h07a1

Seq. No. 32567

Contig ID 293725\_1.R1040 5'-most EST zsg701126009.h1



32568 Seq. No. Contig ID 293779 1.R1040 5'-most EST

zsg701120654.h1

Method BLASTX NCBI GI g1663537 BLAST score 240 E value 4.0e-20 Match length 151 % identity 39

NCBI Description (U55803) disease resistance protein homolog [Glycine max]

Seq. No. 32569

Contig ID 293817 1.R1040 5'-most EST jC-gmf102220103h08a1

Method BLASTX NCBI GI q1077569 BLAST score 346 1.0e-32 E value Match length 164 % identity 41

NCBI Description probable membrane protein YDR109c - yeast (Saccharomyces

cerevisiae) >gi\_747884\_emb\_CAA88663\_ (Z48758) unknown

[Saccharomyces cerevisiae]

Seq. No. 32570

Contig ID 293829 1.R1040 5'-most EST zsg701120720.h1

Method BLASTX NCBI GI q2960364 BLAST score 330 E value 9.0e - 31Match length 127 % identity 46

NCBI Description (AJ224986) cinnamoyl CoA reductase [Populus balsamifera

subsp. trichocarpa]

Seq. No. 32571

Contig ID 293899 1.R1040 5'-most EST zsg701122101.h1

Method BLASTX NCBI GI g2735017 BLAST score 290 E value 2.0e-26 97 Match length % identity 58

NCBI Description (U82481) KI domain interacting kinase 1 [Zea mays]

Seq. No. 32572

Contig ID 293959 1.R1040 5'-most EST zsg701129661.hl

Seq. No. 32573

Contig ID 293970 1.R1040 5'-most EST asn701140095.h1

BLASTX Method NCBI GI q4493908 BLAST score 235



E value 6.0e-20 Match length 87 % identity 45

NCBI Description (AL034558) predicted using hexExon; MAL3P2.30 (PFC0305w),

Putative homologue of Human EB1, len: 511 aa; Similarity to Human EB1 protein. H.sapiens EB1 protein (TR:Q156910) BLAST

Score: 325, sum P(2) = 6.2e-35; 46% identity in

Seq. No. 32574

Contig ID 294089\_1.R1040 5'-most EST zsg701121057.h1

Seq. No. 32575

Contig ID 294097\_1.R1040 5'-most EST zsg701121068.h1

Method BLASTN
NCBI GI g3046856
BLAST score 45
E value 3.0e-16
Match length 164
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXI22, complete sequence [Arabidopsis thaliana]

Seq. No. 32576

Contig ID 294135\_1.R1040 5'-most EST zsg701121119.h1

Seq. No. 32577

Contig ID 294144 1.R1040

5'-most EST uC-gmflminsoy098b03b1

Seq. No. 32578

Contig ID 294184\_1.R1040

5'-most EST g4437061
Method BLASTX
NCBI GI g2497539
BLAST score 336
E value 3.0e-31
Match length 120
% identity 56

NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi\_169703

(M64736) ATP:pyruvate phosphotransferase [Ricinus communis]

Seq. No. 32579

Contig ID 294184 2.R1040

5'-most EST jC-gmle01810031e07d1

Seq. No. 32580

Contig ID 294246\_1.R1040 5'-most EST zsg701130122.h1

Method BLASTX
NCBI GI g3927831
BLAST score 391
E value 3.0e-38
Match length 96
% identity 79



NCBI Description (AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq. No. 32581

Contig ID 294291 1.R1040

5'-most EST uC-gmflminsoy089a05b1

Seq. No. 32582

Contig ID 294292\_1.R1040 5'-most EST jC-gmf102220090c08d1

Seq. No. 32583

Contig ID 294295\_1.R1040 5'-most EST zsg701121395.h1

Method BLASTX
NCBI GI g3033399
BLAST score 144
E value 3.0e-09
Match length 56
% identity 52

NCBI Description (AC004238) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32584

Contig ID 294333\_1.R1040

5'-most EST uC-gmrominsoy275f03b1

Method BLASTN
NCBI GI g886099
BLAST score 36
E value 9.0e-11
Match length 67
% identity 97

NCBI Description Glycine max putative water channel protein (Pip1) mRNA,

complete cds

Seq. No. 32585

Contig ID 294406\_2.R1040 5'-most EST zsg701121561.h1

Method BLASTN
NCBI GI g22073
BLAST score 54
E value 1.0e-21
Match length 58
% identity 98

NCBI Description Mung bean 25S rRNA - 18S rDNA spacer region

Seq. No. 32586

Contig ID 294438 1.R1040

5'-most EST uC-gmflminsoy120e03b1

Method BLASTX
NCBI GI g3289002
BLAST score 166
E value 6.0e-12
Match length 89
% identity 23

NCBI Description (AF073522) CRP1 [Zea mays]

Seq. No. 32587



Contig ID 294475\_1.R1040 5'-most EST jC-gmle01810075g03a1

Seq. No. 32588

Contig ID 294632 1.R1040

5'-most EST uC-gmrominsoy175g11b1

Method BLASTX
NCBI GI g2062169
BLAST score 438
E value 1.0e-43
Match length 107
% identity 53

NCBI Description (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis

thaliana]

Seq. No. 32589

Contig ID 294645\_1.R1040 5'-most EST zsg701122111.h1

Seq. No. 32590

Contig ID 294753\_1.R1040 5'-most EST zsg701122347.h1

Method BLASTX
NCBI GI g4415924
BLAST score 316
E value 2.0e-29
Match length 95
% identity 60

NCBI Description (AC006282) putative glucosyl transferase [Arabidopsis

thaliana]

Seq. No. 32591

Contig ID 294755\_1.R1040 5'-most EST zsg701122354.h1

Seq. No. 32592

Contig ID 294820\_1.R1040

5'-most EST jC-gmf\(\bar{1}\)02220084h03a1

Seq. No. 32593

Contig ID 294859\_1.R1040 5'-most EST zsg701122569.h1

Seq. No. 32594

Contig ID 294893 1.R1040

5'-most EST uC-gmrominsoy031g12b1

Method BLASTN
NCBI GI g169048
BLAST score 226
E value 1.0e-124
Match length 378
% identity 90

NCBI Description Pea farnesyltransferase beta-subunit mRNA, complete cds

Seq. No. 32595

Contig ID 295073\_1.R1040 5'-most EST zsg701122936.h1

Contig ID 295099\_1.R1040

5'-most EST uC-gmflminsoy002b02b1

Method BLASTX
NCBI GI g3335349
BLAST score 413
E value 2.0e-40
Match length 117
% identity 74

NCBI Description (AC004512) Similar to gb\_U46691 putative chromatin

structure regulator (SUPT6H) from Homo sapiens. ESTs

gb T42908, gb AA586170 and gb AA395125 come from this gene.

[Arabidopsis thaliana]

Seq. No. 32597

Contig ID 295114\_1.R1040 5'-most EST zsg701122991.h1

Method BLASTX
NCBI GI g3063458
BLAST score 339
E value 1.0e-31
Match length 132
% identity 51

NCBI Description (AC003981) F22013.20 [Arabidopsis thaliana]

Seq. No. 32598

Contig ID 295156\_1.R1040

5'-most EST jC-gms $\overline{t}$ 02400071e12a1

Method BLASTX
NCBI GI g4314365
BLAST score 331
E value 1.0e-30
Match length 207
% identity 43

NCBI Description (AC006340) putative copia-like retrotransposon Hopscotch

[Arabidopsis thaliana]

Seq. No. 32599

Contig ID 295212\_1.R1040 5'-most EST zsg701123250.h1

Method BLASTX
NCBI GI g4544407
BLAST score 271
E value 3.0e-24
Match length 73
% identity 62

NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32600

Contig ID 295220\_1.R1040 5'-most EST zsg701123155.h1

Seq. No. 32601

Contig ID 295235\_1.R1040

5'-most EST uC-gmrominsoy320d06b1

Method BLASTX



NCBI GI g3549626 BLAST score 166 E value 1.0e-11 Match length 108 % identity 41

NCBI Description (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

Seq. No. 32602

Contig ID 295278\_1.R1040 5'-most EST zsg701123256.h1

Method BLASTX
NCBI GI g2583120
BLAST score 153
E value 1.0e-09
Match length 170
% identity 15

NCBI Description (AC002387) putative receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 32603

Contig ID 295335\_1.R1040 5'-most EST asn701140185.h1

Seq. No. 32604

Contig ID 295367\_1.R1040 5'-most EST zsg701123470.h1

Seq. No. 32605

Contig ID 295386\_1.R1040 5'-most EST zsg701123392.h1

Seq. No. 32606

Contig ID 295405\_1.R1040 5'-most EST zsq701123417.h1

Seq. No. 32607

Contig ID 295413\_1.R1040 5'-most EST jC-gmst02400039a12a1

Method BLASTX
NCBI GI g3107903
BLAST score 257
E value 5.0e-22
Match length 65
% identity 69

NCBI Description (D83719) polycomb-like protein [Daucus carota]

Seq. No. 32608

Contig ID 295471\_1.R1040 5'-most EST uC-gmropic021b08b1

Method BLASTX
NCBI GI g3980384
BLAST score 259
E value 3.0e-22
Match length 124
% identity 42

NCBI Description (AC004561) hypothetical protein [Arabidopsis thaliana]



Contig ID 295614\_1.R1040 5'-most EST zsg701123679.h1

Seq. No. 32610

Contig ID 295641\_1.R1040 5'-most EST zsg701123866.h1

Seq. No. 32611

Contig ID 295713\_1.R1040 5'-most EST jC-gmst02400065h01d1

Method BLASTX
NCBI GI g1055162
BLAST score 194
E value 8.0e-15
Match length 130
% identity 38

NCBI Description (U40029) coded for by C. elegans cDNA yk16b1.3; coded for

by C. elegans cDNA yk8g6.5; coded for by C. elegans cDNA yk8g6.3; coded for by C. elegans cDNA yk6d3.5; coded for by

C. elegans cDNA yk6d3.3; coded for by C. elegans cDNA

yk7e12.5; co

Seq. No. 32612

Contig ID 295725\_1.R1040 5'-most EST zsg701123841.h1

Seq. No. 32613

Contig ID 295776 1.R1040 5'-most EST zsg701123912.h1

Seq. No. 32614

Contig ID 295821\_1.R1040 5'-most EST asn701142424.h1

Method BLASTX
NCBI GI g4191786
BLAST score 225
E value 2.0e-18
Match length 52
% identity 87

NCBI Description (AC005917) unknown protein [Arabidopsis thaliana]

Seq. No. 32615

Contig ID 295846 1.R1040 5'-most EST zsg701124006.h1

Seq. No. 32616

Contig ID 295873\_1.R1040 5'-most EST zsg701124036.h1

Seq. No. 32617

Contig ID 295891\_1.R1040 5'-most EST jC-qmle01810044a06a1

MethodBLASTXNCBI GIg4263778BLAST score342E value4.0e-32



Match length 92 % identity 66

NCBI Description (AC006068) putative serine carboxypeptidase II [Arabidopsis

thaliana]

Seq. No. 32618

Contig ID 295909\_1.R1040 5'-most EST zsg701124081.h1

Seq. No. 32619

Contig ID 295913 1.R1040

5'-most EST uC-gmflminsoy044c03b1

Seq. No. 32620

Contig ID 295978\_1.R1040

5'-most EST jC-gmro02800028f06a1

Seq. No. 32621

Contig ID 296187 1.R1040

5'-most EST g5606708

Seq. No. 32622

Contig ID 296282\_1.R1040

5'-most EST jC-gmst02400074g01a1

Seq. No. 32623

Contig ID 296308\_1.R1040 5'-most EST zsg701124740.h1

Seq. No. 32624

Contig ID 296345\_1.R1040 5'-most EST uC-gmropic104e02b1

Method BLASTX
NCBI GI g1553133
BLAST score 234
E value 3.0e-19
Match length 161
% identity 19

NCBI Description (U64722) actin-fragmin kinase [Physarum polycephalum]

Seq. No. 32625

Contig ID 296424 1.R1040 5'-most EST zsg701127390.h1

Method BLASTX
NCBI GI g2194117
BLAST score 301
E value 1.0e-27
Match length 99
% identity 60

NCBI Description (AC002062) Strong similarity to Arabidopsis receptor

protein kinase PR5K (gb\_ATU48698). [Arabidopsis thaliana]

Seq. No. 32626

Contig ID 296435 1.R1040

5'-most EST g4307200 Method BLASTX NCBI GI g1171429



BLAST score 477 E value 6.0e-48 Match length 147 % identity 47

NCBI Description (U44028) CKC [Arabidopsis thaliana]

Seq. No. 32627

Contig ID 296489 1.R1040 5'-most EST zsg701125024.h1

Seq. No. 32628

Contig ID 296554\_1.R1040 5'-most EST uC-gmropic096g05b1

Seq. No. 32629

Contig ID 296671\_1.R1040 5'-most EST zsg701125390.h1

Method BLASTX
NCBI GI g2213600
BLAST score 213
E value 5.0e-17
Match length 117
% identity 43

NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No. 32630

Contig ID 296679 1.R1040

5'-most EST  $q43972\overline{18}$ 

Seq. No. 32631

Contig ID 296872 1.R1040

5'-most EST uC-gmflminsoy100b07b1

Method BLASTX
NCBI GI g3892709
BLAST score 235
E value 1.0e-19
Match length 114
% identity 53

NCBI Description (AL033545) putative protein [Arabidopsis thaliana]

Seq. No. 32632

Contig ID 296904\_1.R1040 5'-most EST jC-gmfl02220143c12a1

Method BLASTX
NCBI GI g2811226
BLAST score 497
E value 3.0e-50
Match length 142
% identity 69

NCBI Description (AF042669) fimbrin 2 [Arabidopsis thaliana] >gi\_2811232

(AF042671) fimbrin 2 [Arabidopsis thaliana]

Seq. No. 32633

Contig ID 296914 1.R1040 5'-most EST asn701133289.h1

Seq. No. 32634



Contig ID 297000\_1.R1040 5'-most EST uC-gmflminsoy079g06b1

Seq. No. 32635

Contig ID 297192\_1.R1040 5'-most EST jC-gmle01810030h05a2

Seq. No. 32636

Contig ID 297261\_1.R1040 5'-most EST zsg701126236.h1

Seq. No. 32637

Contig ID 297333 1.R1040

5'-most EST uC-gmrominsoy256d12b1

Method BLASTX
NCBI GI g4204302
BLAST score 143
E value 7.0e-09
Match length 41

Match length 41 % identity 66

NCBI Description (AC003027) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 32638

Contig ID 297447\_1.R1040 5'-most EST uC-gmropic012f02b1

Seq. No. 32639

Contig ID 297574\_1.R1040

5'-most EST jC-gmf102220051a08a1

Method BLASTX
NCBI GI g4001805
BLAST score 130
E value 8.0e-12
Match length 122
% identity 36

NCBI Description (AF041476) BAF53a [Mus musculus]

Seq. No. 32640

Contig ID 297593\_1.R1040 5'-most EST fC-gmro700561647w1

Method BLASTX
NCBI GI 94510406
BLAST score 373
E value 2.0e-35
Match length 110
% identity 66

NCBI Description (AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No. 32641

Contig ID 297594 1.R1040

5'-most EST jC-gmle01810090d01a1

Method BLASTX
NCBI GI g3157943
BLAST score 141
E value 1.0e-14
Match length 98
% identity 50



NCBI Description (AC002131) Contains similarity to BAP31 protein gb\_X81816 from Mus musculus. [Arabidopsis thaliana]

Seq. No. 32642

Contig ID 297722\_1.R1040 5'-most EST zsg701127004.h1

Method BLASTX
NCBI GI g2341032
BLAST score 305
E value 4.0e-28
Match length 92
% identity 65

NCBI Description (AC000104) EST gb\_ATTS0956 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 32643

Contig ID 297777\_1.R1040 5'-most EST uC-gmropic111d05b1

Seq. No. 32644

Contig ID 297877 1.R1040

5'-most EST uC-gmrominsoy241e08b1

Seq. No. 32645

Contig ID 297936\_1.R1040 5'-most EST zsg701127433.h1

Seq. No. 32646

Contig ID 298080\_1.R1040

5'-most EST uC-gmflminsoy018e06b1

Method BLASTX
NCBI GI g3885342
BLAST score 398
E value 1.0e-38
Match length 105
% identity 70

NCBI Description (AC005623) putative DNA polymerase [Arabidopsis thaliana]

Seq. No. 32647

Contig ID 298227 1.R1040

5'-most EST uC-gmrominsoy199e07b1

Method BLASTX
NCBI GI g1663648
BLAST score 300
E value 3.0e-27
Match length 151
% identity 46

NCBI Description (U75321) chromaffin granule ATPase II homolog [Mus

musculus]

Seq. No. 32648

Contig ID 298291\_1.R1040 5'-most EST zsg701129887.h1

Seq. No. 32649

Contig ID 298312\_1.R1040 5'-most EST uC-gmropic101d09b1

```
32650
Seq. No.
                  298361 1.R1040
Contig ID
5'-most EST
                  zsg701127922.h1
                  32651
Seq. No.
                  298637 1.R1040
Contig ID
                  uC-gmrominsoy115b09b1
5'-most EST
Seq. No.
                  32652
                  298705 1.R1040
Contig ID
                  zsg701128652.h1
5'-most EST
Method
                  BLASTX
                  g3176726
NCBI GI
BLAST score
                  361
E value
                   9.0e-35
Match length
                   91
% identity
                  75
                  (AC002392) putative serine proteinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   32653
Contig ID
                   298721 1.R1040
5'-most EST
                   asn701134467.hl
Method
                  BLASTX
NCBI GI
                   g3080450
BLAST score
                  185
E value
                   4.0e-14
Match length
                   79
% identity
                   49
                  (AL022605) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   32654
Seq. No.
                   298826 1.R1040
Contig ID
5'-most EST
                   zsg701129278.hl
Method
                  BLASTN
                   g35589
NCBI GI
                   272
BLAST score
                   1.0e-151
E value
Match length
                   272
                   100
% identity
                  Human pancreatic polypeptide(PP) and icosapeptide precursor
NCBI Description
                   >qi 4506032 ref NM 002722.1 PPY Homo sapiens pancreatic
                   polypeptide (PPY) mRNA
                   32655
Seq. No.
Contig ID
                   298841 1.R1040
5'-most EST
                   zsg701129285.hl
                   BLASTN
Method
NCBI GI
                   g177828
BLAST score
                   293
E value
                   1.0e-164
                   293
Match length
                   100
% identity
```

NCBI Description Human alpha-1-antitrypsin mRNA, complete cds



```
Contig ID 298844_1.R1040
5'-most EST zsg701128941.h1
Method BLASTN
NCBI GI q32417
```

BLAST score 238 E value 1.0e-131 Match length 477 % identity 66

NCBI Description Human Hp2 gene fragment for haptoglobin alpha- and

beta-chain

Seq. No. 32657

Contig ID 298852\_1.R1040 5'-most EST zsg701129141.h1

Method BLASTN
NCBI GI g182429
BLAST score 614
E value 0.0e+00
Match length 622
% identity 100

NCBI Description Human fibrinogen beta-chain mRNA, partial cds

Seq. No. 32658

Contig ID 298859\_1.R1040 5'-most EST zsg701128965.h1

Method BLÄSTN
NCBI GI g183269
BLAST score 424
E value 0.0e+00
Match length 460
% identity 98

NCBI Description Human glucagon mRNA, complete cds.

>gi\_4503944 ref NM\_002054.1 GCG Homo sapiens glucagon

(GCG) mRNA

Seq. No. 32659

Contig ID 298861\_1.R1040 5'-most EST zsg701128967.h1

Method BLASTN
NCBI GI g183269
BLAST score 231
E value 1.0e-127
Match length 235
% identity 100

NCBI Description Human glucagon mRNA, complete cds.

>gi\_4503944\_ref\_NM\_002054.1\_GCG\_ Homo sapiens glucagon

(GCG) mRNA

Seq. No. 32660

Contig ID 298865\_1.R1040 5'-most EST zsg701128973.h1

Method BLASTN
NCBI GI g189583
BLAST score 269
E value 1.0e-150
Match length 281
% identity 99



## NCBI Description Human prealbumin mRNA, complete cds

Seq. No. 32661

Contig ID 298891\_1.R1040 5'-most EST zsg701129086.h1

Method BLASTN
NCBI GI g28589
BLAST score 229
E value 1.0e-126
Match length 252
% identity 98

NCBI Description Human messenger RNA for serum albumin (HSA)

Seq. No. 32662

Contig ID 298896\_1.R1040 5'-most EST zsg701129017.h1

Seq. No. 32663

Contig ID 298925\_1.R1040 5'-most EST zsg701129119.h1

Method BLASTN
NCBI GI g1490418
BLAST score 272
E value 1.0e-152
Match length 284
% identity 33

NCBI Description Human ubiquitin gene, complete cds

Seq. No. 32664

Contig ID 298944\_1.R1040 5'-most EST zsg701129095.h1

Method BLASTN
NCBI GI g24444
BLAST score 281
E value 1.0e-157
Match length 285
% identity 100

NCBI Description Human mRNA for alpha1-acid glycoprotein (orosomucoid)

Seq. No. 32665

Contig ID 298950\_1.R1040 5'-most EST zsg701129107.h1

Method BLASTN
NCBI GI g288104
BLAST score 298
E value 1.0e-167
Match length 302
% identity 100

NCBI Description H.sapiens mRNA for 4-hydroxyphenylpyruvate dioxygenase

>gi\_4504476\_ref\_NM\_002150.1\_HPD\_ Homo sapiens
4-hydroxyphenylpyruvate dioxygenase (HPD) mRNA

Seq. No. 32666

Contig ID 298958\_1.R1040 5'-most EST zsg701129116.h1

Method BLASTN NCBI GI g34753



```
BLAST score
                   276
 E value
                   1.0e-154
Match length
                   280
 % identity
                   100
NCBI Description
                   Human MRL3 mRNA for ribosomal protein L3 homologue ( MRL3 =
                   mammalian ribosome L3 )
Seq. No.
                   32667
                   298963 1.R1040
Contig ID
5'-most EST
                   zsg701129122.h1
Seq. No.
                   32668
Contig ID
                   298982_1.R1040
5'-most EST
                   zsg701129148.h1
Method
                   BLASTN
NCBI GI
                   g32429
BLAST score
                   487
E value
                   0.0e+00
Match length
                   503
% identity
                   99
NCBI Description Human mRNA FOR haptoglobin alpha 1S (Hpa 1S)
Seq. No.
                   32669
Contig ID
                   299015 1.R1040
5'-most EST
                   zsg701129187.h1
Method
                   BLASTN
NCBI GI
                   g4503714
BLAST score
                   300
E value
                   1.0e~168
Match length
                   300
% identity
                   100
NCBI Description
                 Homo sapiens fibrinogen, gamma polypeptide (FGG) mRNA
Seq. No.
                   32670
                   299031 1.R1040
Contig ID
5'-most EST
                   zsg701129234.h1
Method
                   BLASTN
NCBI GI
                   g34312
BLAST score
                   288
E value
                  1.0e-161
Match length
                   296
% identity
                   99
NCBI Description Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27)
Seq. No.
                   32671
Contig ID
                  299058 1.R1040
5'-most EST
                  zsg701129264.h1
Method
                  BLASTN
NCBI GI
                  g452047
BLAST score
                  189
E value
                  1.0e-102
Match length
                  261
```

% identity 93

NCBI Description Homo sapiens HnRNP F protein mRNA, complete cds

Seq. No. 32672

299172\_1.R1040 Contig ID



```
5'-most EST
                  q5666766
                  32673
Seq. No.
                  299202 1.R1040
Contig ID
5'-most EST
                  zsq701129448.h1
                  BLASTX
Method
NCBI GI
                  q3036819
BLAST score
                  518
E value
                  1.0e-52
Match length
                  143
% identity
                  72
                  (AJ000058) MCM3 homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  32674
                  299220 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910066a05a1
                  BLASTX
Method
NCBI GI
                  g4056489
BLAST score
                  144
                  8.0e-09
E value
                  104
Match length
                  36
% identity
NCBI Description (AC005896) putative white protein [Arabidopsis thaliana]
                  32675
Seq. No.
Contig ID
                  299233 1.R1040
5'-most EST
                  uC-gmflminsoy119a01b1
Method
                  BLASTX
                  g2979554
NCBI GI
BLAST score
                  381
                  7.0e-37
E value
                  115
Match length
% identity
                   61
                  (AC003680) CDC4 like protein [Arabidopsis thaliana]
NCBI Description
                   32676
Seq. No.
                   299340 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy028b04b1
                   32677
Seq. No.
Contig ID
                   299404 1.R1040
5'-most EST
                  uC-gmrominsoy179b12b1
Method
                   BLASTX
                   g2827635
NCBI GI
BLAST score
                   775
E value
                  1.0e-82
Match length
                   199
% identity
                   75
                  (AL021636) predicted protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32678
Contig ID
                   299425 1.R1040
5'-most EST
                   uC-gmflminsoy047f11b1
```

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Seq. No. 32679 Contig ID 299453\_1.R1040 5'-most EST zsg701129776.h1

```
32680
Seq. No.
                   299497 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy008e06b1
                   32681
Seq. No.
                  299503 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy070c08b1
                   32682
Seq. No.
Contig ID
                  299510 1.R1040
5'-most EST
                  jC-gmro02910059h07a1
Seq. No.
                   32683
Contig ID
                  299526 1.R1040
5'-most EST
                  g5509852
                   32684
Seq. No.
                  299542 1.R1040
Contig ID
5'-most EST
                  q56062\overline{67}
                  BLASTX
Method
NCBI GI
                  g2853087
                   327
BLAST score
E value
                  3.0e-30
Match length
                   95
                   69
% identity
NCBI Description (AL021768) putative protein [Arabidopsis thaliana]
                   32685
Seq. No.
Contig ID
                   299573 1.R1040
                   g5677178
5'-most EST
                  BLASTX
Method
NCBI GI
                   g4204281
BLAST score
                   203
                   1.0e-15
E value
Match length
                   99
% identity
                   38
NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   32686
                   299740 1.R1040
Contig ID
5'-most EST
                   zsg701130174.h1
                   32687
Seq. No.
                   299806 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy138c10b1
Seq. No.
                   32688
```

Contig ID 299932\_1.R1040 5'-most EST asn701131393.h1

Method BLASTX
NCBI GI g3201541
BLAST score 312
E value 1.0e-28
Match length 128
% identity 54

NCBI Description (AJ005077) TCTR2 protein [Lycopersicon esculentum]

```
32689
Seq. No.
                  299992 1.R1040
Contig ID
                  asn701130596.h1
5'-most EST
Method
                  BLASTX
                  g3005931
NCBI GI
BLAST score
                  187
                  2.0e-14
E value
Match length
                  68
                  53
% identity
NCBI Description (AJ005016) ABC transporter [Homo sapiens]
                  32690
Seq. No.
Contig ID
                  300357 1.R1040
                  asn701\overline{1}33603.h2
5'-most EST
Seq. No.
                  32691
                  300814 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy238b11b1
Method
                  BLASTX
NCBI GI
                  g1771381
                  155
BLAST score
                  2.0e-10
E value
Match length
                  81
% identity
                  42
NCBI Description
                  (X95877) phosphoinositide-specific phospholipase C
                   [Nicotiana rustica]
                   32692
Seq. No.
Contig ID
                  300869 1.R1040
5'-most EST
                   jC-qmst02400071c02a1
Method
                  BLASTX
                  q1785851
NCBI GI
BLAST score
                  152
                   8.0e-10
E value
Match length
                   83
% identity
                   36
                  (D50692) c-myc binding protein [Homo sapiens]
NCBI Description
                  >gi 2443310 dbj BAA22408 (AB007191) AMY-1 [Homo sapiens]
                   32693
Seq. No.
Contig ID
                   300980 1.R1040
5'-most EST
                  asn701132877.h1
Seq. No.
                   32694
                   301112 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy022e04b1
                  BLASTX
Method
NCBI GI
                   q1703168
BLAST score
                   219
E value
                   7.0e-18
Match length
                  121
```

44 % identity BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN NCBI Description BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA

LARGE CHAIN) (AP105A) >gi\_482950\_pir\_\_B32105



119

tabacum]

Match length % identity

NCBI Description

component - rat >gi\_203113 (M77245) beta'-chain clathrin associated protein complex AP-1 [Rattus norvegicus]

32695 Seq. No. 301114 1.R1040 Contig ID  $asn701\overline{1}33063.h1$ 5'-most EST BLASTX Method NCBI GI g542058 BLAST score 161 3.0e-11 E value 52 Match length 58 % identity HSR203J protein - common tobacco >gi\_444002\_emb\_CAA54393\_ NCBI Description (X77136) HSR203J [Nicotiana tabacum] 32696 Seq. No. 301138 1.R1040 Contig ID jC-gmro02910017g12a1 5'-most EST BLASTX Method NCBI GI g3242728 BLAST score 321 1.0e-29 E value 152 Match length % identity 44 (AC003040) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 32697 301157 1.R1040 Contig ID uC-gmflminsoy080c03b1 5'-most EST 32698 Seq. No. 301243 1.R1040 Contig ID jC-gmro02910068b05a1 5'-most EST BLASTX Method NCBI GI q3860008 BLAST score 361 3.0e - 34E value Match length 152 % identity 47 (AF091085) unknown [Homo sapiens] NCBI Description 32699 Seq. No. 301343 1.R1040 Contig ID asn701133624.h2 5'-most EST 32700 Seq. No. 301346 1.R1040 Contig ID  $asn701\overline{1}41925.h1$ 5'-most EST Method BLASTX q2739168 NCBI GI BLAST score 260 1.0e-22 E value

4973

(AF032386) aldose-1-epimerase-like protein [Nicotiana



Seq. No. 32701 301475 1.R1040 Contig ID asn701134307.hl 5'-most EST 32702 Seq. No. 301478 1.R1040 Contig ID 5'-most EST asn701133646.h2 Method BLASTN g1675195 NCBI GI 102 BLAST score 3.0e-50 E value 240 Match length % identity Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, NCBI Description complete cds 32703 Seq. No. 301559 1.R1040 Contig ID asn701133893.h1 5'-most EST 32704 Seq. No. 301589 1.R1040 Contig ID asn701134088.hl 5'-most EST Seq. No. 32705 301649 1.R1040 Contig ID asn701134301.h1 5'-most EST 32706 Seq. No. 301683 1.R1040 Contig ID jC-gmf102220077a05d1 5'-most EST BLASTX Method q3184282 NCBI GI BLAST score 296 8.0e-27 E value Match length 70 % identity 76 (AC004136) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 32707 301807 1.R1040 Contig ID 5'-most EST uC-qmflminsoy075h04b1 32708 Seq. No. 301842 1.R1040 Contig ID 5'-most EST asn701134632.h2

32709 Seq. No.

301863 1.R1040 Contig ID 5'-most EST asn701134657.h2

Method BLASTX q2979562 NCBI GI 339 BLAST score 1.0e-31 E value Match length 124 56 % identity

NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]



>gi 3386623 (AC004665) unknown protein [Arabidopsis thaliana]

32710 Seq. No.

302092 1.R1040 Contig ID asn701135586.h1 5'-most EST

Seq. No. 32711

302099 1.R1040 Contig ID asn701135090.h1 5'-most EST

32712 Seq. No.

Contig ID 302312 1.R1040

5'-most EST jC-gmle01810059c05a1

BLASTX Method q3335378 NCBI GI BLAST score 459 8.0e-46 E value Match length 139 69 % identity

(ACO03028) Myb-related transcription activator [Arabidopsis NCBI Description

thaliana]

32713 Seq. No.

302548 1.R1040 Contig ID

5'-most EST jC-gmro02910074b09a1

BLASTX Method g2134102 NCBI GI BLAST score 506 3.0e-51 E value 193 Match length % identity

NCBI Description

kinesin-like protein 1 - African clawed frog
>gi\_562793\_emb\_CAA57539\_ (X82012) kinesin-like protein 1

[Xenopus laevis]

32714 Seq. No.

302584 1.R1040 Contig ID

jC-gmro02910012c04a1 5'-most EST

32715 Seq. No.

302605 1.R1040 Contig ID 5'-most EST asn701136918.hl

BLASTX Method NCBI GI q2618698 BLAST score 301 1.0e-27 E value 91 Match length % identity

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

32716 Seq. No.

302655 1.R1040 Contig ID

uC-gmrominsoy074b12b1 5'-most EST

Seq. No. 32717

302702 1.R1040 Contig ID



```
uC-gmrominsoy099h04b1
5'-most EST
                  BLASTN
Method
                  q938299
NCBI GI
BLAST score
                  130
E value
                  8.0e-67
Match length
                  311
% identity
NCBI Description V.ungiculata mRNA for unknown protein (A3 gene)
Seq. No.
                  32718
                  302746 1.R1040
Contig ID
5'-most EST
                  asn701136609.h1
Method
                  BLASTX
                  a2245065
NCBI GI
                  232
BLAST score
                  1.0e-19
E value
Match length
                  64
                  23
% identity
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
                  32719
Seq. No.
                  302890 1.R1040
Contig ID
5'-most EST
                  g5126428
Seq. No.
                  32720
Contig ID
                  302893 1.R1040
5'-most EST
                  jC-gmro02910010h07a1
                  32721
Seq. No.
                   302931 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810035a08a2
                  BLASTX
Method
NCBI GI
                  q2529707
BLAST score
                   276
                   3.0e-32
E value
Match length
                  158
% identity
NCBI Description (AF001434) Hpast [Homo sapiens]
Seq. No.
                   32722
                   302992 1.R1040
Contig ID
5'-most EST
                   asn701136856.h1
Seq. No.
                   32723
                   303018 1.R1040
Contig ID
5'-most EST
                   asn701136911.hl
Seq. No.
                   32724
                   303157 1.R1040
Contig ID
5'-most EST
                   uC-qmropic110e02b1
Method
                   BLASTX
                   g1363484
NCBI GI
BLAST score
                   251
                   1.0e-21
E value
```

Match length 64 75 % identity

NCBI Description IAA13 protein - Arabidopsis thaliana >gi\_972929 (U18415)



IAA13 [Arabidopsis thaliana] >gi 2459414 (AC002332) auxin inducible protein, IAA13 [Arabidopsis thaliana]

Seq. No. 32725

303183 1.R1040 Contig ID asn701137293.hl 5'-most EST

BLASTX Method g1480014 NCBI GI 151 BLAST score 4.0e-10 E value Match length 36 % identity 89

(D78493) putative delta subunit of ATP synthase [Brassica NCBI Description

32726 Seq. No.

303196 1.R1040 Contig ID

q4298152 5'-most EST Method BLASTX q3176709 NCBI GI 259 BLAST score 2.0e-22 E value 130 Match length % identity 41

(AC002392) putative anthranilate NCBI Description

N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis

thaliana]

Seq. No. 32727

303210 1.R1040 Contig ID

jC-gmf102220086d12a1 5'-most EST

32728 Seq. No.

303300 1.R1040 Contig ID

uC-gmrominsoy028c03b1 5'-most EST

BLASTX Method g114974 NCBI GI BLAST score 382 8.0e-37 E value 110 Match length 66 % identity

NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR NCBI Description

>gi\_67491\_pir\_\_GLJY31 beta-glucosidase (EC 3.2.1.21)

precursor (clone TRE361) - white clover >gi\_21955\_emb\_CAA40058.1\_ (X56734) beta-glucosidase

[Trifolium repens]

32729 Seq. No.

303343 1.R1040 Contig ID

jC-gmro02910023d09a1 5'-most EST

Method BLASTX q2289003 NCBI GI 143 BLAST score E value 1.0e-08 Match length 46 63 % identity

NCBI Description (AC002335) membrane transporter D1 isolog [Arabidopsis



## thaliana]

Seq. No. 32730

Contig ID 303579\_1.R1040 5'-most EST uC-gmropic024c03b1

Seq. No. 32731

Contig ID 303593\_1.R1040 5'-most EST jC-gmle01810091d08a1

Method BLASTX
NCBI GI g3252806
BLAST score 305
E value 9.0e-28

Match length 139 % identity 45

NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32732

Contig ID 303869 1.R1040

5'-most EST jC-gmro02910016b06d1

Seq. No. 32733

Contig ID 304041\_1.R1040

5'-most EST jC-gmf102220067a12a1

Seq. No. 32734

Contig ID 304136\_1.R1040 5'-most EST uC-gmropic024d05b1

Method BLASTX
NCBI GI g4263718
BLAST score 670
E value 1.0e-70
Match length 154
% identity 80

NCBI Description (AC006223) putative DNA topoisomerase III beta [Arabidopsis

thaliana]

Seq. No. 32735

Contig ID 304179\_1.R1040 5'-most EST jC-gmro02910001c02a1

Method BLASTX
NCBI GI g4512665
BLAST score 181
E value 3.0e-13
Match length 53
% identity 64

NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]

>qi 4544472 gb AAD22379.1\_AC006580\_11 (AC006580) unknown

protein [Arabidopsis thaliana]

Seq. No. 32736

Contig ID 304211\_1.R1040 5'-most EST jC-gmst02400025f08a1

Seq. No. 32737

Contig ID 304306 1.R1040

5'-most EST  $g43961\overline{0}5$ 



Seq. No. 32738

Contig ID 304410\_1.R1040

5'-most EST uC-gmrominsoy229f12b1

Seq. No. 32739

Contig ID 304594\_1.R1040 5'-most EST jC-gmle01810066h11a1

Method BLASTX
NCBI GI g140496
BLAST score 157
E value 2.0e-10
Match length 132

% identity 32 NCBI Description HYPOTHETICAL 42.5 KD PROTEIN IN TSM1-ARE1 INTERGENIC REGION

>gi\_83226\_pir\_\_S19457 probable membrane protein YCR044c yeast (Saccharomyces cerevisiae) >gi\_1907186\_emb\_CAA42292\_

(X59720) YCR044c, len:357 [Saccharomyces cerevisiae]

Seq. No. 32740

Contig ID 304629\_1.R1040 5'-most EST asn701139693.h1

Method BLASTX
NCBI GI g1929998
BLAST score 306
E value 1.0e-27
Match length 145
% identity 41

NCBI Description (U77463) NADPH-dependent HC-toxin reductase [Hordeum

vulgare]

Seq. No. 32741

Contig ID 304693\_1.R1040

5'-most EST jC-gmle01810064g04d1

Seq. No. 32742

Contig ID 304803\_1.R1040 5'-most EST asn701140503.h1

Seq. No. 32743

Contig ID 304927\_1.R1040 5'-most EST asn701140133.h1

Seq. No. 32744

Contig ID 304937 1.R1040

5'-most EST uC-gmflminsoy120c02b1

Method BLASTX
NCBI GI 94220524
BLAST score 272
E value 3.0e-24
Match length 92
% identity 61

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 32745

Contig ID 305124\_1.R1040 5'-most EST asn701140533.h1



Method BLASTX
NCBI GI g4262167
BLAST score 509
E value 1.0e-51
Match length 116
% identity 83

NCBI Description (AC005275) putative LRR receptor-linked protein kinase

[Arabidopsis thaliana]

Seq. No. 32746

Contig ID 305156\_1.R1040 5'-most EST asn701140683.h1

Seq. No. 32747

Contig ID 305323\_1.R1040

5'-most EST jC-gmro02910006c08a1

Method BLASTN
NCBI GI g347454
BLAST score 80
E value 6.0e-37
Match length 237
% identity 40

NCBI Description Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3'

end

Seq. No. 32748

Contig ID 305661\_1.R1040 5'-most EST asn701141506.h1

Method BLASTX
NCBI GI g4416307
BLAST score 308
E value 4.0e-28
Match length 104
% identity 53

NCBI Description (AF105716) hypothetical protein [Zea mays]

Seq. No. 32749

Contig ID 305791\_1.R1040

5'-most EST g4397239
Method BLASTN
NCBI GI g169348
BLAST score 50
E value 4.0e-19
Match length 212
% identity 86

NCBI Description P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3'

end

Seq. No. 32750

Contig ID 305867 1.R1040 5'-most EST asn701141850.h1

Seq. No. 32751

Contig ID 305957 1.R1040

5'-most EST g4396382

Seq. No. 32752

% identity

NCBI Description

54



```
306078 1.R1040
Contig ID
                   jC-gms\(\overline{t}\)02400076b03d1
5'-most EST
                   BLASTX
Method
                   g2262159
NCBI GI
                   155
BLAST score
                   3.0e-10
E value
                   46
Match length
                   65
% identity
                   (AC002329) predicted protein similar to S.pombe protein
NCBI Description
                   C5H10.03 [Arabidopsis thaliana]
                   32753
Seq. No.
                   306142 1.R1040
Contig ID
                   jC-gmst02400049g11d1
5'-most EST
Method
                   BLASTX
                   g3493367
NCBI GI
                   156
BLAST score
                   3.0e-10
E value
                   44
Match length
                   70
% identity
                   (AB017159) citrate synthase [Daucus carota]
NCBI Description
                   32754
Seq. No.
                   306384 1.R1040
Contig ID
                   uC-gmrominsoy053h02b1
5'-most EST
Method
                   BLASTX
                   g4263722
NCBI GI
BLAST score
                   364
                   8.0e-35
E value
                   126
Match length
                   56
% identity
                   (ACO06223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
                   32755
Seq. No.
                   306544_1.R1040
Contig ID
                   asn701142952.h2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1176529
                   327
BLAST score
                   3.0e-30
E value
                   138
Match length
                   41
% identity
                   HYPOTHETICAL 100.9 KD PROTEIN C34E10.3 IN CHROMOSOME III
NCBI Description
                   >gi_500726 (U10402) C34E10.3 gene product [Caenorhabditis
                   elegans]
                   32756
Seq. No.
                   306582 1.R1040
Contig ID
5'-most EST
                   g4313715
Method
                   BLASTX
NCBI GI
                   q3861153
                    311
BLAST score
                   2.0e-28
E value
                   111
Match length
```

4981

[Rickettsia prowazekii]

(AJ235272) CYANELLE 50S RIBOSOMAL PROTEIN L20 (rplT)



32757 Seq. No.

306594 1.R1040 Contig ID asn701143167.hl 5'-most EST

32758 Seq. No.

306662 1.R1040 Contig ID uC-gmropic015h12b1 5'-most EST

Seq. No. 32759

306703\_1.R1040 Contig ID

uC-gmrominsoy173e03b1 5'-most EST

BLASTX Method q4103635 NCBI GI BLAST score 222 E value 5.0e-18 112 Match length 38 % identity

(AF026538) ABA-responsive protein [Hordeum vulgare] NCBI Description

Seq. No. 32760

306825 1.R1040 Contig ID

jC-gmf102220050a02d1 5'-most EST

32761 Seq. No.

Contig ID 306827 1.R1040

jC-gmf102220050a03d1 5'-most EST

Method BLASTX NCBI GI q417576 144 BLAST score 5.0e-09 E value 71 Match length 45 % identity

NCBI Description

60S RIBOSOMAL PROTEIN YL16A >gi\_322960\_pir\_S28944 ribosomal protein L6.e.A, cytosolic - yeast (Saccharomyces cerevisiae) >gi\_218509\_dbj\_BAA01077\_ (D10225) ribosomal

protein YL16 [Saccharomyces cerevisiae]

>gi\_914877\_emb\_CAA86505\_ (Z46373) YL16a gene, len: 176, CAI: 0.64, R16A YEAST Q02326 60S ribosomal protein YL16A

[Saccharomyces cerevisiae]

32762 Seq. No.

306837 1.R1040 Contig ID

5'-most EST jC-gmf102220050a10d1

32763 Seq. No.

306839 1.R1040 Contig ID

5'-most EST  $jC-gmf\overline{1}02220050a12a1$ 

32764 Seq. No.

Contig ID 306841 1.R1040

jC-gmf102220050b01d1 5'-most EST

BLASTX Method g2341032 NCBI GI 263 BLAST score E value 8.0e-23 93 Match length



% identity 60
NCBI Description (AC000104) EST gb\_ATTS0956 comes from this gene.
[Arabidopsis thaliana]

Seq. No. 32765

Contig ID 306850 1.R1040

5'-most EST jC-gmf102220050b07a1

Seq. No. 32766

Contig ID 306873\_1.R1040

5'-most EST jC-gmle01810092g03d1

Method BLASTX
NCBI GI g3152583
BLAST score 229
E value 6.0e-19
Match length 90
% identity 54

NCBI Description (AC002986) Contains similarity to inhibitor of apoptosis

protein gb\_U45881 from D. melanogaster. [Arabidopsis

thaliana]

Seq. No. 32767

Contig ID 306888\_1.R1040

5'-most EST jC-gmle01810050c02d1

Method BLASTN
NCBI GI g2351071
BLAST score 40
E value 5.0e-13
Match length 116
% identity 84

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MVA3, complete sequence [Arabidopsis thaliana]

Seq. No. 32768

Contig ID 306910\_1.R1040

5'-most EST jC-gmfl02220050e04d1

Seq. No. 32769

Contig ID 306923\_1.R1040

5'-most EST jC-gmle01810036e03d1

Seq. No. 32770

Contig ID 306925 1.R1040

5'-most EST jC-gmst02400065e10d1

Seq. No. 32771

Contig ID 306932\_1.R1040

5'-most EST jC-gmf102220050f05d1

Seq. No. 32772

Contig ID 306944 1.R1040 5'-most EST jC-gmfI02220050f11d1

Method BLASTN
NCBI GI g2924257
BLAST score 379
E value 0.0e+00
Match length 483



% identity NCBI Description Tobacco chloroplast genome DNA Seq. No. 32773 306951 1.R1040 Contig ID jC-gmle01810050f02d1 5'-most EST 32774 Seq. No. 306972 1.R1040 Contig ID jC-gmf102220050h03a1 5'-most EST BLASTX Method g3668077 NCBI GI 125 BLAST score 3.0e-09 E value Match length 67 % identity 55 (AC004667) hypothetical protein [Arabidopsis thaliana] NCBI Description 32775 Seq. No. 306975 1.R1040 Contig ID jC-gmle01810050h04d1 5'-most EST BLASTX Method g2447013 NCBI GI BLAST score 167 1.0e-11 E value 63 Match length % identity 52 (D37949) defective F1F0-ATPase alpha subunit precursor NCBI Description [Saccharomyces cerevisiae] 32776 Seq. No. 307016 1.R1040 Contig ID jC-gmle01810051b05d15'-most EST BLASTX Method g3033392 NCBI GI 283 BLAST score 3.0e-25 E value 85 Match length 65 % identity (AC004238) putative translation initiation factor NCBI Description EIF-2B-epsilon subunit [Arabidopsis thaliana] 32777 Seq. No. 307024 1.R1040 Contig ID jC-gmf102220051b10d1 5'-most EST BLASTN Method q3319365 NCBI GI 77 BLAST score 5.0e-35 E value Match length 193 % identity 88

NCBI Description Arabidopsis thaliana BAC T24M8

Seq. No. 32778

Contig ID 307035\_1.R1040 5'-most EST jC-gmle01810051c06d1



Seq. No. 32779

Contig ID 307047\_1.R1040 5'-most EST jC-gmfl02220051d01d1

Method BLASTX
NCBI GI g3047125
BLAST score 174
E value 2.0e-12
Match length 38
% identity 76

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 32780

Contig ID 307063\_1.R1040

5'-most EST jC-gmle01810051e12d1

Seq. No. 32781

Contig ID 307078\_1.R1040 5'-most EST jC-gmle01810067b08d1

Seq. No. 32782

Contig ID 307091\_1.R1040 5'-most EST jC-gmf102220051f04d1

Method BLASTX
NCBI GI g4512682
BLAST score 306
E value 6.0e-28
Match length 71
% identity 82

NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]

Seq. No. 32783

Contig ID 307097\_1.R1040

5'-most EST jC-gmle01810051f07d1

Seq. No. 32784

Contig ID 307115\_1.R1040 5'-most EST jC-gmle01810051g07d1

Seq. No. 32785

Contig ID 307126\_1.R1040

5'-most EST uC-gmflminsoy014e07b1

Method BLASTX
NCBI GI g2244816
BLAST score 753
E value 6.0e-80
Match length 248
% identity 27

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32786

Contig ID 307129\_1.R1040 5'-most EST jC-gmfl02220051h03a1

Method BLASTX
NCBI GI g1652745
BLAST score 184
E value 3.0e-13
Match length 156



% identity 32
NCBI Description (D90908) hypothetical protein [Synechocystis sp.]

Seq. No. 32787

Contig ID 307143\_1.R1040 5'-most EST jC-gmf102220051h12a1

Seq. No. 32788

Contig ID 307153\_1.R1040

5'-most EST jC-gmf\overline{1}02220052a07a1

Method BLASTX
NCBI GI g2317910
BLAST score 405
E value 2.0e-45
Match length 152
% identity 60

NCBI Description (U89959) CER1 protein [Arabidopsis thaliana]

Seq. No. 32789

Contig ID 307154\_1.R1040 5'-most EST jC-gmle01810052a07d1

Seq. No. 32790

Contig ID 307159\_1.R1040

5'-most EST  $jC-gmf\overline{10}2220052a10d1$ 

Seq. No. 32791

Contig ID 307219\_1.R1040

5'-most EST jC-gmle01810073f06d1

Method BLASTX
NCBI GI g3336894
BLAST score 207
E value 2.0e-16
Match length 85
% identity 55

NCBI Description (AJ225049) Hsp20.2 protein [Lycopersicon peruvianum]

Seq. No. 32792

Contig ID 307247\_1.R1040

5'-most EST jC-gmfl02220052g01d1

Seq. No. 32793

Contig ID 307271\_1.R1040

5'-most EST jC-gmfl02220052h04a1

Seq. No. 32794

Contig ID 307273\_1.R1040

5'-most EST jC-gmle01810052h05d1

Seq. No. 32795

Contig ID 307275\_1.R1040

5'-most EST jC-gmf102220052h06d1

Seq. No. 32796

Contig ID 307282 1.R1040 5'-most EST jC-gmfl02220052h11a1



32797 Seq. No.

307288 1.R1040 Contig ID

5'-most EST jC-gmf102220053a02d1

32798 Seq. No.

307327\_1.R1040 Contig ID

5'-most EST jC-gmf102220053c03a1

Method BLASTX NCBI GI g1903357 BLAST score 496 4.0e-50 E value Match length 140

% identity NCBI Description (AC000104) Strong similarity to Arabidopsis 2A6

(gb X83096). [Arabidopsis thaliana]

Seq. No. 32799

307357 1.R1040 Contig ID

5'-most EST jC-gmf102220053e01a1

63

Seq. No. 32800

Contig ID 307358 1.R1040

5'-most EST jC-gmle01810053e01d1

Seq. No. 32801

Contig ID 307361 1.R1040

5'-most EST g5126430 Method BLASTX NCBI GI g3063691 BLAST score 329 E value 3.0e-43Match length 107

% identity 80

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

32802 Seq. No.

307361 2.R1040 Contig ID

5'-most EST jC-qmle01810053e03a1

32803 Seq. No.

307363 1.R1040 Contig ID

5'-most EST jC-gmf102220053e04d1

Seq. No. 32804

Contig ID 307380 1.R1040

5'-most EST jC-gmle01810053a07d1

Seq. No. 32805

307383 1.R1040 Contig ID

5'-most EST jC-qmle01810053b10d1

Seq. No. 32806

Contig ID 307387 1.R1040

5'-most EST  $jC-gmf\overline{1}02220053f07d1$ 

Seq. No. 32807

307397 1.R1040 Contig ID



jC-qmle01810053b07d1 5'-most EST

32808 Seq. No.

307419 1.R1040 Contig ID jC-qmf102220053h04d1

5'-most EST

Seq. No. 32809

307422 1.R1040 Contig ID

uC-gmflminsoy002d08b1 5'-most EST

32810 Seq. No.

Contig ID 307434 1.R1040

uC-gmrominsoy100b10b1 5'-most EST

BLASTX Method q4262239 NCBI GI 444 BLAST score E value 7.0e-44 Match length 145 % identity 63

(AC006200) putative membrane transporter [Arabidopsis NCBI Description

thaliana]

32811 Seq. No.

307434 2.R1040 Contig ID

jC-gmle01810002f05d15'-most EST

32812 Seq. No.

307453 1.R1040 Contig ID

5'-most EST jC-gmf102220054b03d1

32813 Seq. No.

307485 1.R1040 Contig ID

jC-gmf102220054d04a1 5'-most EST

Seq. No. 32814

307521 1.R1040 Contig ID

5'-most EST jC-qmf102220054f03d1

32815 Seq. No.

307527 1.R1040 Contig ID

5'-most EST jC-gmle01810047g12d1

32816 Seq. No.

307529 1.R1040 Contig ID

jC-gmle01810080h02d1 5'-most EST

32817 Seq. No.

307561 1.R1040 Contig ID

jC-gmle01810054h07d1 5'-most EST

32818 Seq. No.

307611 1.R1040 Contiq ID

jC-gmle01810055c11a1 5'-most EST

32819 Seq. No.

307641 1.R1040 Contig ID 5'-most EST

jC-gmf102220055e11d1



32820 Seq. No. 307675 1.R1040 Contig ID jC-gmle01810055h01d15'-most EST 32821 Seq. No. 307704 1.R1040 Contig ID jC-gmf102220056a07d1 5'-most EST 32822 Seq. No. 307722 1.R1040 Contig ID  $jC-gmf\overline{1}02220056b09a1$ 5'-most EST 32823 Seq. No. 307725 1.R1040 Contig ID jC-gmle01810056b11d1 5'-most EST 32824 Seq. No. 307756 1.R1040 Contig ID jC-qmst02400040b11d1 5'-most EST 32825 Seq. No. 307770 1.R1040 Contig ID uC-gmropic029b11b1 5'-most EST Seq. No. 32826 307781 1.R1040 Contig ID  $jC-gmf\overline{1}02220056f02d1$ 5'-most EST 32827 Seq. No. 307801 1.R1040 Contig ID jC-gmle01810057g05d15'-most EST 32828 Seq. No. 307803 1.R1040 Contig ID jC-gmf102220057b02d1 5'-most EST 32829 Seq. No. 307824 1.R1040 Contig ID q5677492 5'-most EST 32830 Seq. No. 307825 1.R1040 Contig ID jC-gmle01810056h12d1 5'-most EST BLASTX Method q1483218 NCBI GI 275 BLAST score 3.0e-24E value 73 Match length

70 % identity

(X99793) induced upon wounding stress [Arabidopsis NCBI Description

thaliana]

32831 Seq. No.

307833 1.R1040 Contig ID jC-gmle01810057a06d1 5'-most EST



```
32832
Seq. No.
                   307882 1.R1040
Contig ID
                   jC-gmro02910033f12d1
5'-most EST
                   32833
Seq. No.
Contig ID
                   307890 1.R1040
                   uC-qmflminsoy055h09b1
5'-most EST
                   BLASTX
Method
                   g2648588
NCBI GI
                   294
BLAST score
                   2.0e-26
E value
                   156
Match length
                   41
% identity
                    (AE000968) Glu-tRNA amidotransferase, subunit A (gatA-1)
NCBI Description
                    [Archaeoglobus fulgidus]
                    32834
Seq. No.
                    307909 1.R1040
Contig ID
                   jC-gmle01810057f06d1
5'-most EST
                    32835
Seq. No.
                    307936 1.R1040
Contig ID
                    jC-gmf\overline{1}02220057h06d1
5'-most EST
                    32836
Seq. No.
                    307971 1.R1040
Contig ID
                    jC-gmro02910036f01d1
5'-most EST
                    32837
Seq. No.
                    307995 1.R1040
Contig ID
                    jC-gmf\overline{1}02220058g10a1
5'-most EST
                    32838
Seq. No.
                    307997 1.R1040
Contig ID
                    jC-gms\(\overline{t}\)02400046h02d1
5'-most EST
                    32839
Seq. No.
                    307997 2.R1040
Contig ID
                    jC-qmf102220101g05d1
5'-most EST
                    32840
Seq. No.
                    308004 1.R1040
Contig ID
                    jC-gmf102220059b01d1
5'-most EST
                    32841
Seq. No.
                    308017 1.R1040
Contig ID
                    uC-qmrominsoy212a10b1
5'-most EST
                    BLASTX
Method
NCBI GI
                    g2894560
BLAST score
                    563
                    7.0e-58
E value
```

187 Match length % identity

NCBI Description (AL021890) putative protein [Arabidopsis thaliana]

32842 Seq. No.

308039\_1.R1040 Contig ID



jC-gmf102220080a03d1 5'-most EST BLASTX Method g3335372 NCBI GI 216 BLAST score 3.0e-17 E value 65 Match length 65 % identity (AC003028) putative SRG1 protein [Arabidopsis thaliana] NCBI Description 32843 Seq. No. 308044 1.R1040 Contig ID uC-gmflminsoy049b06b1 5'-most EST BLASTX Method q4467146 NCBI GI BLAST score 761 2.0e-84 E value 203 Match length 70 % identity (AL035540) galactosidase like protein [Arabidopsis NCBI Description thaliana] Seq. No. 32844 308046 1.R1040 Contig ID jC-qmf102220060e12a1 5'-most EST BLASTX Method NCBI GI g3152614 BLAST score 258 E value 5.0e-22 Match length 163 % identity 45 (AC004482) unknown protein [Arabidopsis thaliana] NCBI Description 32845 Seq. No. 308057 1.R1040 Contig ID jC-gmst02400044e05d1 5'-most EST 32846 Seq. No. 308067\_1.R1040 Contig ID g5688407 5'-most EST 32847 Seq. No. 308070 1.R1040 Contig ID jC-gmf102220060h12a1 5'-most EST

BLASTX Method g3420057 NCBI GI BLAST score 653 2.0e-68 E value 197 Match length % identity 31

(AC004680) putative ABC transporter [Arabidopsis thaliana] NCBI Description

32848 Seq. No.

308176 1.R1040 Contig ID jC-qmf102220061f03a1 5'-most EST

Seq. No. 32849

308235 1.R1040 Contig ID



5'-most EST g5605735

Seq. No. 32850

Contig ID 308252\_1.R1040 5'-most EST jC-gmf102220062b04a1

Seq. No. 32851

Contig ID 308273 1.R1040

5'-most EST jC-gmro02910047g01d1

Seq. No. 32852

Contig ID 308292\_1.R1040

5'-most EST  $jC-gmf\overline{102220127g02a1}$ 

Method BLASTX
NCBI GI g2864613
BLAST score 142
E value 1.0e-08
Match length 103
% identity 33

NCBI Description (AL021811) S-receptor kinase -like protein [Arabidopsis

thaliana] >gi 4049333 emb CAA22558 (AL034567) S-receptor

kinase-like protein [Arabidopsis thaliana]

Seq. No. 32853

Contig ID 308325\_1.R1040

5'-most EST jC-gmf102220062h03d1

Seq. No. 32854

Contig ID 308368\_1.R1040 5'-most EST jC-gmfl02220063b11d1

Seq. No. 32855

Contig ID 308385\_1.R1040 5'-most EST fC-gmle700555329d3

Seq. No. 32856

Contig ID 308427 1.R1040

5'-most EST jC-qmf102220063e08d1

Seq. No. 32857

Contig ID 308476\_1.R1040 5'-most EST uC-gmronoir068e09b1

Method BLASTX
NCBI GI g3287695
BLAST score 293
E value 2.0e-26
Match length 100
% identity 56

NCBI Description (AC003979) Similar to hypothetical protein C34B7.2

gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis

thaliana]

Seq. No. 32858

Contig ID 308543\_1.R1040 5'-most EST jC-gmst02400063f06d1

Method BLASTX NCBI GI g419760



```
249
BLAST score
                   2.0e-22
E value
                   70
Match length
% identity
                   47
                   P-glycoprotein atpgp1 - Arabidopsis thaliana
NCBI Description
                   >qi 3849833 emb CAA43646 (X61370) P-glycoprotein
                   [Arabidopsis thaliana]
                   32859
Seq. No.
                   308567 1.R1040
Contig ID
                   jC-gmf102220065c03d1
5'-most EST
Seq. No.
                   32860
                   308581 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220065c12d1
                   32861
Seq. No.
                   308638 1.R1040
Contig ID
                   jC-gmf102220137a08a1
5'-most EST
Seq. No.
                   32862
                   308687 1.R1040
Contiq ID
                   jC-gmf102220067e06a1
5'-most EST
Method
                   BLASTX
                   q2244831
NCBI GI
BLAST score
                   246
                   8.0e-21
E value
Match length
                   129
% identity
                   47
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   32863
Seq. No.
                   308730 1.R1040
Contig ID
                   g5753626
5'-most EST
                   32864
Seq. No.
                   308779 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220068d06d1
                   32865
Seq. No.
                   308848 1.R1040
Contig ID
                   jC-gmro02910047h07d1
5'-most EST
                   BLASTX
Method
                   q1708971
NCBI GI
BLAST score
                   215
E value
                   3.0e-17
                   60
Match length
                   60
% identity
```

(R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR NCBI Description (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)

>gi\_421871\_pir\_\_S32156 mandelonitrile lyase (EC 4.1.2.10) black cherry >gi\_288116\_emb\_CAA51194\_ (X72617)
mandelonitrile lyase [Prunus serotina] >gi\_1730332 (U78814) (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus serotina] >gi 1090776 prf 2019441A mandelonitrile lyase

[Prunus serotina]



```
32866
Seq. No.
                   308893 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220069c07a1
Method
                   BLASTX
                   g4006915
NCBI GI
                   203
BLAST score
                   1.0e-15
E value
                   121
Match length
                   38
% identity
                  (Z99708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   32867
Seq. No.
                   308914 1.R1040
Contig ID
                   jC-gmf\overline{1}02220139b01d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2979548
BLAST score
                   328
                   2.0e-30
E value
                   119
Match length
                   49
% identity
                   (AC003680) putative 7-ethoxycoumarin O-deethylase
NCBI Description
                   [Arabidopsis thaliana]
                   32868
Seq. No.
                   308930_1.R1040
Contig ID
                   jC-qmle01810078e09d1
5'-most EST
Seq. No.
                   32869
                   308935 1.R1040
Contig ID
                   jC-qmle01810035a04d1
5'-most EST
                   32870
Seq. No.
                   308949 1.R1040
Contig ID
                   uC-gmropic066e06b1
5'-most EST
                   32871
Seq. No.
                   308953 1.R1040
Contig ID
                   jC-gms\overline{t}02400011f01a1
5'-most EST
                   BLASTX
Method
                   g3941543
NCBI GI
                   256
BLAST score
                   5.0e-22
E value
                   69
Match length
                   70
% identity
                   (AF069497) pelota [Arabidopsis thaliana]
NCBI Description
                   >gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1)
                    [Arabidopsis thaliana]
                    32872
Seq. No.
                    308972 1.R1040
Contig ID
                    jC-gmf102220069h08a1
```

5'-most EST

32873 Seq. No.

309054 1.R1040 Contig ID  $jC-gmf\overline{1}02220070f01d1$ 5'-most EST

Method BLASTX g4454464 NCBI GI



BLAST score 384 E value 5.0e-37 Match length 91 % identity 81

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 32874

Contig ID 309063 1.R1040 5'-most EST jC-gmfl02220070f06a1

Seq. No. 32875

Contig ID 309095\_1.R1040 5'-most EST jC-gmf102220070h05d1

Seq. No. 32876

Contig ID 309118\_1.R1040 5'-most EST jC-gmfl02220071a10a1

Seq. No. 32877

Contig ID 309121\_1.R1040 5'-most EST jC-gmst02400025a11d1

Seq. No. 32878

Contig ID 309133\_1.R1040 5'-most EST jC-gmf102220071b06a1

Seq. No. 32879

Contig ID 309159\_1.R1040

5'-most EST g4299702

Seq. No. 32880

Contig ID 309164\_1.R1040 5'-most EST jC-gmfl02220071d02a1

Method BLASTX
NCBI GI g2262100
BLAST score 749
E value 1.0e-79
Match length 192
% identity 72

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 32881

Contig ID 309174\_1.R1040

5'-most EST uC-gmflminsoy071h11b2

Method BLASTX
NCBI GI g3445204
BLAST score 344
E value 3.0e-32
Match length 86
% identity 79

NCBI Description (AC004786) putative GTP-binding protein [Arabidopsis

thaliana]

Seq. No. 32882

Contig ID 309176\_1.R1040 5'-most EST jC-gmfl02220071d07a1



Seq. No. 32883

Contig ID 309190\_1.R1040 5'-most EST jC-gmfl02220071e07d1

Seq. No. 32884

Contig ID 309194\_1.R1040

5'-most EST jC-gmle01810093f02d1

Seq. No. 32885

Contig ID 309202\_1.R1040

5'-most EST jC-gmst02400031b02d1

Seq. No. 32886

Contig ID 309222\_1.R1040

5'-most EST jC-gmf102220071g06d1

Method BLASTN
NCBI GI g3413321
BLAST score 42
E value 2.0e-14
Match length 102
% identity 85

NCBI Description M.sativa PG3 gene

Seq. No. 32887

Contig ID 309225\_1.R1040

5'-most EST jC-gmf102220071g08a1

Seq. No. 32888

Contig ID 309252 1.R1040

5'-most EST jC-gmf102220071h11a1

Seq. No. 32889

Contig ID 309298 1.R1040

5'-most EST jC-gmf102220072d01d1

Seq. No. 32890

Contig ID 309304\_1.R1040

5'-most EST jC-gmf102220072c08a1

Seq. No. 32891

Contig ID 309308\_1.R1040

5'-most EST  $jC-gmf\overline{1}02220092g12d1$ 

Seq. No. 32892

Contig ID 309331\_1.R1040

5'-most EST  $jC-gmf\overline{1}02220072e02d1$ 

Seq. No. 32893

Contig ID 309335\_1.R1040

5'-most EST jC-gmf102220072e04d1

Seq. No. 32894

Contig ID 309351\_1.R1040 5'-most EST jC-gmf102220072f06a1

Method BLASTX NCBI GI g3281861

BLAST score 195



E value 6.0e-15
Match length 90
% identity 46

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 32895

Contig ID 309375\_1.R1040 5'-most EST jC-gmfl02220081h01a1

Seq. No. 32896

Contig ID 309389\_1.R1040 5'-most EST jC-gmf102220072h12a1

Seq. No. 32897

Contig ID 309401\_1.R1040

5'-most EST jC-gmf102220073c10a1

Seq. No. 32898

Contig ID 309420\_1.R1040

5'-most EST jC-gmf\(\bar{1}\)02220073b08a1

Seq. No. 32899

Contig ID 309447\_1.R1040

5'-most EST  $jC-gmf\overline{1}022220073d01d1$ 

Seq. No. 32900

Contig ID 309452\_1.R1040

5'-most EST jC-gmf102220073d04a1

Method BLASTX
NCBI GI g2244890
BLAST score 221
E value 6.0e-18
Match length 119
% identity 38

NCBI Description (Z97338) unnamed protein product [Arabidopsis thaliana]

Seq. No. 32901

Contig ID 309455 1.R1040

5'-most EST  $jC-gmf\overline{1}02220073d07d1$ 

Seq. No. 32902

Contig ID 309458\_1.R1040 5'-most EST jC-gmf102220073f05a1

Method BLASTX
NCBI GI g3152592
BLAST score 190
E value 6.0e-15
Match length 52
% identity 75

NCBI Description (AC002986) Contains similarity to 8A-2V protein gb\_Y10496

from Mus musculus. [Arabidopsis thaliana]

Seq. No. 32903

Contig ID 309473 1.R1040

5'-most EST  $g43004\overline{2}1$ 

Seq. No. 32904



```
309476 1.R1040
Contig ID
                   jC-gmf\overline{1}02220073e12d1
5'-most EST
                   32905
Seq. No.
                   309541 1.R1040
Contig ID
                   jC-gmf102220075a07d1
5'-most EST
                   32906
Seq. No.
                   309602 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400001d10d1
                   32907
Seq. No.
                   309621 1.R1040
Contig ID
                   jC-qmro02910050b11d1
5'-most EST
                   32908
Seq. No.
                   309638 1.R1040
Contig ID
                   jC-qmf102220075h10d1
5'-most EST
                   {\tt BLASTX}
Method
                   q1655536
NCBI GI
                   176
BLAST score
                   1.0e-12
E value
                   39
Match length
                   79
% identity
                  (Y09095) chloride channel [Arabidopsis thaliana]
NCBI Description
                   >qi 1742957 emb CAA96059 (Z71447) CLC-c chloride channel
                   protein [Arabidopsis thaliana]
                   32909
Seq. No.
                   309662 1.R1040
Contig ID
                   jC-qmf102220077b01d1
5'-most EST
                   32910
Seq. No.
                   309678 1.R1040
Contig ID
                   jC-gmf102220076d05a1
5'-most EST
                   BLASTX
Method
                   g2618701
NCBI GI
                   394
BLAST score
                   5.0e-38
E value
Match length
                   150
% identity
                  (AC002510) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   32911
Seq. No.
                   309706 1.R1040
Contig ID
```

jC-gmle01810072a06d1 5'-most EST

32912 Seq. No.

Contig ID 309731 1.R1040 jC-qmf102220077a07d1 5'-most EST

Seq. No. 32913

309743 1.R1040 Contig ID 5'-most EST jC-qmf102220078g09a1

Seq. No. 32914

309773 1.R1040 Contig ID



5'-most EST jC-gmro02910075a06d1

Method BLASTN
NCBI GI g168214
BLAST score 107
E value 8.0e-53
Match length 290
% identity 85

NCBI Description Hevea brasiliensis 3-hydroxy-3-methylglutaryl-coenzyme A

reductase (hmgr3) mRNA, complete cds

Seq. No. 32915

Contig ID 309786\_1.R1040 5'-most EST jC-gmfl02220077d05a1

Method BLASTX
NCBI GI g4314356
BLAST score 299
E value 7.0e-27
Match length 144
% identity 43

NCBI Description (AC006340) putative anthocyanidin-3-glucoside

rhamnosyltransferase [Arabidopsis thaliana]

Seq. No. 32916

Contig ID 309805\_1.R1040

5'-most EST jC-gmf102220077f05a1

Seq. No. 32917

Contig ID 309806 1.R1040

5'-most EST jC-gmfl02220077e06d1

Seq. No. 32918

Contig ID 309826 1.R1040

5'-most EST jC-gmfl02220077f08d1

Seq. No. 32919

Contig ID 309849 1.R1040

5'-most EST jC-gmf102220077h01a1

Seq. No. 32920

Contig ID 309902 1.R1040

5'-most EST uC-gmrominsoy260b11b1

Seq. No. 32921

Contig ID 309959\_1.R1040

5'-most EST jC-gmf102220079b01d1

Seq. No. 32922

Contig ID 309969 1.R1040

5'-most EST jC-gmf102220080h02d1

Seq. No. 32923

Contig ID 310019 1.R1040

5'-most EST g5175497

Seq. No. 32924

Contig ID 310076\_1.R1040

5'-most EST jC-gmst02400017f07d1



Method BLASTX
NCBI GI g1497987
BLAST score 142
E value 1.0e-08
Match length 82
% identity 33

NCBI Description (U62798) SCARECROW [Arabidopsis thaliana]

Seq. No. 32925

Contig ID 310101\_1.R1040

5'-most EST jC-gmst02400060a07d1

Seq. No. 32926

Contig ID 310110\_1.R1040 5'-most EST jC-gmf102220080b01a1

Seq. No. 32927

Contig ID 310178 1.R1040 5'-most EST jC-gmfl02220080f07d1

Seq. No. 32928

Contig ID 310181\_1.R1040 5'-most EST jC-gmfl02220080f09d1

Seq. No. 32929

Contig ID 310202\_1.R1040 5'-most EST jC-gmst02400018e07d1

Seq. No. 32930

Contig ID 310351\_1.R1040 5'-most EST jC-gmfl02220082b07d1

Seq. No. 32931

Contig ID 310364\_1.R1040

5'-most EST  $g42602\overline{4}8$  Method BLASTX NCBI GI g4218120 BLAST score 209 E value 2.0e-16 Match length 53 % identity 70

NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis

thaliana]

Seq. No. 32932

Contig ID 310399\_1.R1040 5'-most EST jC-gmfl02220083b01d1

Seq. No. 32933

Contig ID 310406\_1.R1040 5'-most EST jC-gmfl02220083a11a1

Seq. No. 32934

Contig ID 310418\_1.R1040 5'-most EST jC-gmf102220083d12a1

Seq. No. 32935



Contig ID 310446 1.R1040 5'-most EST jC-gmf102220094a12a1

Seq. No. 32936 Contig ID 310447 1.R1040

5'-most EST jC-gmf102220083e02a1

Method BLASTX g2702268 NCBI GI BLAST score 588 6.0e-61 E value Match length 163 % identity 64

(AC003033) putative cellulase [Arabidopsis thaliana] NCBI Description

Seq. No. 32937

Contig ID 310451 1.R1040

5'-most EST jC-gmf102220083h10a1

32938 Seq. No.

Contig ID 310452 1.R1040

5'-most EST jC-gmf102220083f08a1

32939 Seq. No.

310465 4.R1040 Contig ID

5'-most EST jC-gmf102220099f03a1

32940 Seq. No.

Contig ID 310479 1.R1040

5'-most EST jC-gmf102220083g08a1

Seq. No. 32941

Contig ID 310505 1.R1040

5'-most EST jC-qmf102220083h12d1

Seq. No.

32942 Contig ID

310511 1.R1040 5'-most EST

 $jC-gmf\overline{1}02220101f11d1$ 

32943 Seq. No.

Contig ID 310554 1.R1040

5'-most EST  $jC-gmf\overline{1}02220084e02d1$ 

Seq. No. 32944

310579 1.R1040 Contig ID

5'-most EST jC-gmf102220084h09d1

32945 Seq. No.

Contig ID 310587 1.R1040

5'-most EST jC-gmf\(\bar{1}\)02220112d07d1

Seq. No. 32946

Contig ID 310593 1.R1040

5'-most EST jC-gmst02400020h09a1

Method BLASTX NCBI GI g3201611 BLAST score 270 E value 2.0e-23

5001 . .



Match length % identity 61

NCBI Description (AC004669) unknown protein [Arabidopsis thaliana]

Seq. No. Contig ID 32947

5'-most EST

310603 1.R1040

jC-gmst02400031a12d1 BLASTX

Method NCBI GI BLAST score

q3287857 379

E value Match length 3.0e-36

% identity

105 69

NCBI Description

3-HYDROXYBUTYRYL-COA DEHYDROGENASE (BETA-HYDROXYBUTYRYL-COA

DEHYDROGENASE) (BHBD) >gi 1209052 (U32229) HbdA

[Bradyrhizobium japonicum]

Seq. No.

32948

Contig ID

310605 1.R1040

5'-most EST

jC-qmf102220115b11d1

Method NCBI GI BLASTX g1345132

BLAST score

186

E value Match length 7.0e-14

% identity

55 69

NCBI Description

(U47029) ERECTA [Arabidopsis thaliana]

>gi 1389566 dbj\_BAA11869 (D83257) receptor protein kinase [Arabidopsis thaliana] >gi 3075386 (AC004484) receptor

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.

32949

Contig ID

310623 1.R1040

5'-most EST

jC-gmf102220085c01a1

Seq. No.

32950

Contig ID

310640 1.R1040

5'-most EST

jC-gmle01810088e01a1

Seq. No.

32951

Contia ID

310654 1.R1040

5'-most EST

jC-gmf102220085f04d1

Seq. No.

32952

Contig ID

310665 1.R1040

5'-most EST

jC-gmf102220085h03d1

Seq. No.

32953

Contig ID

310684 1.R1040

5'-most EST

jC-gmf102220090b10d1

Method NCBI GI BLASTX q2529663

BLAST score

E value

195

7.0e-15

Match length % identity

66

NCBI Description (AC002535) putative lysophospholipase [Arabidopsis





thaliana] >gi\_3738277 (AC005309) putative lysophospholipase [Arabidopsis thaliana]

Seq. No. 32954

Contig ID 310685\_1.R1040 5'-most EST jC-gmf102220085h10a1

Seq. No. 32955

Contig ID 310702\_1.R1040

5'-most EST jC-gmf102220088b06a1

Method BLASTX
NCBI GI g2618686
BLAST score 406
E value 1.0e-39
Match length 136
% identity 54

NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32956

Contig ID 310717\_1.R1040 5'-most EST jC-gmfl02220086f09a1

Seq. No. 32957

Contig ID 310727\_1.R1040 5'-most EST jC-gmf102220086b08d1

Seq. No. 32958

Contig ID 310737\_1.R1040 5'-most EST jC-gmro02910019e03d1

Seq. No. 32959

Contig ID 310772\_1.R1040 5'-most EST jC-qmf102220086d10d1

Method BLASTX
NCBI GI g4512664
BLAST score 290
E value 4.0e-26
Match length 64
% identity 84

NCBI Description (AC006931) putative ribose phosphate pyrophosphokinase

[Arabidopsis thaliana]

>gi\_4544471\_gb\_AAD22378.1\_AC006580\_10 (AC006580) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana]

Seq. No. 32960

Contig ID 310805\_1.R1040

5'-most EST jC-gmle01810028f10d1

Seq. No. 32961

Contig ID 310890 1.R1040

5'-most EST jC-gmle01810049e02d1

32962

Seq. No.

Contig ID 310906 1.R1040

5'-most EST jC-qmf102220089b05d1

Seq. No. 32963



Contig ID 310921\_1.R1040

5'-most EST jC-gmf\overline{1}02220089c03a1

Method BLASTX
NCBI GI 9731400
BLAST score 159
E value 1.0e-10
Match length 171
% identity 6

NCBI Description VACUOLAR PROTEIN 8 >gi\_1077594\_pir\_\_S50446 hypothetical

protein YEL013w - yeast (Saccharomyces cerevisiae)

>gi\_602380 (U18530) Yel013wp [Saccharomyces cerevisiae]

Seq. No. 32964

Contig ID 310922 1.R1040

5'-most EST  $jC-gmf\overline{1}02220089c03d1$ 

Seq. No. 32965

Contig ID 310970\_1.R1040

5'-most EST jC-gmfl02220089e12a1

Seq. No. 32966

Contig ID 310999 1.R1040

5'-most EST jC-gmst02400003a01d1

Method BLASTX
NCBI GI g4063751
BLAST score 154
E value 4.0e-10
Match length 58
% identity 50

NCBI Description (AC005851) putative white protein [Arabidopsis thaliana]

>gi\_4510409 gb AAD21495.1 (AC006929) putative white

protein [Arabidopsis thaliana]

Seq. No. 32967

Contig ID 311016 1.R1040

5'-most EST  $jC-gmf\overline{1}02220112h12d1$ 

Seq. No. 32968

Contig ID 311042\_1.R1040 5'-most EST iC-gmle018100736

5'-most EST jC-gmle01810073e12d1 Method BLASTN

Method BLASTN
NCBI GI g1707656
BLAST score 43
E value 7.0e-15
Match length 206
% identity 91

NCBI Description P.sativum mRNA for DnaJ-like protein

Seq. No. 32969

Contig ID 311050 1.R1040

5'-most EST jC-gmf $\overline{1}$ 02220090e07a1

Seq. No. 32970

Contig ID 311053 1.R1040

5'-most EST jC-gmf102220090d07d1

Method BLASTX NCBI GI g4455250



BLAST score E value 3.0e-16 Match length 61 % identity 64

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No.

32971

311086 1.R1040 Contig ID 5'-most EST jC-gmf102220091g03a1

Method BLASTX g4371280 NCBI GI BLAST score 211 8.0e-17 E value Match length 48 % identity 88

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.

32972

Contiq ID 311095 1.R1040

5'-most EST jC-gmf102220090d04d1

Seq. No. 32973

Contig ID 311120 1.R1040

5'-most EST jC-gmf102220090e09d1

Seq. No. 32974

Contig ID 311139 1.R1040

5'-most EST jC-gmf102220090f08d1

32975 Seq. No.

Contig ID 311162 1.R1040

5'-most EST jC-gmf102220090g09d1

32976 Seq. No.

Contig ID 311208 1.R1040

5'-most EST jC-gmf102220091b09a1

32977 Seq. No.

Contig ID 311256 1.R1040

5'-most EST jC-qmf102220091e09a1

BLASTX Method NCBI GI q3176709 BLAST score 457 1.0e-45 E value Match length 150 % identity 57

NCBI Description (AC002392) putative anthranilate

N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis

thaliana]

Seq. No. 32978

Contig ID 311269 1.R1040

5'-most EST jC-qmro02800042d06d1

Method BLASTX NCBI GI q3355471 BLAST score 180 E value 5.0e-13



Match length 44 % identity 68

NCBI Description (AC004218) putative lysophospholipase [Arabidopsis

thaliana]

Seq. No. 32979

Contig ID 311330\_2.R1040

5'-most EST jC-gmst02400008h07d1

Seq. No. 32980

Contig ID 311347\_1.R1040

5'-most EST jC-gmf102220092d03d1

Method BLASTN NCBI GI g1044867

BLAST score 43 E value 8.0e-15 Match length 47

% identity 98

NCBI Description Glycine max mRNA for cinnamic acid 4-hydroxylase (CYP73)

---

Seq. No. 32981

Contig ID 311372 1.R1040

5'-most EST jC-gmfl02220092f05d1

Method BLASTX

NCBI GI g4538965

BLAST score 172

E value 1.0e-12

Match length 69
% identity 54

NCBI Description (AL049488) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32982

Contig ID 311377 1.R1040

5'-most EST  $jC-gmf\overline{102220092f12a1}$ 

Method BLASTX
NCBI GI g4530126
BLAST score 604
E value 1.0e-62
Match length 210
% identity 57

NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1

[Phaseolus vulgaris]

Seq. No. 32983

Contig ID 311380\_1.R1040

5'-most EST  $jC-gmf\overline{1}02220092g02d1$ 

Method BLASTX
NCBI GI g4101626
BLAST score 402
E value 8.0e-39
Match length 89
% identity 79

NCBI Description (AF005096) desaturase/cytochrome b5 protein [Ricinus

communis]

Seq. No. 32984

Contig ID 311396\_1.R1040

5006



Method BLASTX
NCBI GI g3004564
BLAST score 175
E value 2.0e-12
Match length 67
% identity 54

NCBI Description (AC003673) putative receptor Ser/Thr protein kinase

[Arabidopsis thaliana]

Seq. No. 32985

Contig ID 311418 1.R1040 5'-most EST jC-gmfI02220093b03d1

Seq. No. 32986

Contig ID 311508\_1.R1040

5'-most EST jC-gmf\(\bar{1}\)02220094f12d1

Seq. No. 32987

Contig ID 311510 1.R1040

5'-most EST jC-gmf102220096d02a1

Seq. No. 32988

Contig ID 311524\_1.R1040

5'-most EST jC-gmf102220094d01d1

Seq. No. 32989

Contig ID 311527 1.R1040

5'-most EST jC-gmf102220094b10d1

Seq. No. 32990

Contig ID 311559 1.R1040

5'-most EST jC-gmf102220094f01d1

Seq. No. 32991

Contig ID 311577\_1.R1040

5'-most EST  $jC-gmf\overline{1}02220094e08d1$ 

Seq. No. 32992

Contig ID 311625 1.R1040

5'-most EST  $jC-gmf\overline{10}2220094h07d1$ 

Seq. No. 32993

Contig ID 311659\_1.R1040

5'-most EST jC-gmf102220096c07a1

Seq. No. 32994

Contig ID 311670\_1.R1040

5'-most EST jC-gmst02400068e03d1

Seq. No. 32995

Contig ID 311698\_1.R1040

5'-most EST jC-gmro02800043f09a1

Seq. No. 32996

Contig ID 311717 1.R1040

5'-most EST uC-gmrominsoy201h09b1



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Seq. No.
                  32997
                  311792 1.R1040
Contig ID
                  jC-gmf102220133h10a1
5'-most EST
                  BLASTX
Method
                  g3341978
NCBI GI
BLAST score
                  171
                  5.0e-12
E value
Match length
                  100
% identity
                  43
NCBI Description (AF044603) cytokinin oxidase [Zea mays]
Seq. No.
                  32998
Contig ID
                  311805 1.R1040
5'-most EST
                  jC-gmf102220139a10d1
                  BLASTX
Method
NCBI GI
                  q4314378
BLAST score
                  147
                  3.0e-09
E value
Match length
                  43
                  58
% identity
                 (AC006232) putative lipase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  32999
                  311821 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220099e04a1
                  33000
Seq. No.
                  311834 1.R1040
Contig ID
5'-most EST
                  q5676970
                  BLASTX
Method
                  g2664212
NCBI GI
BLAST score
                  462
E value
                  5.0e-46
Match length
                  134
% identity
                  65
NCBI Description
                  (AJ222645) asparaginyl-tRNA synthetase [Arabidopsis
                  thaliana]
Seq. No.
                  33001
                  311844 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810090g12d1
Seq. No.
                   33002
                  311856 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220099a06a1
Seq. No.
                  33003
                  311859 1.R1040
Contig ID
5'-most EST
                  q5753537
```

Contig ID 311869\_1.R1040 5'-most EST jC-gmfl02220099e01a1

Seq. No. 33005

Contig ID 311879\_1.R1040

5008



jC-gmf102220099b01d1 5'-most EST BLASTX Method g3152577 NCBI GI BLAST score 432 1.0e-42 E value 149 Match length % identity 61 (AC002986) Contains similarity to Kinesin-like protein C NCBI Description gb D21138 from A. thaliana. [Arabidopsis thaliana] 33006 Seq. No. 311880 1.R1040 Contig ID jC-gmf102220099c07a1 5'-most EST

Seq. No. 33007 Contig ID 311895 1.R1040

jC-qmf102220099d06d1 5'-most EST

BLASTX Method q4038030 NCBI GI 448 BLAST score 2.0e-44 E value 167 Match length % identity 23

(AC005936) putative protein kinase, 5' partial [Arabidopsis NCBI Description

thaliana]

33008 Seq. No.

Contig ID 311928 1.R1040

jC-gmf102220099e06a1 5'-most EST

33009 Seq. No.

311937 1.R1040 Contig ID

jC-gmf102220099f04d1 5'-most EST

33010 Seq. No.

311945 1.R1040 Contig ID

jC-gmro02800024e03d1 5'-most EST

BLASTX Method g3434969 NCBI GI BLAST score 150 2.0e-09 E value 57 Match length 56 % identity

(AB008104) ethylene responsive element binding factor 2 NCBI Description

[Arabidopsis thaliana]

33011 Seq. No.

311953 1.R1040 Contig ID jC-gmr002800042g05d1 5'-most EST

BLASTX Method NCBI GI q4539006 BLAST score 382 9.0e-37 E value Match length 90 80 % identity

NCBI Description (AL049481) putative protein [Arabidopsis thaliana]



Contig ID 311979\_1.R1040 5'-most EST jC-gmfI02220100c04a1

Seq. No. 33013

Contig ID 312053\_1.R1040

5'-most EST jC-gmst02400045h12d1

Seq. No. 33014

Contig ID 312068\_1.R1040

5'-most EST  $jC-gmf\overline{1}02220101d05d1$ 

Seq. No. 33015

Contig ID 312076 1.R1040

5'-most EST jC-gmfl02220101d09d1

Seq. No. 33016

Contig ID 312087 1.R1040

5'-most EST jC-gmfl02220101e05a1

Method BLASTX
NCBI GI g1143445
BLAST score 404
E value 1.0e-39
Match length 114
% identity 68

NCBI Description (X88797) cinnamyl alcohol dehydrogenase [Eucalyptus gunnii]

Seq. No. 33017

Contig ID 312156\_1.R1040 5'-most EST jC-gmf102220102b01a1

Method BLASTX
NCBI GI g2894600
BLAST score 259
E value 3.0e-22
Match length 82
% identity 57

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 33018

Contig ID 312187 1.R1040

5'-most EST jC-gmle01810031b04d1

Method BLASTX
NCBI GI g2924784
BLAST score 482
E value 4.0e-48
Match length 173
% identity 51

NCBI Description (AC002334) similar to jasmonate inducible protein

[Arabidopsis thaliana]

Seq. No. 33019

Contig ID 312263\_1.R1040 5'-most EST jC-qmfl02220103f07d1

Seq. No. 33020

Contig ID 312285 1.R1040 5'-most EST jC-gmf102220103c03a1



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33021
Seq. No.
                   312296 1.R1040
Contig ID
                   q4260293
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2245020
                   185
BLAST score
                   1.0e-13
E value
                   132
Match length
                   39
% identity
                  (Z97341) growth regulator homolog [Arabidopsis thaliana]
NCBI Description
                   33022
Seq. No.
                   312331 1.R1040
Contig ID
                   uC-gmrominsoy315f02b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3882273
BLAST score
                   260
                   3.0e-22
E value
                   175
Match length
% identity
                   (AB018319) KIAA0776 protein [Homo sapiens]
NCBI Description
                   33023
Seq. No.
                   312354 1.R1040
Contig ID
                   jC-qmf102220103f12d1
5'-most EST
                   BLASTN
Method
                   g3021356
NCBI GI
                   80
BLAST score
                    6.0e-37
E value
                    108
Match length
% identity
                    94
                   Cyamopsis tetragonoloba mRNA for UDP-galactose 4-epimerase,
NCBI Description
                    clone GEPI48
                    33024
Seq. No.
                    312358 1.R1040
Contig ID
                    uC-gmrominsoy308h09b1
5'-most EST
                    33025
Seq. No.
                    312391 1.R1040
 Contig ID
                    jC-gmr002910068a04d1
 5'-most EST
                    33026
 Seq. No.
                    312439 1.R1040
 Contig ID
                    jC-gmf\overline{1}02220104c12a1
 5'-most EST
                    33027
 Seq. No.
                    312446 1.R1040
 Contig ID
                    jC-gms\(\overline{t}\)02400004a04d1
 5'-most EST
```

Contig ID 5'-most EST

312463\_1.R1040

most EST jC-gmf\(\bar{1}\)02220113h11d1

Method BLASTN
NCBI GI g861154
BLAST score 106



E value Match length 214 87 % identity

NCBI Description V.faba VFCWINV1 mRNA for cell wall invertase I

Seq. No.

33029

Contig ID 5'-most EST 312497 1.R1040 jC-gmst02400053d10a1

Seq. No.

33030

Contig ID

312513 1.R1040

5'-most EST

jC-gmle01810061b01d1

Seq. No.

33031

Contig ID

312519 1.R1040

5'-most EST

 $jC-gms\overline{t}02400056f08d1$ 

Seq. No.

33032

Contig ID

312549 1.R1040

5'-most EST

 $jC-gmf\overline{1}02220106b09a1$ 

Method

BLASTX

NCBI GI

g4559356 218

BLAST score E value

Match length

2.0e-17

% identity

183

NCBI Description

(AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No.

33033

Contig ID

312555 1.R1040

5'-most EST

jC-gmf102220106c01a1

Seq. No.

33034

Contig ID

312673 1.R1040

5'-most EST

jC-qmf102220108d10a1

Seq. No.

33035

Contig ID

312755 1.R1040

5'-most EST

jC-qmf102220112d06d1

Seq. No.

33036

Contig ID

312763 1.R1040 jC-gmf102220112e07d1

5'-most EST

33037

Seq. No. Contig ID

312771 1.R1040

5'-most EST

g5057800

Method

BLASTX

NCBI GI

q2129929

BLAST score

376

E value Match length 7.0e-36

174 44

% identity

NCBI Description

DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 tomato >gi 1049068 (U28403) RNA polymerase II subunit 2

[Solanum lycopersicum]



Seq. No. 3303 Contig ID 3127

312788\_1.R1040

5'-most EST jC-gmf102220143g10d1

Method BLASTX
NCBI GI g2244732
BLAST score 201
E value 2.0e-15
Match length 40

% identity 82 NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No. 33039

Contig ID 312822\_1.R1040 5'-most EST jC-gmf102220113c06d1

Method BLASTX
NCBI GI g2506139
BLAST score 335
E value 2.0e-31
Match length 86

Match length 86 % identity 71

NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)

(ARCHAIN) >gi\_1314049\_emb\_CAA91901\_ (Z67962)

-

archain/delta-COP [Oryza sativa]

Seq. No. 33040

Contig ID 312860\_1.R1040

5'-most EST jC-gmle01810000c08d1

Seq. No. 33041

Contig ID 312876\_1.R1040

5'-most EST  $jC-gmf\overline{1}02220113h08d1$ 

Seq. No. 33042

Contig ID 312882\_1.R1040

5'-most EST jC-gmf\overline{1}02220114a02a1

Seq. No. 33043

Contig ID 312928\_1.R1040 5'-most EST jC-gmf102220114c09a1

Seq. No. 33044

Contig ID 312970 1.R1040 5'-most EST jC-gmfl02220114f02a1

Method BLASTX
NCBI GI g3785994
BLAST score 331
E value 1.0e-30
Match length 122
% identity 53

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33045

Contig ID 313033 1.R1040 5'-most EST jC-gmle01810063g12a1 Method BLASTX

Method BLASTX
NCBI GI g4519258
BLAST score 154



E value 5.0e-10
Match length 168
% identity 29

NCBI Description (AB017914) L-zip+NBS+LRR [Oryza sativa]

Seq. No. 33046

Contig ID 313182\_1.R1040 5'-most EST jC-gmf102220125d11a1

Method BLASTX
NCBI GI g2832692
BLAST score 196
E value 6.0e-15
Match length 129
% identity 36

NCBI Description (AL021713) putative protein [Arabidopsis thaliana]

Seq. No. 33047

Contig ID 313183\_1.R1040

5'-most EST jC-gmf102220135e12d1

Method BLASTX
NCBI GI g2760326
BLAST score 165
E value 3.0e-11
Match length 83
% identity 42

NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No. 33048

Contig ID 313189\_2.R1040

5'-most EST jC-gmst02400037h07d2

Seq. No. 33049

Contig ID 313211 1.R1040

5'-most EST uC-gmrominsoy286d02b1

Seq. No. 33050

Contig ID 313232\_1.R1040

5'-most EST jC-gmf102220125f05d1

Seq. No. 33051

Contig ID 313262 1.R1040

5'-most EST jC-gmro02910031f01a1

Method BLASTX
NCBI GI g4263795
BLAST score 195
E value 9.0e-15
Match length 69
% identity 72

NCBI Description (AC006068) putative glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 33052

Contig ID 313266\_1.R1040 5'-most EST jC-gmfl02220125h04d1

Method BLASTX NCBI GI g2959781 BLAST score 274



E value 4.0e-24

Match length 75 % identity 75

NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No. 33053

Contig ID 313271 1.R1040

5'-most EST jC-gmfl02220125h08a1

Seq. No. 33054

Contig ID 313289\_1.R1040

5'-most EST jC-gmfl02220131a02a1

Method BLASTX
NCBI GI g3249110
BLAST score 430
E value 2.0e-42
Match length 153

% identity 58 NCBI Description (AC003114) T12M4.6 [Arabidopsis thaliana]

Seq. No. 33055

Contig ID 313341 1.R1040

5'-most EST jC-gmle01810002a07d1

Seq. No. 33056

Contig ID 313466 1.R1040

5'-most EST jC-gmle01810047b10a1

Seq. No. 33057

Contig ID 313468 1.R1040

5'-most EST jC-gmf102220128h09a1

Seq. No. 33058

Contig ID 313520 1.R1040

5'-most EST jC-gmf102220130d03a1

Method BLASTX
NCBI GI g2467272
BLAST score 294
E value 2.0e-26
Match length 183
% identity 24

NCBI Description (Z99759) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 33059

Contig ID 313560 1.R1040

5'-most EST jC-gmfl02220130f07d1

Seq. No. 33060

Contig ID 313626\_1.R1040

5'-most EST jC-gmf102220131a10d1

Seq. No. 33061

Contig ID 313663\_1.R1040

5'-most EST jC-gmf\(\bar{1}\)02220131f01d1

Method BLASTX 94530126

BLAST score 412



4.0e-40 E value 140 Match length 56 % identity

(AF078082) receptor-like protein kinase homolog RK20-1 NCBI Description

[Phaseolus vulgaris]

33062 Seq. No.

313667 1.R1040 Contig ID

uC-gmrominsoy0001h10a1 5'-most EST

33063 Seq. No.

313704 1.R1040 Contig ID

jC-gmf102220132aa03d1 5'-most EST

Seq. No. 33064

313778 1.R1040 Contig ID

jC-gmf102220132ae10a1 5'-most EST

BLASTN Method g167227 NCBI GI BLAST score 212 1.0e-115 E value 460

Match length 87 % identity

Canavalia ensiformis urease (ure) mRNA, complete cds NCBI Description

33065 Seq. No.

313847 1.R1040 Contig ID

jC-gmf102220133f09a1 5'-most EST

33066 Seq. No.

313851 1.R1040 Contig ID uC-gmropic104d10b1 5'-most EST

BLASTX Method NCBI GI g1773014 670 BLAST score E value 2.0e-70 Match length 217 % identity 62

(Y10338) chloride channel Stclc1 [Solanum tuberosum] NCBI Description

33067 Seq. No.

313964 1.R1040 Contig ID

5'-most EST jC-gmf102220138a06d1

Seq. No. 33068

313966 1.R1040 Contig ID

5'-most EST jC-gmro02910008h03a1

BLASTX Method NCBI GI q4558550 BLAST score 659 E value 3.0e-69 Match length 156 79 % identity

(ACO07138) putative protein transport factor [Arabidopsis NCBI Description

thaliana]

33069 Seq. No.



Contig ID 314024\_1.R1040 5'-most EST jC-gmle01810048c01d1

Seq. No. 33070

Contig ID 314102\_1.R1040 5'-most EST jC-gmf102220139d01d1

Seq. No. 33071

Contig ID 314128\_1.R1040

5'-most EST jC-gmf102220139g07a1

Seq. No. 33072

Contig ID 314143\_1.R1040

5'-most EST jC-gmfl02220139h05d1

Seq. No. 33073

Contig ID 314172\_1.R1040

5'-most EST jC-gmf102220140c03d1

Seq. No. 33074

Contig ID 314180\_1.R1040

5'-most EST g5510346
Method BLASTX
NCBI GI g509810
BLAST score 145
E value 5.0e-09
Match length 38
% identity 71

NCBI Description (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No. 33075

Contig ID 314242\_1.R1040

5'-most EST jC-gmfl02220141d01d1

Method BLASTN
NCBI GI g2104674
BLAST score 38
E value 5.0e-12
Match length 134
% identity 86

NCBI Description V.faba mRNA for transcription factor containing bZIP

Seq. No. 33076

Contig ID 314259\_1.R1040

5'-most EST jC-gmfl02220141d11d1

Seq. No. 33077

Contig ID 314362\_1.R1040

5'-most EST jC-gmf102220142d05d1

Seq. No. 33078

Contig ID 314363\_1.R1040 5'-most EST jC-gmfl02220142c06a1

Method BLASTN
NCBI GI g3641869
BLAST score 133
E value 1.0e-68
Match length 277



% identity 87
NCBI Description Cicer arietinum epicotyl EST, clone Can133

Seq. No. 33079

Contig ID 314365\_1.R1040 5'-most EST jC-gmf102220142c07d1

Seq. No. 33080

Contig ID 314394\_1.R1040 5'-most EST jC-gmf102220142e04a1

Seq. No. 33081

Contig ID 314409\_1.R1040 5'-most EST jC-gmf102220142f02a1

Seq. No. 33082

Contig ID 314467\_1.R1040

5'-most EST  $g55101\overline{4}0$ 

Seq. No. 33083

Contig ID 314477\_1.R1040

5'-most EST jC-gmfl02220143b08a1

Seq. No. 33084

Contig ID 314488\_1.R1040

5'-most EST jC-gmf102220143c03d1

Seq. No. 33085

Contig ID 314518\_1.R1040

5'-most EST jC-gmf102220143d12a1

Seq. No. 33086

Contig ID 314546\_1.R1040

5'-most EST jC-gmf102220143f06a1

Method BLASTX
NCBI GI g2147484
BLAST score 359
E value 6.0e-34
Match length 93
% identity 84

NCBI Description homeotic protein - Phalaenopsis sp >gi\_1173622 (U34743) homeobox protein [Phalaenopsis sp. 'hybrid SM9108']

Seq. No. 33087

Contig ID 314584\_1.R1040

5'-most EST  $jC-gms\overline{t}02400055e10d1$ 

Method BLASTX
NCBI GI g2811226
BLAST score 339
E value 1.0e-31
Match length 94
% identity 72

NCBI Description (AF042669) fimbrin 2 [Arabidopsis thaliana] >gi\_2811232

(AF042671) fimbrin 2 [Arabidopsis thaliana]

Seq. No. 33088

Contig ID 314665\_1.R1040



5'-most EST jC-gmf102220144g10a1

Seq. No. 33089

Contig ID 314716\_1.R1040 5'-most EST jC-gmf102220145e07a1

Seq. No. 33090

Contig ID 314729\_1.R1040

5'-most EST jC-gmfl02220145g05a1

Seq. No. 33091

Contig ID 314822\_1.R1040

5'-most EST uC-gmflminsoy010h04b1

Seq. No. 33092

Contig ID 314831\_1.R1040

5'-most EST jC-gmf\(\bar{1}\)02220146h06a1

Method BLASTX
NCBI GI g1351945
BLAST score 230
E value 5.0e-19
Match length 69
% identity 68

NCBI Description FLORAL HOMEOTIC PROTEIN APETALA2 >gi\_533709 (U12546)

APETALA2 protein [Arabidopsis thaliana]

>gi\_2464888\_emb\_CAB16765\_ (Z99707) APETALA2 protein

[Arabidopsis thaliana]

Seq. No. 33093

Contig ID 314910\_1.R1040

5'-most EST jC-gmle01810016b08a1

Method BLASTX
NCBI GI g556853
BLAST score 189
E value 4.0e-14
Match length 154
% identity 34

NCBI Description (Z37996) incomplete orf, len: 744, CAI: 0.14 [Saccharomyces

cerevisiae]

Seq. No. 33094

Contig ID 314911\_1.R1040

Seq. No. 33095

Contig ID 314912\_1.R1040

5'-most EST jC-gmle01810016b10a1

33096

Method BLASTX
NCBI GI g4531442
BLAST score 277
E value 2.0e-24
Match length 162
% identity 43

NCBI Description (AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.

Contig ID 314913\_1.R1040

5019



5'-most EST jC-gmle01810016a09d1

Seq. No. 33097

Contig ID 314932\_1.R1040 5'-most EST jC-qmle01810016d01a1

Seq. No. 33098

Contig ID 314938\_1.R1040

5'-most EST jC-gmr002910052e01a1

Method BLASTN
NCBI GI g310560
BLAST score 57
E value 6.0e-23
Match length 57
% identity 100

NCBI Description Soybean ascorbate peroxidase mRNA, complete cds

Seq. No. 33099

Contig ID 314979\_1.R1040 5'-most EST jC-gmle01810000f04a1

Method BLASTX
NCBI GI g133872
BLAST score 180
E value 4.0e-13
Match length 125
% identity 31

NCBI Description 30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)

>gi\_282838\_pir\_\_S26494 ribosomal protein S1, chloroplast spinach >gi\_322404\_pir\_\_A44121 small subunit ribosomal
protein CS1, CS-S2 - spinach >gi\_18060\_emb\_CAA46927\_
(X66135) ribosomal protein S1 [Spinacia oleracea]
>gi\_170143 (M82923) chloroplast ribosomal protein S1

[Spinacia oleracea]

Seq. No. 33100

Contig ID 314985 1.R1040

.5'-most EST jC-gmle01810000f08a1

Method BLASTX
NCBI GI g1477565
BLAST score 191
E value 2.0e-14
Match length 143
% identity 7

NCBI Description (U50078) p532 [Homo sapiens]

>gi 4557026 ref NP 003913.1\_pHERC1\_ hect (homologous to the

E6-AP (UBE3A) carboxyl terminus) domain and RCC1

(CHC1)-like domain (RLD)

Seq. No. 33101

Contig ID 314987\_1.R1040

5'-most EST jC-gmle01810065b03a1

Method BLASTN
NCBI GI g402243
BLAST score 184
E value 7.0e-99
Match length 455
% identity 85



NCBI Description Neurospora crassa 740R23 1A ubiquitin/ribosomal protein S27a fusion protein (ubi/crp-6) mRNA, complete cds

Seq. No. 33102

Contig ID 314990\_1.R1040

5'-most EST jC-gmle01810016f12a1

Method BLASTX
NCBI GI g1168347
BLAST score 235
E value 1.0e-19
Match length 94
% identity 53

NCBI Description ALCOHOL DEHYDROGENASE (ADH-T) >gi 282375 pir A42654

alcohol dehydrogenase (EC 1.1.1.1), thermostable - Bacillus

stearothermophilus >gi\_216230\_dbj\_BAA14411\_ (D90421) alcohol dehydrogenase [Bacillus stearothermophilus]

Seq. No. 33103

Contig ID 315019 1.R1040

5'-most EST jC-gmle01810000h12a1

Method BLASTX
NCBI GI g1723472
BLAST score 141
E value 1.0e-08
Match length 75
% identity 44

NCBI Description HYPOTHETICAL 25.9 KD PROTEIN C6C3.07 IN CHROMOSOME I

>gi 1204247 emb CAA93620 (Z69731) unknown

[Schizosaccharomyces pombe]

Seq. No.

Contig ID 315024 1.R1040

5'-most EST jC-gmle01810001a05a1

33104

Method BLASTX
NCBI GI g3461817
BLAST score 318
E value 2.0e-29
Match length 141
% identity 46

NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]

Seq. No. 33105

Contig ID 315026\_1.R1040 5'-most EST jC-gmle01810091c11a1

Method BLASTX
NCBI GI g4335745
BLAST score 303
E value 2.0e-27
Match length 134
% identity 46

NCBI Description (AC006284) putative hydrolase (contains an

esterase/lipase/thioesterase active site serine domain

(prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 33106

Contig ID 315033 1.R1040

5'-most EST jC-gmle01810017h02d2



```
Method
                  q1813489
NCBI GI
BLAST score
                  154
E value
                  4.0e-10
Match length
                  70
                  50
% identity
                  (U64312) amidase [Bacillus firmus]
NCBI Description
                  33107
Seq. No.
                  315060 1.R1040
Contig ID
                  jC-gmle01810001c11d1
5'-most EST
                   33108
Seq. No.
                   315071 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810001d10a1
                   33109
Seq. No.
                   315072 1.R1040
Contig ID
                   jC-gmle01810048c11a1
5'-most EST
Seq. No.
                   33110
                   315081 1.R1040
Contig ID
                   jC-gmle01810001e09d1
5'-most EST
                   33111
Seq. No.
Contig ID
                   315083 1.R1040
                   jC-gmst02400004c11d1
5'-most EST
Seq. No.
                   33112
                   315086 1.R1040
Contig ID
                   jC-qmle01810017c11a2
5'-most EST
Method
                   BLASTX
                   q4006910
NCBI GI
                   196
BLAST score
                   6.0e-15
E value
Match length
                   72
% identity
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                   33113
Seq. No.
                   315087_1.R1040
Contig ID
5'-most EST
                   jC-gmle01810001f03a1
```

315098 1.R1040 Contig ID

5'-most EST jC-gmle01810001g01a1

33115 Seq. No.

Contig ID 315099 1.R1040

jC-gmle01810001h01a1 5'-most EST

33116 Seq. No.

315123 1.R1040 Contig ID

5'-most EST jC-qmle01810001h10d1

Seq. No.

315174\_1.R1040 Contig ID

5022

```
5'-most EST jC-gmle01810018c11a2
```

Method BLASTX
NCBI GI g2275204
BLAST score 240
E value 8.0e-20
Match length 53
% identity 79

NCBI Description (AC002337) DNA binding protein isolog [Arabidopsis

thaliana]

Seq. No. 33118

Contig ID 315191\_1.R1040

5'-most EST jC-gmle01810041h12d1

Seq. No. 33119

Contig ID 315221\_1.R1040 5'-most EST fC-gmro700763905d4

Seq. No. 33120

Contig ID 315245 1.R1040

5'-most EST jC-gmle01810002h07a1

Seq. No. 33121

Contig ID 315252\_1.R1040

5'-most EST jC-gmle01810008f04d1

Method BLASTX
NCBI GI g4510389
BLAST score 618
E value 3.0e-64
Match length 172
% identity 70

NCBI Description (AC007017) putative solute carrier protein [Arabidopsis

thaliana]

Seq. No. 33122

Contig ID 315259\_1.R1040

5'-most EST jC-gmle01810019g05a2

Seq. No. 33123

Contig ID 315277\_1.R1040

5'-most EST jC-gmle01810083f02d1

Method BLASTX
NCBI GI g3822403
BLAST score 409
E value 5.0e-40
Match length 106
% identity 70

NCBI Description (AF087932) hydroperoxide lyase [Arabidopsis thaliana]

Seq. No. 33124

Contig ID 315278\_1.R1040 5'-most EST uC-gmropic014b08b1

Seq. No. 33125

Contig ID 315293 1.R1040

5'-most EST jC-gmle01810019g12a2



Contig ID 315297\_1.R1040

5'-most EST jC-gmle01810003h03a1

Method BLASTX
NCBI GI g3063473
BLAST score 345
E value 2.0e-32
Match length 97
% identity 72

NCBI Description (AC003981) F22013.35 [Arabidopsis thaliana]

Seq. No. 33127

Contig ID 315313 1.R1040

5'-most EST jC-gmle01810004a08d1

Method BLASTX
NCBI GI g1352934
BLAST score 194
E value 8.0e-15
Match length 61
% identity 59

NCBI Description HYPOTHETICAL 161.2 KD PROTEIN IN NMD5-HOM6 INTERGENIC

REGION >gi\_1078403\_pir\_\_S57160 sulfite reductase homolog

YJR137c - yeast (Saccharomyces cerevisiae) >gi\_1015876\_emb\_CAA89669\_ (Z49637) ORF YJR137c

[Saccharomyces cerevisiae]

Seq. No. 33128

Contig ID 315315\_1.R1040

5'-most EST jC-gmle01810004a10a1

Method BLASTX
NCBI GI g3426037
BLAST score 256
E value 3.0e-37
Match length 169
% identity 35

NCBI Description (AC005168) putative ABC transporter protein [Arabidopsis

thaliana]

Seq. No. 33129

Contig ID 315317 1.R1040

5'-most EST jC-gmle01810004a11d1

Method BLASTX
NCBI GI g1931652
BLAST score 677
E value 4.0e-71
Match length 226
% identity 63

NCBI Description (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog

[Arabidopsis thaliana]

Seq. No. 33130

Contig ID 315354 1.R1040

Seq. No. 33131

Contig ID 315383 1.R1040

5'-most EST jC-gmle01810094b07d1



```
BLASTX
Method
                   q1399380
NCBI GI
BLAST score
                   368
E value
                   3.0e-35
Match length
                   93
% identity
                   69
                  (U43683) S-adenosyl-L-methionine:delta24-sterol-C-
NCBI Description
                  methyltransferase [Glycine max]
Seq. No.
                   33132
                   315395 1.R1040
Contig ID
                   jC-gmle01810004f06d1
5'-most EST
Seq. No.
                   33133
Contig ID
                   315467 1.R1040
5'-most EST
                   jC-gmle01810005b05d1
Seq. No.
                   33134
Contig ID
                   315509 1.R1040
                   jC-gmle01810005d07d1
5'-most EST
Seq. No.
                   33135
                   315547 1.R1040
Contig ID
                   jC-qmle01810005f08d1
5'-most EST
                   33136
Seq. No.
Contig ID
                   315604 1.R1040
5'-most EST
                   q4397395
Method
                   BLASTX
NCBI GI
                   g1621461
BLAST score
                   547
                   6.0e-56
E value
Match length
                   224
                   50
% identity
NCBI Description (U73103) laccase [Liriodendron tulipifera]
                   33137
Seq. No.
                   315608 1.R1040
Contig ID
5'-most EST
                   g5677524
                   33138
Seq. No.
Contig ID
                   315630 1.R1040
5'-most EST
                   jC-gmle01810006b11d1
                   33139
Seq. No.
                   315651 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810062d11d1
                   BLASTX
Method
                   g2864618
NCBI GI
BLAST score
                   156
E value
                   2.0e-10
Match length
                   44
% identity
```

NCBI Description

315658\_1.R1040 Contig ID

(AL021811) putative protein [Arabidopsis thaliana]



33141

5'-most EST jC-gmle01810006d04a1

Contig ID 315670\_1.R1040 5'-most EST jC-gmle01810006d11d1

Seq. No. 33142

Seq. No.

Contig ID 315704\_1.R1040 5'-most EST jC-gmro02910006b01a1

Method BLASTX
NCBI GI g4092534
BLAST score 317
E value 6.0e-29
Match length 221
% identity 35

NCBI Description (AF097830) suppressor of forked protein; Su(f) protein

[Drosophila virilis]

Seq. No. 33143

Contig ID 315743 1.R1040

5'-most EST jC-gmle01810007a04a1

Seq. No. 33144

Contig ID 315749\_1.R1040 5'-most EST jC-gmle01810007f05a1

Method BLASTX
NCBI GI g1084643
BLAST score 347
E value 1.0e-32
Match length 98
% identity 62

NCBI Description STE23 protein - yeast (Saccharomyces cerevisiae) >gi\_625109

(U19729) Ste23p [Saccharomyces cerevisiae]

Seq. No. 33145

Contig ID 315765\_1.R1040

5'-most EST jC-gmle01810007c04a1

Method BLASTX
NCBI GI g3738306
BLAST score 605
E value 7.0e-63
Match length 166
% identity 63

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 33146

Contig ID 315822\_1.R1040 5'-most EST jC-gmle01810007h12d1

Seq. No. 33147

Contig ID 315834 1.R1040

5'-most EST jC-gmle01810008b02d1

Seq. No. 33148

Contig ID 315836 1.R1040

5'-most EST jC-gmle01810027b04d1



Seq. No. Contig ID

315911 1.R1040 jC-gmle01810009f03a1

Seq. No.

33150

Contig ID

5'-most EST

315948 1.R1040

5'-most EST

uC-qmflminsoy070h04b1

Seq. No.

33151

Contig ID 5'-most EST 315949 1.R1040

Method

jC-gmle01810009c08d1 BLASTX

NCBI GI BLAST score E value

g3335367 256 4.0e-22

Match length % identity

59 69

NCBI Description

(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.

33152

Contig ID

315965 1.R1040

5'-most EST

jC-gmle01810009d06d1

Seq. No.

33153

Contig ID

316063 2.R1040

5'-most EST

jC-gmle01810092d11d1

Seq. No.

33154

Contig ID

316063 3.R1040

5'-most EST

jC-gmle01810045f08d1

Seq. No.

33155

Contig ID

316074 1.R1040

5'-most EST

jC-gmle01810010f10d1

Seq. No.

33156

Contig ID

316076 1.R1040

5'-most EST

jC-gmle01810010c09a1

Seq. No.

33157

Contig ID

316194 1.R1040

5'-most EST

jC-gmle01810011c07a1 BLASTX

Method NCBI GI

q3123100

BLAST score

197

E value

5.0e-15

Match length

65

% identity

58

NCBI Description

HYPOTHETICAL 15.9 KD PROTEIN C4A8.02C IN CHROMOSOME I

>gi 4490640 emb CAB11472.1 (Z98762) SPAC4A8.02c, unknown, len:142aa, similar eg. to YJBQ \_ECOLI, P32698, hypothetical

15.7 kd protein, (138aa), fast  $\overline{a}$  scores, opt:403, E(): 2.4e-32, (41.0% identity in 134 aa overlap)

[Schizosaccharomyces pombe]

Seq. No.

33158

Contig ID

316212 1.R1040



```
jC-gmle01810011d06a1
5'-most EST
                  33159
Seq. No.
Contig ID
                  316221 1.R1040
                  jC-gmst02400049c09a1
5'-most EST
                  33160
Seq. No.
                  316282 1.R1040
Contig ID
5'-most EST
                  q4260071
Method
                  BLASTX
                  g3297815
NCBI GI
BLAST score
                  187
                  4.0e-17
E value
                  72
Match length
% identity
                  65
                  (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  33161
                  316305 1.R1040
Contig ID
                  jC-gmle01810012a07d1
5'-most EST
Seq. No.
                  33162
                  316313 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400031c03a1
Seq. No.
                  33163
                  316313 2.R1040
Contig ID
5'-most EST
                  jC-gmle01810012b02a1
                  33164
Seq. No.
                  316313 3.R1040
Contig ID
                  uC-gmflminsoy019h04b1
5'-most EST
Seq. No.
                  33165
                  316350 1.R1040
Contig ID
                   jC-gmle01810012d05a1
5'-most EST
                  BLASTX
Method
                  g2924521
NCBI GI
                   269
BLAST score
                   3.0e-23
E value
Match length
                  134
% identity
                   45
NCBI Description (AL022023) putative protein [Arabidopsis thaliana]
Seq. No.
                   33166
Contig ID
                   316422_1.R1040
5'-most EST
                   fC-gmst700839356d1
                   BLASTX
Method
NCBI GI
                   q3256035
                   470
BLAST score
E value
                   1.0e-46
Match length
                   199
```

% identity NCBI Description

(Y14274) putative serine/threonine protein kinase [Sorghum

bicolor

47

Seq. No.

33167

```
316489 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810026f10d1
                  33168
Seq. No.
                  316517 1.R1040
Contig ID
5'-most EST
                  q4303947
                  33169
Seq. No.
                  316537_1.R1040
Contig ID
                  jC-gmle01810014f11d1
5'-most EST
                  BLASTX
Method
                  g2289786
NCBI GI
                  189
BLAST score
E value
                  5.0e-14
                  82
Match length
                  45
% identity
NCBI Description (D88153) HYA22 [Homo sapiens]
                  33170
Seq. No.
                  316631 1.R1040
Contig ID
                  jC-gmle01810036g02d1
5'-most EST
                  33171
Seq. No.
                  316754 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810048g09a1
Seq. No.
                  33172
                  316847 1.R1040
Contig ID
                  jC-gmle01810017h04a2
5'-most EST
                  33173
Seq. No.
                  317053 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810042h07d1
                   33174
Seq. No.
                   317065 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810020b10a1
Seq. No.
                   33175
Contig ID
                   317070 1.R1040
5'-most EST
                   jC-gmle01810020b12d1
                   33176
Seq. No.
Contig ID
                   317076 1.R1040
5'-most EST
                   jC-gmle01810020c06a1
                   33177
Seq. No.
```

Contig ID 317092 1.R1040

jC-gmle01810020g06d15'-most EST

Method BLASTX NCBI GI a3608147 BLAST score 159 1.0e-10 E value 79 Match length 43 % identity

(AC005314) putative chloroplast 31 kDa ribonucleoprotein NCBI Description

precursor [Arabidopsis thaliana]



```
Seq. No.
                  33178
Contig ID
                  317141 1.R1040
5'-most EST
                  jC-gmst02400060a05d1
                  BLASTX
Method
NCBI GI
                  q2947062
BLAST score
                  208
                  2.0e-16
E value
Match length
                  79
                  54
% identity
                  (AC002521) unknown protein [Arabidopsis thaliana]
NCBI Description
                  33179
Seq. No.
Contig ID
                  317164 1.R1040
5'-most EST
                  uC-gmrominsoy186g02b1
Method
                  BLASTX
NCBI GI
                  g2191175
BLAST score
                  189
                   5.0e-14
E value
Match length
                   123
% identity
                   (AF007270) A IG002P16.24 gene product [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   33180
                   317164 2.R1040
Contig ID
                   jC-gmle01810020g12d1
5'-most EST
Method
                   BLASTX
                   g2335096
NCBI GI
BLAST score
                   147
E value
                   5.0e-09
Match length
                   129
% identity
                  (AC002339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   33181
Seq. No.
                   317227 1.R1040
Contig ID
5'-most EST
                   uC-gmropic056d09b1
Seq. No.
                   33182
Contig ID
                   317248 1.R1040
5'-most EST
                   jC-gmle01810021c12d1
                   33183
Seq. No.
                   317251 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810021d02d1
                   33184
Seq. No.
                   317274 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810021e07d1
Method
                   BLASTX
```

NCBI GI g2213586
BLAST score 177
E value 1.0e-12
Match length 73
% identity 49

NCBI Description (AC000348) T7N9.6 [Arabidopsis thaliana]



Contig ID 317285\_1.R1040

5'-most EST jC-gmle01810073a09d1

Method BLASTX
NCBI GI g3894197
BLAST score 303
E value 1.0e-27
Match length 64
% identity 84

NCBI Description (AC005662) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33186

Contig ID 317316 1.R1040

5'-most EST jC-gmle01810091e09d1

Seq. No. 33187

Contig ID 317348 1.R1040

5'-most EST jC-gmro02910001a02d1

Seq. No. 33188

Contig ID 317350\_1.R1040

5'-most EST jC-gmle01810022b07a1

Seq. No. 33189

Contig ID 317379 1.R1040

5'-most EST g5687996
Method BLASTN
NCBI GI g4115370
BLAST score 41
E value 1.0e-13

Match length 89 % identity 87

NCBI Description Arabidopsis thaliana chromosome II BAC F27D4 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 33190

Contig ID 317380 1.R1040

5'-most EST jC-gmle01810022c05a1

Seq. No. 33191

Contig ID 317481 1.R1040

5'-most EST jC-gmle01810055b02a1

Method BLASTX
NCBI GI g3355467
BLAST score 267
E value 4.0e-23
Match length 139
% identity 39

NCBI Description (AC004218) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33192

Contig ID 317486 1.R1040

5'-most EST jC-gmle01810023b05a1

Method BLASTX
NCBI GI g2501644
BLAST score 303



E value 2.0e-27 Match length 153 % identity 42

NCBI Description URICASE (URATE OXIDASE) >gi\_2131155\_pir\_\_JC5140 urate

oxidase (EC 1.7.3.3) - yeast (Pichia jadinii)

>gi\_1741860\_dbj\_BAA06804\_ (D32043) uricase [Candida utilis]

Seq. No. 33193

Contig ID 317512\_1.R1040 5'-most EST jC-gmle01810023d07a1

Seq. No. 33194

Contig ID 317513\_1.R1040 5'-most EST jC-gmle01810023d07d1

Seq. No. 33195

Contig ID 317531\_1.R1040 5'-most EST jC-gmle01810023e06a1

Seq. No. 33196

Contig ID 317597\_1.R1040 5'-most EST jC-gmle01810093b04a1

Seq. No. 33197

Contig ID 317651\_1.R1040 5'-most EST jC-gmle01810024f10a1

Seq. No. 33198

Contig ID 317682\_1.R1040

5'-most EST jC-gmst02400068d08d1

Method BLASTX
NCBI GI g2262113
BLAST score 237
E value 8.0e-20
Match length 56
% identity 73

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 33199

Contig ID 317728\_1.R1040

5'-most EST jC-gmle01810025c04a1 Method BLASTN

Method BLASTN
NCBI GI g170073
BLAST score 76
E value 1.0e-34
Match length 118
% identity 92

NCBI Description Soybean calmodulin (SCaM-3) mRNA, complete cds

Seq. No. 33200

Contig ID 317748 1.R1040

5'-most EST jC-gmro02910007d04d1

Seq. No. 33201

Contig ID 317804 1.R1040

5'-most EST jC-gmle01810025g10d1



Contig ID 317832\_1.R1040 5'-most EST jC-gmle01810026a08d1

Seq. No. 33203

Contig ID 317833\_1.R1040

5'-most EST g5126688

Seq. No. 33204

Contig ID 317836\_1.R1040 5'-most EST jC-gmle01810027d04a1

Method BLASTN
NCBI GI g3378649
BLAST score 35
E value 3.0e-10
Match length 119

% identity 87

NCBI Description M.sativa mRNA translated from abscisic activated gene

Seq. No. 33205

Contig ID 317849 1.R1040 5'-most EST jC-gmle01810026b06a1

Method BLASTX
NCBI GI g417674
BLAST score 758
E value 1.0e-80
Match length 238

% identity 62

NCBI Description 60S RIBOSOMAL PROTEIN L7 >gi\_103356\_pir\_\_S21500 ribosomal

protein L7.e - fruit fly (Drosophila melanogaster)
>gi 8484 emb CAA33207 (X15109) ribosomal protein

[Drosophila melanogaster]

Seq. No. 33206

Contig ID 317884 1.R1040

5'-most EST jC-gmle01810026d06a1

Seq. No. 33207

Contig ID 317935\_1.R1040

5'-most EST jC-gmle01810026h03a1

Method BLASTX
NCBI GI g2213611
BLAST score 283
E value 2.0e-25
Match length 73
% identity 75

NCBI Description (AC000103) F21J9.5 [Arabidopsis thaliana]

Seq. No. 33208

Contig ID 317938\_1.R1040

5'-most EST jC-gmle01810027a01a1

Seq. No. 33209

Contig ID 317940 1.R1040

5'-most EST jC-gmle01810042h08d1

Seq. No. 33210



Contig ID 317982\_1.R1040 5'-most EST jC-gmst02400002e02d1

Seq. No. 33211

Contig ID 317997\_1.R1040 5'-most EST jC-gmle01810035f12d1

Seq. No. 33212

Contig ID 318029\_1.R1040 5'-most EST jC-gmle01810027f09d1

Seq. No. 33213

Contig ID 318075\_1.R1040

5'-most EST jC-gmle01810028b02a1

Seq. No. 33214

Contig ID 318100\_1.R1040 5'-most EST jC-gmst02400076d09a1

Method BLASTX
NCBI GI g2444174
BLAST score 604
E value 3.0e-78
Match length 176
% identity 79

NCBI Description (U94781) unconventional myosin [Helianthus annuus]

Seq. No. 33215

Contig ID 318109\_1.R1040
51-most FST 3C-cmrc02910061

5'-most EST jC-gmro02910061e02d1

Method BLASTX
NCBI GI g2832241
BLAST score 186
E value 1.0e-13
Match length 87
% identity 28

NCBI Description (AF030864) nonphototropic hypocotyl 1 [Arabidopsis

thaliana]

Seq. No. 33216

Contig ID 318121\_1.R1040 5'-most EST jC-gmle01810064b01a1

5 MOSC EST JC GMIEOTOTOVO+DOTAL

Seq. No. 33217

Contig ID 318132\_1.R1040

5'-most EST jC-gmle01810035f08d1

Seq. No. 33218

Contig ID 318144\_1.R1040 5'-most EST jC-gmle01810028f05d1

Seq. No. 33219

Contig ID 318146\_1.R1040 5'-most EST uC-gmropic0001g04a1

Method BLASTX
NCBI GI g2088651
BLAST score 201
E value 3.0e-15



Match length 55 % identity

(AF002109) hypersensitivity-related gene 201 isolog NCBI Description

[Arabidopsis thaliana]

33220 Seq. No.

318151 1.R1040 Contig ID

5'-most EST jC-gmle01810028f09d1

33221 Seq. No.

318185 1.R1040 Contig ID

jC-gmle01810028h08d1 5'-most EST

BLASTX Method g3935150 NCBI GI 321 BLAST score 1.0e-29 E value 75 Match length

77 % identity (AC005106) T25N20.14 [Arabidopsis thaliana] NCBI Description

33222 Seq. No.

318209 1.R1040 Contig ID jC-gmle01810029b01a1 5'-most EST

Seq. No. 33223

318210 1.R1040 Contig ID

jC-gmle01810029b01d1 5'-most EST

33224 Seq. No.

Contig ID 318223 1.R1040

5'-most EST jC-gmle01810029b10d1

33225 Seq. No.

318254\_1.R1040 Contig ID

5'-most EST jC-gmle01810029d08d1

33226 Seq. No.

318279 1.R1040 Contig ID

5'-most EST jC-gmle01810029f05a1

Seq. No.

33227

318349 1.R1040 Contig ID

jC-gmle01810030c02d1 5'-most EST

33228 Seq. No.

318370 1.R1040 Contig ID fC-qmst700605413r1 5'-most EST

BLASTX Method NCBI GI g2746079 256 BLAST score E value 5.0e-22 65 Match length % identity 74

(AF015310) BTH1 [Brassica napus] NCBI Description

Seq. No. 33229

318376 1.R1040 Contig ID

5035

```
jC-gmle01810030d11a2
5'-most EST
Method
                  BLASTX
                  g3413511
NCBI GI
BLAST score
                  441
                  1.0e-43
E value
                  129
Match length
% identity
                  66
                  (AJ000265) glucose-6-phosphate isomerase [Spinacia
NCBI Description
                  oleracea]
                  33230
Seq. No.
                  318377 1.R1040
Contig ID
                   jC-gmle01810030d11d1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4220528
BLAST score
                   506
                   2.0e-51
E value
                  106
Match length
                   89
% identity
                  (AL035356) glucose-6-phosphate isomerase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   33231
                   318388 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810078h03d1
                   33232
Seq. No.
                   318452 1.R1040
Contig ID
                   jC-gmle01810031a05a2
5'-most EST
                   BLASTX
Method
                   g2262157
NCBI GI
```

311 2.0e-44

BLAST score E value 173 Match length % identity 60

(AC002329) putative ligand-gated ion channel protein NCBI Description

[Arabidopsis thaliana]

33233 Seq. No. 318458 1.R1040 Contig ID 5'-most EST jC-gmle01810033e03d1

33234 Seq. No. 318459 1.R1040 Contig ID 5'-most EST jC-gmle01810033e05d1

33235 Seq. No. 318490 1.R1040 Contig ID 5'-most EST jC-gmle01810033g05d1

Seq. No. 33236 Contig ID 318511 1.R1040 5'-most EST jC-gmst02400016c09d1 Method BLASTX

NCBI GI q4262162 BLAST score 277 2.0e-24 E value



Match length 69 % identity 72

NCBI Description (AC005275) putative glycosylation enzyme [Arabidopsis

thaliana]

Seq. No. 33237

Contig ID 318536\_1.R1040

5'-most EST jC-gmle01810033e09d1

Seq. No. 33238

Contig ID 318552\_1.R1040

5'-most EST jC-gmle01810033d03d1

Method BLASTX
NCBI GI g3941543
BLAST score 381
E value 1.0e-36
Match length 90
% identity 80

NCBI Description (AF069497) pelota [Arabidopsis thaliana]

>gi\_4469016\_emb\_CAB38277\_ (AL035602) pelota (PEL1)

[Arabidopsis thaliana]

Seq. No. 33239

Contig ID 318560 1.R1040

5'-most EST jC-gmle01810031h03d1

Seq. No. 33240

Contig ID 318570 1.R1040

5'-most EST jC-gmle01810032a01d1

Seq. No. 33241

Contig ID 318588 1.R1040

5'-most EST g5752954

Method BLASTX

NCBI GI g2462839

BLAST score 156

E value 4.0e-10

Match length 63

% identity 56

NCBI Description (AF000657) unknown protein [Arabidopsis thaliana]

Seq. No. 33242

Contig ID 318597 1.R1040

5'-most EST jC-gmle01810032c09d1

Seq. No. 33243

Contig ID 318597\_2.R1040

5'-most EST jC-gmro02910046h05d1

Seq. No. 33244

Contig ID 318603 1.R1040

5'-most EST jC-gmle01810033g06d1

Seq. No. 33245

Contig ID 318605\_1.R1040

5'-most EST jC-gmle01810033g10d1



Contig ID 318654\_1.R1040

5'-most EST jC-gmle01810094f09d1

Seq. No. 33247

Contig ID 318680\_1.R1040

5'-most EST jC-gmle01810033b01a2

Seq. No. 33248

Contig ID 318697\_1.R1040

5'-most EST jC-gmle01810033c01d1

Seq. No. 33249

Contig ID 318742 1.R1040

5'-most EST jC-gmle01810033e08a2

Seq. No. 33250

Contig ID 318748 1.R1040

5'-most EST jC-gmle01810033e12d1

Seq. No. 33251

Contig ID 318801 1.R1040

5'-most EST jC-gmle01810034a06d1

Seq. No. 33252

Contig ID 318809\_1.R1040

5'-most EST jC-gmle01810034a11d1

Seq. No. 33253

Contig ID 318848 1.R1040

5'-most EST jC-gmle01810034e02d1

Method BLASTX
NCBI GI g4559327
BLAST score 257
E value 4.0e-22
Match length 122
% identity 48

NCBI Description (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33254

Contig ID 318891 1.R1040

5'-most EST jC-gmle01810034h09d1

Seq. No. 33255

Contig ID 318919 1.R1040

5'-most EST jC-gmle01810035b04a2

Seq. No. 33256

Contig ID 318923\_1.R1040

5'-most EST jC-gmro02910075g03d1

Method BLASTX
NCBI GI g3935170
BLAST score 239
E value 4.0e-20
Match length 59
% identity 76

NCBI Description (AC004557) F17L21.13 [Arabidopsis thaliana]



Contig ID 319060\_1.R1040 5'-most EST jC-gmle01810036a12a2

Seq. No. 33258

Contig ID 319070\_1.R1040

5'-most EST jC-gmle01810036b12a2

Method BLASTN
NCBI GI g945086
BLAST score 71
E value 2.0e-31
Match length 107
% identity 92

NCBI Description Glycine max transcription factor TFIIB mRNA, complete cds

Seq. No. 33259

Contig ID 319071 1.R1040

5'-most EST jC-gmle01810036d01d1

Method BLASTX
NCBI GI g3063710
BLAST score 196
E value 5.0e-15
Match length 59
% identity 53

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 33260

Contig ID 319074 1.R1040

5'-most EST jC-gmle01810036h02d1

Seq. No. 33261

Contig ID 319155 1.R1040

5'-most EST jC-gmle01810037c10a2

Method BLASTX
NCBI GI g2262177
BLAST score 299
E value 5.0e-27
Match length 126
% identity 59

NCBI Description (AC002329) hypothetical protein similar to T18A10.3

[Arabidopsis thaliana]

Seq. No. 33262

Contig ID 319184\_1.R1040

5'-most EST jC-gmle01810037f08a2

Method BLASTX
NCBI GI g2494301
BLAST score 672
E value 8.0e-71
Match length 161
% identity 80

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 2 GAMMA SUBUNIT

(EIF-2-GAMMA) >gi 1049318 (U37354) initiation factor eIF-2

gamma subunit [Schizosaccharomyces pombe]

Seq. No. 33263



```
319211 1.R1040
Contig ID
                   jC-gmro02910013f08d1
5'-most EST
                   33264
Seq. No.
                   319222 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810038b04d1
```

```
Seq. No.
                   33265
                   319231 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810038d07d1
```

33266 Seq. No. Contig ID 319294 1.R1040 5'-most EST jC-gmle01810040d07a1 33267 Seq. No.

319352 1.R1040

5'-most EST jC-gmle01810040h10d1 BLASTN Method g3335331 NCBI GI BLAST score 36 1.0e-10 E value 56 Match length 91 % identity

Contig ID

Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, NCBI Description complete sequence [Arabidopsis thaliana]

33268 Seq. No. 319356 1.R1040 Contig ID 5'-most EST jC-qmle01810041a02a1 Method BLASTX g2829870 NCBI GI 249 BLAST score

E value 3.0e-21 89 Match length % identity 25

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

33269 Seq. No. Contig ID 319360 1.R1040 5'-most EST jC-qmle01810041a06a1

33270 Seq. No. Contig ID 319429 1.R1040 5'-most EST jC-qmle01810041f11a1 Method BLASTX NCBI GI g2077896 BLAST score 393

5.0e-38 E value Match length 153 % identity

(AB003470) beta-D-glucosidase [Aspergillus kawachii] NCBI Description

Seq. No. 33271 319467 1.R1040 Contig ID 5'-most EST jC-gmle01810042d10a1



 Seq. No.
 33272

 Contig ID
 319482\_1.R1040

 5'-most EST
 jC-gmle01810042b06a1

Seq. No. 33273

Contig ID 319692\_1.R1040 5'-most EST jC-gmle01810044c09a1

Seq. No. 33274

Contig ID 319703\_1.R1040 5'-most EST jC-gmle01810043e05d1

Seq. No. 33275

Contig ID 319706\_1.R1040 5'-most EST jC-gmle01810043e07d1

Seq. No. 33276

Contig ID 319738 1.R1040 5'-most EST jC-gmle01810043g03d1

Seq. No. 33277

Contig ID 319770\_1.R1040

5'-most EST jC-gmst02400073e09d1

Seq. No. 33278

Contig ID 319818 1.R1040

5'-most EST jC-gmle01810044b11d1

Seq. No. 33279

Contig ID 319840\_1.R1040

5'-most EST jC-gmle01810044c11a1

Method BLASTX
NCBI GI g3560136
BLAST score 505
E value 3.0e-51
Match length 166
% identity 55

NCBI Description (AL031534) 2-isopropylmalate synthase. [Schizosaccharomyces

pombe]

Seq. No. 33280

Contig ID 319841\_1.R1040

5'-most EST jC-gmle01810044c11d1

Seq. No. 33281

Contig ID 320112\_1.R1040

5'-most EST jC-gmle01810046e06a1

Seq. No. 33282

Contig ID 320136\_1.R1040

5'-most EST jC-gmle01810046d05a1

Method BLASTX
NCBI GI g3688186
BLAST score 557
E value 2.0e-57
Match length 139
% identity 73

5041



NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 33283

Contig ID 320192 1.R1040

5'-most EST jC-gmle01810046f05d1

Method BLASTX
NCBI GI g4314371
BLAST score 148
E value 1.0e-09
Match length 40
% identity 65

NCBI Description (AC006340) putative G9a protein [Arabidopsis thaliana]

Seq. No. 33284

Contig ID 320313\_1.R1040 5'-most EST uC-gmropic014b11b1

Seq. No. 33285

Contig ID 320315 1.R1040

5'-most EST jC-gmst02400020da07d1

Seq. No. 33286

Contig ID 320407\_1.R1040

5'-most EST jC-gmle01810048b12d1

Seq. No. 33287

Contig ID 320438 1.R1040

5'-most EST jC-gmle01810048d09d1

Seq. No. 33288

Contig ID 320446 1.R1040

5'-most EST jC-gmle01810048e03a1

Seq. No. 33289

Contig ID 320447 1.R1040

5'-most EST jC-gmle01810048e03d1

Seq. No. 33290

Contig ID 320552\_1.R1040

5'-most EST jC-gmle01810049d06d1

Seq. No. 33291

Contig ID 320558 1.R1040

Seq. No. 33292

Contig ID 320642\_1.R1040

5'-most EST jC-gmle01810050e10a1

Method BLASTN
NCBI GI g11576
BLAST score 433
E value 0.0e+00
Match length 465
% identity 98

NCBI Description Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,

NADH dehydrogenase and ORF

```
Seq. No.
                   320768 1.R1040
- Contig ID
5'-most EST
                   jC-qmle01810051f07a1
Seq. No.
                   33294
Contig ID
                   320770 1.R1040
5'-most EST
                   jC-gmle01810051f08a1
Seq. No.
                   33295
Contig ID
                   320810 1.R1040
5'-most EST
                   jC-gmle01810073b08a1
Seq. No.
                   33296
                   321044 1.R1040
Contig ID
 5'-most EST
                   fC-qmro700565358r2
Method
                   BLASTX
```

Method BLASTX
NCBI GI g642134
BLAST score 299
E value 4.0e-27
Match length 88
% identity 64

NCBI Description (D45355) protein kinase [Arabidopsis thaliana]

>gi\_3063704\_emb\_CAA18595.1\_ (AL022537) protein kinase AME3

[Arabidopsis thaliana]

Seq. No. 33297

Contig ID 321155 1.R1040

5'-most EST uC-gmflminsoy024c03b1

Seq. No. 33298

Contig ID 321256\_1.R1040

5'-most EST jC-gmle01810056a07a1

Method BLASTX
NCBI GI g3445210
BLAST score 368
E value 4.0e-35
Match length 139
% identity 47

NCBI Description (AC004786) putative flavonol 3-o-glucosyltransferase

[Arabidopsis thaliana]

Seq. No. 33299

Contig ID 321264\_1.R1040

5'-most EST jC-gmle01810056b03a1

Method BLASTX
NCBI GI g3892055
BLAST score 1195
E value 1.0e-132
Match length 243
% identity 88

NCBI Description (AC002330) putative transport protein [Arabidopsis

thaliana]

Seq. No. 33300

Contig ID 321373\_1.R1040

5'-most EST jC-gmst02400065b02d1



Contig ID 321416 1.R1040

5'-most EST jC-gmro02910067f02d1

Seq. No. 33302

Contig ID 321418\_1.R1040

5'-most EST jC-gmle01810059d04d1

Seq. No. 33303

Contig ID 321419 1.R1040

5'-most EST jC-gmle01810059d05a1

Method BLASTX
NCBI GI g4432821
BLAST score 296
E value 2.0e-26
Match length 207

NCBI Description (AC006593) putative transmembrane protein [Arabidopsis

thaliana]

Seq. No. 33304

% identity

Contig ID 321438 1.R1040

5'-most EST jC-gmle01810059e03a1

Seq. No. 33305

Contig ID 321512 1.R1040

5'-most EST jC-gmle01810059h10d1

Seq. No. 33306

Contig ID 321531\_1.R1040

5'-most EST jC-gmle01810060b01d1

Seq. No. 33307

Contig ID 321560 1.R1040

5'-most EST jC-gmle01810060c09a1

Seq. No. 33308

Contig ID 321569\_1.R1040

5'-most EST jC-gmle01810060d01d1

Seq. No. 33309

Contig ID 321577\_1.R1040

5'-most EST jC-gmle01810087h11a1

Seq. No. 33310

Contig ID 321582 1.R1040

5'-most EST jC-gmle01810060d09d1

Method BLASTX
NCBI GI g1871180
BLAST score 280
E value 8.0e-25
Match length 131
% identity 53

NCBI Description (U90439) unknown protein [Arabidopsis thaliana]

Seq. No. 33311

Contig ID 321604\_1.R1040



```
5'-most EST jC-gmle01810060e11d1
Method BLASTX
NCBI GI g2191168
BLAST score 273
E value 5.0e-24
Match length 70
```

80

NCBI Description (AF007270) contains similarity to myosin heavy chain

[Arabidopsis thaliana]

Seq. No. 33312

% identity

Contig ID 321608\_1.R1040

5'-most EST jC-gmr002800027g09d1

Seq. No. 33313

Contig ID 321627 1.R1040

5'-most EST jC-gmle01810062h02d1

Seq. No. 33314

Contig ID 321632 1.R1040

5'-most EST jC-gmst02400028c02a1

Seq. No. 33315

Contig ID 321633 1.R1040

5'-most EST g5752600
Method BLASTX
NCBI GI g3702343
BLAST score 555
E value 9.0e-57
Match length 223
% identity 53

NCBI Description (AC005397) putative homeotic gene regulator [Arabidopsis

thaliana]

Seq. No.

Contig ID 321729 1.R1040

5'-most EST jC-gmle01810061h03a1

33316

Method BLASTX
NCBI GI g3482941
BLAST score 215
E value 3.0e-17
Match length 111
% identity 46

NCBI Description (AC005315) putative ligand-gated ionic channel [Arabidopsis

thaliana]

Seq. No. 33317

Contig ID 321737 1.R1040

5'-most EST jC-gmle01810061g12a1

Seq. No. 33318

Contig ID 321798\_1.R1040 5'-most EST fC-gmle700685876b1

Seq. No. 33319

Contig ID 321964\_1.R1040

5'-most EST jC-gmle01810063d05d1



Method NCBI GI q3786006 BLAST score 361 E value 2.0e-34 Match length 83 % identity 78

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33320

Contig ID 322022 1.R1040 5'-most EST fC-gmro700646449r1

Method BLASTX NCBI GI a4468151 BLAST score 158 E value 2.0e-10 Match length 56 % identity 41

NCBI Description (AJ131999) sucrose synthase [Craterostigma plantagineum]

Seq. No. 33321

Contig ID 322035 1.R1040

5'-most EST jC-gmro02800028b04d1

Seq. No. 33322

Contig ID 322089 1.R1040

5'-most EST jC-gmle01810064b08d1

Seq. No. 33323

Contig ID 322118 1.R1040 5'-most EST jC-gmle01810064c11a1

Seq. No. 33324

Contig ID 322148 1.R1040 5'-most EST fC-qmle7000786512d1

Seq. No. 33325

322182 1.R1040 Contig ID 5'-most EST jC-qmle01810064f11d1

Seq. No. 33326

Contig ID 322203 1.R1040

5'-most EST g4396088 Method BLASTX NCBI GI g3249098 BLAST score 207 E value 3.0e-16 Match length 97 % identity 46

NCBI Description (AC003114) ESTs gb\_T04610, gb N38459, gb T45174, qb R30481

and gb\_N64971 come from this gene. [Arabidopsis thaliana]

Seq. No. 33327

Contig ID 322266 1.R1040 5'-most EST

jC-gmle01810065d04d1

Seq. No. 33328

Contig ID 322276 1.R1040



```
5'-most EST
                   jC-qmle01810065d12d1
Seq. No.
                   33329
                   322297 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810065f08d1
Method
                  BLASTX
NCBI GI
                  q1408460
BLAST score
                  252
E value
                  1.0e-21
Match length
                  124
% identity
NCBI Description
                   (U40161) type 2A protein serine/threonine phosphatase 55
                  kDa B regulatory subunit [Arabidopsis thaliana]
                   33330
Seq. No.
Contig ID
                   322310 1.R1040
5'-most EST
                  jC-gmle01810065g11d1
Method
                  BLASTN
NCBI GI
                  q2764523
BLAST score
                  114
E value
                   3.0e-57
Match length
                  342
% identity
                  83
NCBI Description Pisum sativum mRNA for Rieske iron-sulfur protein Tic55
Seq. No.
                  33331
                  322322 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400044g03d1
Seq. No.
                  33332
                  322344 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810066c12d1
Seq. No.
                  33333
                  322347 1.R1040
Contig ID
5'-most EST
                  jC-qmle01810066d03d1
Seq. No.
                  33334
                  322365 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910019a06d1
Seq. No.
                  33335
                  322382 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400032h02a1
Method
                  BLASTX
NCBI GI
                  g1350528
BLAST score
                  147
```

E value 3.0e-09 Match length 39 64 % identity

NCBI Description (L47602) ABA-responsive and embryogenesis-associated gene;

LEA-like protein [Picea glauca]

Seq. No. 33336

Contig ID 322391 1.R1040

5'-most EST jC-gmle01810067a02d1



322395 1.R1040 Contig ID

5'-most EST jC-gmst02400074f02d1

Seq. No. 33338

Contig ID 322406 1.R1040

5'-most EST jC-gmle01810073a03d1

Seq. No. 33339

Contig ID 322474 1.R1040

5'-most EST jC-gmle01810067g03a1

Seq. No. 33340

Contig ID 322488 1.R1040

5'-most EST jC-gmle01810067h01d1

33341 Seq. No.

Contig ID 322501 1.R1040

5'-most EST jC-gmst02400027a09d1

33342 Seq. No.

Contig ID 322524 1.R1040

5'-most EST jC-gmle01810068b08a1

33343 Seq. No.

Contig ID 322532 1.R1040

5'-most EST jC-qmle01810068c02a1

Method BLASTX NCBI GI g1710055 BLAST score 328 E value 2.0e-30 Match length 118

% identity

NCBI Description RDS1 PROTEIN >gi\_1363621\_pir\_\_S58477 rds1 protein - fission

yeast (Schizosaccharomyces pombe) >gi\_1184029\_emb\_CAA54544\_

(X77328) rds1 [Schizosaccharomyces pombe]

33344 Seq. No.

322554 1.R1040 Contig ID

5'-most EST jC-qmle01810071d01a1

Seq. No. 33345

322578\_1.R1040 Contig ID

5'-most EST jC-gmle01810068e10d1

Seq. No. 33346

322583 1.R1040 Contig ID

5'-most EST jC-gmle01810068f02d1

Seq. No. 33347

322609 1.R1040 Contig ID

5'-most EST jC-gmle01810068g10d1

Seq. No. 33348

Contig ID 322615 1.R1040

5'-most EST jC-gmle01810068h05a1



Contig ID 322618\_1.R1040

5'-most EST jC-gmle01810068h08a1

Seq. No. 33350

Contig ID 322650 1.R1040

Seq. No. 33351

Contig ID 322682 1.R1040

5'-most EST jC-gmle01810070a11a1

Seq. No. 33352

Contig ID 322705 1.R1040

5'-most EST jC-gmle01810070c04d1

Method BLASTX
NCBI GI g3924606
BLAST score 324
E value 1.0e-30
Match length 89

Match length 89 % identity 75

NCBI Description (AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33353

Contig ID 322740 1.R1040

5'-most EST jC-gmle01810070e12a1

Method BLASTX
NCBI GI g2827534
BLAST score 685
E value 2.0e-72
Match length 150
% identity 86

NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 33354

Contig ID 322741\_1.R1040

5'-most EST jC-gmle01810070f11d1

Seq. No. 33355

Contig ID 322763 1.R1040

5'-most EST jC-gmle01810070g02d1

Seq. No. 33356

Contig ID 322775 1.R1040

5'-most EST jC-gmle01810070h09a1

Seq. No. 33357

Contig ID 322776 1.R1040

5'-most EST jC-gmle01810070h09d1

Seq. No. 33358

Contig ID 322850 1.R1040

5'-most EST jC-gmle01810071d12a1

Seq. No. 33359

Contig ID 322857 1.R1040

5'-most EST jC-gmle01810071e05d1



```
Seq. No.
                  33360
                  322864 1.R1040
Contig ID
5'-most EST
                  fC-qmro700565119r2
Seq. No.
                  33361
Contig ID
                  322871 1.R1040
5'-most EST
                  jC-gmle01810071f03d1
                  BLASTX
Method
NCBI GI
                  q3881976
BLAST score
                  497
E value
                  2.0e-50
Match length
                  118
                  76
% identity
                  (AJ012409) hypothetical protein [Homo sapiens]
NCBI Description
                  33362
Seq. No.
Contig ID
                  322878 1.R1040
5'-most EST
                  jC-gmle01810071f08d1
                  33363
Seq. No.
Contig ID
                  322886 1.R1040
5'-most EST
                  jC-gmle01810071g02d1
                  33364
Seq. No.
Contig ID
                  322908 1.R1040
                  jC-gmle01810071h06d1
5'-most EST
Seq. No.
                  33365
                  322922 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810072b04d1
Seq. No.
                  33366
Contig ID
                  322953 1.R1040
5'-most EST
                  jC-qmle01810072d06d1
Method
                  BLASTX
NCBI GI
                  g1710055
BLAST score
                  188
E value
                  4.0e-14
Match length
                  100
% identity
                  39
                  RDS1 PROTEIN >gi 1363621 pir S58477 rds1 protein - fission
NCBI Description
                  yeast (Schizosaccharomyces pombe) >gi 1184029 emb CAA54544
                  (X77328) rds1 [Schizosaccharomyces pombe]
Seq. No.
                  33367
                  322972_1.R1040
Contig ID
5'-most EST
                  jC-gmst02400006b09d1
```

Method BLASTX NCBI GI g2739309 BLAST score 394 4.0e-38 E value Match length 91 % identity 47

NCBI Description (Y15990) P-glycoprotein-like protein [Arabidopsis thaliana]

Seq. No. 33368

5050



Contig ID 322994 1.R1040 5'-most EST jC-gmle01810072h12d1

Seq. No. 33369

Contig ID 323119 1.R1040

5'-most EST jC-gmle01810073h08a1

Method BLASTX NCBI GI q3402751 BLAST score 283 E value 6.0e-25 Match length 154

% identity 21

NCBI Description (AL031187) putative protein [Arabidopsis thaliana]

Seq. No. 33370

323132 1.R1040 Contig ID

5'-most EST jC-gmle01810075a03a1

Seq. No. 33371

Contig ID 323213 1.R1040

5'-most EST jC-gmst02400058b01d1

Method BLASTX NCBI GI g2344887 BLAST score 676 E value 5.0e-71 Match length 174 % identity 79

NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 33372

Contig ID 323233 1.R1040

5'-most EST jC-gmle01810093c06d1

Seq. No. 33373

323269 1.R1040 Contig ID 5'-most EST fC-gmle700875686r1

Seq. No. 33374

323279 1.R1040 Contig ID 5'-most EST jC-gmle01810077f11d1

Method BLASTX NCBI GI g3335348 BLAST score 243 E value 2.0e-20 Match length 71

% identity 68

(AC004512) T8F5.20 [Arabidopsis thaliana] NCBI Description

Seq. No. 33375

Contig ID 323283 1.R1040 5'-most EST jC-gmle01810078b07d1

Seq. No. 33376

Contig ID 323378 1.R1040 5'-most EST jC-gmst02400024e07d1

Seq. No. 33377

```
Contig ID
                   323461 1.R1040
5'-most EST
                   uC-gmflminsoy081d01b1
Method
                   BLASTX
NCBI GI
                   q4539389
BLAST score
                   653
E value
                   1.0e-68
Match length
                   136
% identity
                   94
                   (AL035526) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   323507 1.R1040
5'-most EST
                   jC-gmle01810080d06d1
Seq. No.
                   33379
Contig ID
                   323512 1.R1040
5'-most EST
                   jC-gmle01810080d08d1
Method
                   BLASTX
NCBI GI
                   g4455328
BLAST score
                   239
                   7.0e-20
E value
Match length
                   55
% identity
                   76
NCBI Description
                  (AL035525) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   33380
Contig ID
                   323549 1.R1040
5'-most EST
                   jC-gmle01810080f09a1
Method
                   BLASTX
NCBI GI
                   g3511147
BLAST score
                   484
E value
                   1.0e-48
Match length
                   135
% identity
                   67
NCBI Description
                   (AF061329) PR-4 type protein [Vitis vinifera]
Seq. No.
                   33381
Contig ID
                   323558 1.R1040
5'-most EST
                   jC-gmle01810089d11d1
                   BLASTX
                   q4314384
                   344
                   2.0e-32
                   101
% identity
NCBI Description
```

Method NCBI GI BLAST score E value Match length

(AC006232) putative cysteine proteinase [Arabidopsis

thalianal

Seq. No. 33382 Contig ID

323599 1.R1040 5'-most EST jC-gmle01810082a07a1

42

Method BLASTX NCBI GI g119791 BLAST score 175 E value 2.0e-12 Match length 101

% identity

5052





NCBI Description 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR

(3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)

>gi\_1084385\_pir\_\_S22450 3-oxoacyl-[acyl-carrier-protein]
reductase (EC 1.1.1.100) precursor - Cuphea lanceolata
>gi\_18046\_emb\_CAA45866\_ (X64566) 3-oxoacyl-[acyl-carrier

protein] reductase [Cuphea lanceolata]

>gi\_228929\_prf\_\_1814446A beta ketoacyl-ACP reductase

[Cuphea lanceolata]

Seq. No. 33383

Contig ID 323601\_1.R1040

Seq. No. 33384

Contig ID 323697 1.R1040

5'-most EST jC-gmle01810082f10a1

Method BLASTX
NCBI GI g479413
BLAST score 987
E value 1.0e-107

Match length 216 % identity 91

NCBI Description myosin-like protein - Arabidopsis thaliana

Seq. No. 33385

Contig ID 323815 1.R1040

5'-most EST jC-gmle01810083e02d1

Seq. No. 33386

Contig ID 323831\_1.R1040

5'-most EST jC-gmle01810083e11a1

Seq. No. 33387

Contig ID 323850 1.R1040

5'-most EST jC-gmle01810083f10a1

Method BLASTX
NCBI GI g731810
BLAST score 404
E value 3.0e-39
Match length 109

% identity 67

NCBI Description PROBABLE 60S RIBOSOMAL PROTEIN YIL052C

>gi\_626886\_pir\_\_S48427 ribosomal protein L34.e.B, cytosolic
- yeast (Saccharomyces cerevisiae) >gi\_557816\_emb\_CAA86170\_
(Z38060) spliced ribosomal protein, len: 121, CAI: 0.77,
RL34\_RAT P11250 60S RIBOSOMAL PROTEIN L34 [Saccharomyces

cerevisiael

Seq. No. 33388

Contig ID 323872\_1.R1040
5'-most EST iC-gml-01810083

5'-most EST jC-gmle01810083g11a1
Method BLASTX

NCBI GI g4006908 BLAST score 217 E value 4.0e-17 Match length 78 % identity 53





## NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 33389

Contig ID 323923 1.R1040

5'-most EST jC-gmle01810084c01d1

Seq. No. 33390

Contig ID 323996 1.R1040

5'-most EST uC-gmrominsoy109g10b1

Seq. No. 33391

Contig ID 324020 1.R1040

5'-most EST jC-gmle01810084h03a1

Seq. No. 33392

Contig ID 324042 1.R1040

5'-most EST jC-gmle01810085a08d1

Seq. No. 33393

Contig ID 324063 1.R1040

5'-most EST jC-gmle01810085c02a1

Method BLASTX
NCBI GI g2492509
BLAST score 159
E value 1.0e-10
Match length 114
% identity 39

NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG >gi\_2146083\_pir\_\_S73497

cell division protein ftsH - Mycoplasma pneumoniae (SGC3) (ATCC 29342) >gi\_1673833 (AE000018) Mycoplasma pneumoniae, cell division protein FtsH; similar to Swiss-Prot Accession Number P37476, from B. subtilis [Mycoplasma pneumoniae]

Seg. No. 33394

Contig ID 324112 1.R1040

5'-most EST jC-qmle01810085f06d1

Seq. No. 33395

Contig ID 324133 1.R1040

5'-most EST jC-gmle01810085g11a1

Seq. No. 33396

Contig ID 324161 1.R1040

5'-most EST jC-gmst02400063d12d1

Seq. No. 33397

Contig ID 324193 1.R1040

5'-most EST jC-qmst02400036d05d2

Method BLASTX
NCBI GI g2191194
BLAST score 132
E value 6.0e-09
Match length 83
% identity 48

NCBI Description (AF007271) contains weak to the SAPB protein (TR:E236624)

[Arabidopsis thaliana]



Contig ID 324231 1.R1040

5'-most EST jC-gmle01810086e02a1

Seq. No. 33399

Contig ID 324238\_1.R1040

5'-most EST jC-gmle01810086e06a1

Method BLASTX
NCBI GI g2765817
BLAST score 382
E value 1.0e-36
Match length 175

% identity 53

NCBI Description (Z95352) AtMlo-h1 [Arabidopsis thaliana]

>gi 3892049 gb AAC78258.1 AAC78258 (AC002330) AtMlo-h1

[Arabidopsis thaliana]

Seq. No. 33400

Contig ID 324262 1.R1040

5'-most EST jC-gmle01810086f07a1

Method BLASTX
NCBI GI g3913996
BLAST score 305
E value 3.0e-31
Match length 109
% identity 68

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR

 $>gi_2208927_dbj_BAA20482_ (D85610)$  ATP-dependent protease

Lon [Spinacia oleracea]

Seq. No. 33401

Contig ID 324322\_1.R1040

5'-most EST jC-gmle01810087a08d1

Seq. No. 33402

Contig ID 324382\_1.R1040

5'-most EST jC-gmle01810087d11a1

Seq. No. 33403

Contig ID 324400 1.R1040

5'-most EST jC-gmle01810087e09a1

Method BLASTX
NCBI GI g1172441
BLAST score 167
E value 3.0e-11
Match length 53
% identity 68

NCBI Description POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi 99685 pir S21883

DNA-binding protein POSF21 - Arabidopsis thaliana >gi\_16429\_emb\_CAA43366 (X61031) posF21 [Arabidopsis

thaliana]

Seq. No. 33404

Contig ID 324501\_1.R1040 5'-most EST jC-gmle01810088b11a1

Method BLASTX NCBI GI g3176709



BLAST score E value 1.0e-16 126 Match length 35 % identity

NCBI Description (AC002392) putative anthranilate

N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis

thaliana]

33405 Seq. No.

324526 1.R1040 Contig ID

5'-most EST jC-gmle01810088d03d1

Method BLASTX q2765817 NCBI GI BLAST score 312 2.0e-28 E value 106 Match length % identity 67

(Z95352) AtMlo-h1 [Arabidopsis thaliana] NCBI Description

>gi 3892049 gb AAC78258.1 AAC78258 (AC002330) AtMlo-hl

[Arabidopsis thaliana]

Seq. No. 33406

324639 1.R1040 Contig ID

5'-most EST g5752874

Seq. No. 33407

324663 1.R1040 Contig ID

5'-most EST q5677301

Seq. No. 33408

324676 1.R1040 Contig ID

5'-most EST jC-gmle01810089c10a1

Seq. No. 33409

324686 1.R1040 Contig ID

5'-most EST jC-qmle01810089d03a1

Seq. No. 33410

324742 1.R1040 Contig ID

5'-most EST jC-qmro02910009d08a1

Method BLASTX g1272349 NCBI GI BLAST score 346 E value 2.0e-32 Match length 137 52 % identity

NCBI Description (U51740) secreted glycoprotein 3 [Ipomoea trifida]

Seq. No. 33411

324826 1.R1040 Contig ID

5'-most EST jC-gmle01810090c04d1

Seq. No. 33412

324844 1.R1040 Contig ID

5'-most EST jC-gmle01810090d03d1

Method BLASTX NCBI GI g2809246



BLAST score 276 E value 9.0e-27 Match length 107 % identity 52

NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]

Seq. No. 33413

Contig ID 324878\_1.R1040 5'-most EST jC-gmle01810090e11a1

Method BLASTX
NCBI GI g4185136
BLAST score 411
E value 6.0e-40
Match length 216
% identity 40

NCBI Description (AC005724) putative trehalose-6-phosphate synthase

[Arabidopsis thaliana]

Seq. No. 33414

Contig ID 325006\_1.R1040

5'-most EST jC-gmle01810091c12d1

Seq. No. 33415

Contig ID 325066\_1.R1040 5'-most EST uC-gmropic100f07b1

Method BLASTX
NCBI GI g2864618
BLAST score 413
E value 3.0e-40
Match length 131
% identity 57

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 33416

Contig ID 325068\_1.R1040

5'-most EST jC-gmle01810091f10d1

Seq. No. 33417

Contig ID 325075 1.R1040

5'-most EST jC-gmle01810094h06d1

Seq. No. 33418

Contig ID 325111\_1.R1040

5'-most EST jC-gmle01810092a04d1

Seq. No. 33419

Contig ID 325157\_1.R1040

5'-most EST jC-gmle01810092d11a1

Seq. No. 33420

Contig ID 325265 1.R1040

5'-most EST jC-gmro02800032a06d1

Method BLASTX
NCBI GI g3924602
BLAST score 152
E value 8.0e-10
Match length 51

5057



% identity 51

NCBI Description (AF069442) predicted OR23 protein of unknown function [Arabidopsis thaliana]

Seq. No. 33421

Contig ID

325314 1.R1040

5'-most EST

uC-gmflminsoy054h11b1

Method NCBI GI BLASTX g4220477

BLAST score

284

E value

8.0e-38

Match length % identity

133 68

NCBI Description

(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.

33422

Contig ID

325321 1.R1040

5'-most EST

jC-gmle01810093d12a1

Seq. No.

33423

Contig ID

325372\_1.R1040

5'-most EST

jC-gmst02400036g05d2

Seq. No.

33424

Contig ID

325462 1.R1040

5'-most EST

jC-gmle01810094h07d1

Seq. No.

33425

Contig ID

325477 1.R1040

5'-most EST

jC-gmle01810094d12a1

Method

BLASTN

NCBI GI

g1839634

BLAST score

292

E --- l--

1.0e-163

E value

502

Match length

91

% identity
NCBI Description

heat shock protein 70=allergenic polypeptide {C-terminal, variable region} [Cladosporium herbarum, IMI 96220, mRNA

Partial, 1061 nt]

Seq. No.

33426

Contig ID

325484 1.R1040

5'-most EST

jC-gmle01810094e04a1

Method NCBI GI BLASTX

BLAST score

g2980784

DLMD1 SCOLE

651

E value

3.0e-68

Match length

201

% identity

12

NCBI Description

(AL022198) puative protein [Arabidopsis thaliana]

Seq. No.

33427

Contig ID

325675 1.R1040

5'-most EST

jC-gmst02400064a11d1

Seq. No.

33428

Contig ID

325725 1.R1040

5058



jC-qmro02800026c03a1 5'-most EST BLASTX Method g2244866 NCBI GI 323 BLAST score 6.0e-30 E value Match length 134 58 % identity (Z97337) hypothetical protein [Arabidopsis thaliana] NCBI Description 33429 Seq. No. 325785 1.R1040 Contig ID 5'-most EST jC-gmro02910071c01a1 BLASTX Method q2459431 NCBI GI 298 BLAST score 7.0e-27 E value Match length 91 % identity 63 (AC002332) unknown protein [Arabidopsis thaliana] NCBI Description 33430 Seq. No. 325792 1.R1040 Contig ID 5'-most EST jC-gmro02800027d02d1 33431 Seq. No. 325805 1.R1040 Contig ID jC-gmro02910022a11a1 5'-most EST Method BLASTX g2832304 NCBI GI BLAST score 210 2.0e-30 E value Match length 149 % identity 49 (AF044489) receptor-like protein kinase [Oryza sativa] NCBI Description 33432 Seq. No. 325884 1.R1040 Contig ID 5'-most EST jC-gmro02800028e10a1 BLASTX Method NCBI GI g3261631 BLAST score 177 2.0e-12 E value 105 Match length % identity 42 (Z79700) accA2 [Mycobacterium tuberculosis] NCBI Description 33433 Seq. No. 325981 1.R1040 Contig ID 5'-most EST jC-gmro02800029e04a1 Seq. No. 33434

Contig ID 326038 1.R1040

5'-most EST jC-gmro02800030a04d1

BLASTX Method NCBI GI q2129623 BLAST score 204 E value 5.0e-16



Match length 53 % identity

immunophilin FKBP15-2 - Arabidopsis thaliana >gi 1272408 NCBI Description

(U52047) immunophilin [Arabidopsis thaliana]

Seq. No. 33435

326093 1.R1040 Contig ID jC-gmro02800042c08d1 5'-most EST

Method BLASTX NCBI GI g3785990 BLAST score 203 E value 8.0e-16 Match length 55

73 % identity

NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]

>gi 4220487 (AC006069) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 33436

Contig ID 326100 1.R1040

5'-most EST jC-gmro02800030e11d1

33437 Seq. No.

326152 1.R1040 Contig ID

5'-most EST jC-gmro02800031a04d1

33438 Seq. No.

326177 1.R1040 Contig ID

5'-most EST jC-gmro02800031b07a1

Method BLASTX NCBI GI g1762584 BLAST score 114 4.0e-09 E value Match length 61

% identity

NCBI Description (U63373) polygalacturonase isoenzyme 1 beta subunit homolog

[Arabidopsis thaliana]

33439 Seq. No.

Contig ID 326216 1.R1040

5'-most EST jC-gmro02800031d09d1

Seq. No. 33440

Contig ID 326292 1.R1040

5'-most EST g4301729

Seq. No. 33441

Contig ID 326300 1.R1040

5'-most EST jC-gmro02800032a05d1

Seq. No. 33442

Contig ID 326318 1.R1040

5'-most EST q4284526 Method BLASTX NCBI GI q4335745 BLAST score 362 E value 2.0e-34



Match length 159 % identity 47

NCBI Description (AC006284) putative hydrolase (contains an

esterase/lipase/thioesterase active site serine domain

(prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 33443

Contig ID 326500 1.R1040

5'-most EST jC-gmro02800033d09d1

Seq. No. 33444

Contig ID 326611 1.R1040

Seq. No. 33445

Contig ID 326612 1.R1040

5'-most EST jC-gmro02800034f07a1

Method BLASTX
NCBI GI g1730576
BLAST score 246
E value 6.0e-21
Match length 82
% identity 56

NCBI Description PROLINE IMINOPEPTIDASE (PROLYL AMINOPEPTIDASE)

>gi\_1084134\_pir\_\_JC4184 prolyl aminopeptidase (EC 3.4.11.5)

- Aeromonas sobria >gi 1236731 dbj\_BAA06380\_ (D30714)

prolyl aminopeptidase [Aeromonas sobria]

Seq. No. 33446

Contig ID 326622\_1.R1040

5'-most EST jC-gmro02800035a04a1
Method BLASTX
NCBI GI g4510368
BLAST score 170

BLAST score 170 E value 5.0e-12 Match length 106 % identity 40

NCBI Description (AC007017) putative transcription factor E2F5 [Arabidopsis

thaliana]

Seq. No.

33447

Contig ID 326711\_1.R1040

5'-most EST  $g42604\overline{1}5$ 

Seq. No.

33448

Contig ID 326733 1.R1040

5'-most EST uC-gmrominsoy235e07b1

Method BLASTX
NCBI GI g2739381
BLAST score 350
E value 5.0e-33
Match length 126
% identity 60

NCBI Description (AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.

33449

Contig ID

326800\_1.R1040



```
jC-gmro02800038d09a1
5'-most EST
                  33450
Seq. No.
Contig ID
                   326823 1.R1040
                  uC-gmropic008h09b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2344900
                  277
BLAST score
                  2.0e-24
E value
                  112
Match length
                   47
% identity
                  (AC002388) EREBP isolog [Arabidopsis thaliana]
NCBI Description
                   33451
Seq. No.
                   326831 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800038f08d1
Method
                   BLASTN
                   q1432053
NCBI GI
BLAST score
                   62
                   3.0e-26
E value
                   170
Match length
% identity
                   84
NCBI Description Oryza sativa asparagine synthetase mRNA, complete cds
                   33452
Seq. No.
                   326949 1.R1040
Contig ID
                   jC-gmro02800039e09a1
5'-most EST
Method
                   BLASTX
                   g100099
NCBI GI
                   422
BLAST score
                   2.0e-41
E value
Match length
                   138
% identity
                   56
                  DNA-binding protein VBP1 - fava bean >gi 1372966 (M81827)
NCBI Description
                   CREB-like protein [Vicia faba]
                   33453
Seq. No.
                   326950 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910024g05d1
                   BLASTX
Method
NCBI GI
                   g2865394
BLAST score
                   141
                   1.0e-08
E value
Match length
                   49
                   57
% identity
                  (AF036949) basic leucine zipper protein [Zea mays]
NCBI Description
```

327214 1.R1040 Contig ID

jC-gmro02800042g07d1 5'-most EST

Seq. No. 33455

327251 1.R1040 Contig ID

5'-most EST uC-gmrominsoy048h09b1

Seq. No. 33456

Contig ID 327345 1.R1040



jC-qmro02800044h04a1 5'-most EST

Method BLASTX NCBI GI g2344899 BLAST score 419 E value 6.0e-41Match length 123

% identity

NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No.

33457 327355 1.R1040 Contig ID

5'-most EST jC-gmro02910011f07d1

59

Seq. No.

33458

Contig ID

327360 1.R1040

5'-most EST

jC-gmro02910001b02d1

Method BLASTX NCBI GI g3875246 BLAST score 172 E value 3.0e-12

59 Match length % identity 51

NCBI Description (Z81490) similar to WD domain, G-beta repeats (2 domains);

cDNA EST EMBL:T00482 comes from this gene; cDNA EST

EMBL: T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gene;

Seq. No. 33459

327408 1.R1040 Contig ID

5'-most EST jC-gmro02910001f06d1

Seq. No. 33460

327416 1.R1040 Contig ID

5'-most EST jC-gmro02910001g01d1

Seq. No. 33461

Contig ID 327471 1.R1040

5'-most EST jC-gmro02910039a12d1

33462 Seq. No.

Contig ID 327490 1.R1040

5'-most EST jC-gmro02910002c11d1

Seq. No. 33463

327495 1.R1040 Contig ID

jC-gmro02910007e03d1 5'-most EST

Method BLASTX NCBI GI q4490309 BLAST score 273 E value 4.0e-24 Match length 74

% identity 72

NCBI Description (AL035678) peroxidase ATP17a-like protein [Arabidopsis

thaliana]

Seq. No. 33464

Contig ID 327498 1.R1040



```
5'-most EST
                   jC-gmro02910002d04d1
                  33465
Seq. No.
                  327512 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910002d11d1
                  33466
Seq. No.
                  327580_1.R1040
Contig ID
5'-most EST
                   jC-gmro02910002h12d1
Method
                  BLASTX
NCBI GI
                  g4235430
BLAST score
                  216
                  2.0e-17
E value
                  56
Match length
                  71
% identity
NCBI Description
                  (AF098458) latex-abundant protein [Hevea brasiliensis]
Seq. No.
                   33467
                   327599_1.R1040
Contig ID
5'-most EST
                  jC-gmst02400069e02a1
Seq. No.
                   33468
                   327716_1.R1040
Contig ID
5'-most EST
                   jC-gmro02910004e12d1
Seq. No.
                   33469
                   327718 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910016a08a1
Method
                   BLASTX
NCBI GI
                  g4510339
BLAST score
                   468
E value
                   7.0e-47
Match length
                  163
                   57
% identity
                  (AC006921) putative ABC transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                   33470
Seq. No.
                   327719 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910004f03d1
                   BLASTX
Method
NCBI GI
                   g4510339
BLAST score
                   223
E value
                   3.0e-18
Match length
                   62
% identity
                   61
NCBI Description
```

(AC006921) putative ABC transporter protein [Arabidopsis

thaliana]

33471 Seq. No.

Contig ID 327729 1.R1040

5'-most EST uC-gmflminsoy065c02b1

Seq. No. 33472

Contig ID 327751 1.R1040

5'-most EST jC-qmst02400051d03d1

Method BLASTX



NCBI GI g3335169 BLAST score 160 E value 8.0e-11 Match length 70 % identity 47

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi\_4455197\_emb\_CAB36520\_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 33473

Contig ID 327939\_1.R1040 5'-most EST jC-gmro02910007f07a1

Method BLASTX
NCBI GI g2464865
BLAST score 516
E value 2.0e-52
Match length 136
% identity 69

NCBI Description (Z99707) pectinesterase like protein [Arabidopsis thaliana]

Seq. No. 33474

Contig ID 327940\_1.R1040

5'-most EST jC-gmro02910007f07d1

Method BLASTX
NCBI GI g3152618
BLAST score 361
E value 2.0e-34
Match length 97
% identity 67

NCBI Description (AC004482) putative pectinesterase [Arabidopsis thaliana]

>gi\_3242724 (AC003040) putative pectinesterase [Arabidopsis

thaliana]

Seq. No. 33475

Contig ID 327993\_1.R1040

5'-most EST jC-gmro02910008h07a1

Seq. No. 33476

Contig ID 327999\_1.R1040 5'-most EST jC-gmro02910006e11a1

Method BLASTX
NCBI GI g1669341
BLAST score 182
E value 2.0e-13
Match length 57
% identity 65

NCBI Description (D45066) AOBP (ascorbate oxidase promoter-binding protein)

[Cucurbita maxima]

Seq. No. 33477

Contig ID 328018\_1.R1040 5'-most EST uC-gmropic070h10b1

Seq. No. 33478

Contig ID 328023\_1.R1040 5'-most EST uC-gmronoir064f05b1



328063 1.R1040 Contig ID 5'-most EST uC-gmronoir042e08b1

BLASTX Method NCBI GI g4539343 BLAST score 614 7.0e-64 E value 181 Match length 70 % identity

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

33480 Seq. No.

328076 1.R1040 Contig ID 5'-most EST jC-gmst02400027f03a1

Seq. No. 33481

328194 1.R1040 Contig ID 5'-most EST jC-gmro02910007h12a1

33482 Seq. No.

328339 2.R1040 Contig ID 5'-most EST jC-gmro02910008g10d1

Method BLASTX NCBI GI g4107480 BLAST score 155 3.0e-10 E value

59 Match length % identity 35

(AL035085) putative mitochondrial carrier protein NCBI Description

[Schizosaccharomyces pombe]

Seq. No. 33483

328484 1.R1040 Contig ID 5'-most EST uC-gmronoir060d02b1

BLASTX Method NCBI GI q2462833 BLAST score 207 E value 5.0e-16 236 Match length 24 % identity

(AF000657) highly similar to froha and frohb, potential NCBI Description

frohc [Arabidopsis thaliana]

Seq. No. 33484

328495 1.R1040 Contig ID 5'-most EST uC-gmropic044c09b1

Method BLASTX NCBI GI q3367574 BLAST score 181 3.0e-13 E value Match length 109 % identity 40

NCBI Description (AL031135) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33485

Contig ID 328567 1.R1040

5'-most EST jC-gmro02910040e08d1



Contig ID 328593\_1.R1040 5'-most EST jC-gmro02910011e10d1

Seq. No. 33487

Contig ID 328631\_1.R1040

5'-most EST jC-gmro02910035g04d1

Seq. No. 33488

Contig ID 328661\_1.R1040

5'-most EST jC-gmro02910012b07a1

Method BLASTX
NCBI GI g2832636
BLAST score 186
E value 9.0e-14
Match length 61
% identity 54

NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]

>gi\_4455157\_emb\_CAA16697.1\_ (AL021687) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 33489

Contig ID 328670 1.R1040

5'-most EST jC-gmro02910012b11d1

Seq. No. 33490

Contig ID 328757\_1.R1040

5'-most EST jC-gmro02910012g09d1

Seq. No. 33491

Contig ID 328773\_1.R1040

5'-most EST jC-gmro02910012h06d1

Method BLASTX
NCBI GI g3337361
BLAST score 168
E value 1.0e-11
Match length 54
% identity 56

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 33492

Contig ID 328804\_1.R1040 5'-most EST fC-gmro7000747276r1

Method BLASTX
NCBI GI g2459419
BLAST score 224
E value 4.0e-18
Match length 99
% identity 47

NCBI Description (AC002332) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33493

Contig ID 328817\_1.R1040

5'-most EST jC-gmro02910013b09d1

Method BLASTX NCBI GI g2708749



BLAST score 248
E value 3.0e-21
Match length 135
% identity 49

NCBI Description (AC003952) putative senescence-assoc. rhodanese-like

protein [Arabidopsis thaliana]

Seq. No. 33494

Contig ID 328828\_1.R1040 5'-most EST jC-gmro02910013c04a1

Method BLASTX
NCBI GI g2245055
BLAST score 162
E value 6.0e-11
Match length 67
% identity 49

NCBI Description (Z97342) resistance gene homolog (fragment) [Arabidopsis

thaliana]

Seq. No. 33495

Contig ID 328849\_1.R1040

5'-most EST jC-gmst02400014c12d1

Method BLASTX
NCBI GI g2117619
BLAST score 189
E value 3.0e-14
Match length 72
% identity 50

NCBI Description peroxidase (EC 1.11.1.7) 4 precursor - wheat

>gi\_732976\_emb\_CAA59487\_ (X85230) peroxidase [Triticum

aestivum]

Seq. No. 33496

Contig ID 328849\_2.R1040

5'-most EST jC-gmro02910074c05d1

Seq. No. 33497

Contig ID 328879\_1.R1040

5'-most EST jC-gmro02910013e08a1

Method BLASTX
NCBI GI g2851577
BLAST score 887
E value 8.0e-96
Match length 229
% identity 69

NCBI Description SERINE CARBOXYPEPTIDASE III PRECURSOR (CP-MIII)

>qi 1877219 emb CAA70817 (Y09604) serine carboxypeptidase

III, CP-MIII [Hordeum vulgare]

Seq. No. 33498

Contig ID 328933\_1.R1040 5'-most EST uC-gmropic025h11b1

Method BLASTX
NCBI GI g2464901
BLAST score 263
E value 9.0e-23
Match length 79



% identity 70

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 33499

Contig ID 328993 1.R1040

5'-most EST jC-gmst02400020dc08d1

Method BLASTX
NCBI GI g3928097
BLAST score 216
E value 3.0e-17
Match length 88
% identity 49

NCBI Description (AC005770) unknown protein, 5' partial [Arabidopsis

thaliana]

Seq. No. 33500

Contig ID 329011\_1.R1040 5'-most EST uC-gmronoir030d10b1

Method BLASTX
NCBI GI g1888357
BLAST score 359
E value 5.0e-34
Match length 83
% identity 77

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]

>gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 33501

Contig ID 329059\_1.R1040

5'-most EST jC-gmro02910015a06d1

Seq. No. 33502

Contig ID 329077 1.R1040

5'-most EST jC-gmro02910015c10d1

Method BLASTX
NCBI GI g3377507
BLAST score 525
E value 2.0e-53
Match length 119
% identity 87

NCBI Description (AF056026) auxin transport protein EIR1 [Arabidopsis

thaliana] >gi\_3661620 (AF093241) putative auxin efflux carrier AGR [Arabidopsis thaliana] >gi\_3746886 (AF087459) polar-auxin-transport efflux component AGRAVITROPIC 1 [Arabidopsis thaliana] >gi\_4206709 (AF086906) root gravitropism control protein [Arabidopsis thaliana]

Seq. No. 33503

Contig ID 329171 1.R1040

5'-most EST jC-gmro02910016c04a1

Method BLASTX
NCBI GI g3334667
BLAST score 349
E value 1.0e-38
Match length 118
% identity 70





```
NCBI Description (Y10493) putative cytochrome P450 [Glycine max]
```

Contig ID 329194 1.R1040

5'-most EST jC-gmst02400065f11d1

Seq. No. 33505

Contig ID 329277 1.R1040

5'-most EST jC-gmro02910016h11d1

Method BLASTX
NCBI GI g3176684
BLAST score 422
E value 3.0e-41
Match length 128

Match length 128 % identity 62

NCBI Description (AC003671) Contains similarity to equilibratiave nucleoside

transporter 1 gb\_U81375 from Homo sapiens. ESTs gb\_N65317, gb\_T20785, gb\_AA586285 and gb\_AA712578 come from this gene.

[Arabidopsis thaliana]

Seq. No. 33506

Contig ID 329290 1.R1040

5'-most EST jC-gmr002910018b01a1

Method BLASTX
NCBI GI g4165018
BLAST score 226
E value 4.0e-33
Match length 155
% identity 53

NCBI Description (D89053) Acyl-CoA synthetase 3 [Homo sapiens]

Seq. No. 33507

Contig ID 329291 1.R1040

5'-most EST jC-gmro02910017d03a1

Seq. No. 33508

Contig ID 329326\_1.R1040

5'-most EST jC-gmro02910024a12a1

Seq. No. 33509

Contig ID 329368 1.R1040

5'-most EST jC-gmro02910019b01d1

Seq. No. 33510

Contig ID 329370 1.R1040

5'-most EST jC-gmro02910059g03d1

Method BLASTX
NCBI GI g3738298
BLAST score 399
E value 8.0e-39
Match length 150
% identity 55

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

>gi\_4249394 (AC006072) unknown protein [Arabidopsis

thaliana]

Seq. No. 33511



Contig ID 329460\_1.R1040 5'-most EST jC-gmro02910020e09d1

Seq. No. 33512

Contig ID 329587\_1.R1040

5'-most EST g4397439

Method BLASTX

NCBI GI g2244915

BLAST score 164

E value 2.0e-20

Match length 146
% identity 36

NCBI Description (Z97339) strong homology to reverse transcriptase

[Arabidopsis thaliana]

Seq. No. 33513

Contig ID 329690\_1.R1040

5'-most EST jC-gmro02910022f05d1

Seq. No. 33514

Contig ID 329775\_1.R1040

5'-most EST jC-gmro02910022f10a1

Seq. No. 33515

Contig ID 329828\_1.R1040

5'-most EST jC-gmro02910023a08a1

Seq. No. 33516

Contig ID 329830\_1.R1040

5'-most EST jC-gmro02910023b08a1

Seq. No. 33517

Contig ID 329919\_1.R1040

5'-most EST jC-gmro02910023f03d1

Seq. No. 33518

Contig ID 330002 1.R1040

5'-most EST jC-gmro02910024b08d1

Seq. No. 33519

Contig ID 330066\_1.R1040

5'-most EST jC-gmro02910024f10a1

Method BLASTX
NCBI GI g3395431
BLAST score 340
E value 7.0e-32
Match length 92
% identity 68

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 33520

Contig ID 330120 1.R1040

5'-most EST jC-gmro02910051h03d1

Seq. No. 33521

Contig ID 330137 1.R1040

5'-most EST jC-gmro02910025a04a1



Contig ID 330191 1.R1040

uC-gmrominsoy320a01b1 5'-most EST

BLASTX Method NCBI GI q4006908 226 BLAST score 9.0e-19 E value 107 Match length 44 % identity

(Z99708) putative protein [Arabidopsis thaliana] NCBI Description

33523 Seq. No.

330216 1.R1040 Contig ID

5'-most EST jC-gmst02400043a09d1

33524 Seq. No.

330330 1.R1040 Contig ID

5'-most EST jC-gmro02910026e03a1

33525 Seq. No.

330409 1.R1040 Contig ID

5'-most EST jC-gmro02910071a02d1

33526 Seq. No.

330421 1.R1040 Contig ID

5'-most EST uC-gmrominsoy028h10b1

BLASTX Method NCBI GI g3128185 BLAST score 332 6.0e-31 E value 171 Match length

47 % identity

(AC004521) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 33527

330422 1.R1040 Contig ID

5'-most EST jC-gmst02400062b03d1

Seq. No. 33528

Contig ID 330427 1.R1040

jC-gmro02910057f12a1 5'-most EST

Method BLASTN NCBI GI q2245682 BLAST score 192 1.0e-104 E value Match length 411 87 % identity

Glycine max peroxidase precursor (GMIPER1) mRNA, complete NCBI Description

Seq. No. 33529

Contig ID 330437 1.R1040

5'-most EST jC-gmro02910027b04d1

Method BLASTX NCBI GI g2702272 BLAST score 295



E value 2.0e-26
Match length 135
% identity 13

NCBI Description (AC003033) hypothetical protein [Arabidopsis thaliana]

Seq. No.

33530

Contig ID

330460 1.R1040

5'-most EST

uC-gmrominsoy186f11b1

Seq. No.

33531

Contig ID

330468 1.R1040

5'-most EST

jC-gmro02910027e04d1

Method NCBI GI BLAST score BLASTX g4567249 465

E value Match length 2.0e-46 117 73

% identity
NCBI Description

(AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.

33532

Contig ID

330486 1.R1040

5'-most EST

jC-gmro02910027g02d1

Seq. No.

33533

Contig ID 5'-most EST

330518\_1.R1040 uC-gmropic040g03b1

Seq. No.

33534

Contig ID

330598 1.R1040

5'-most EST

jC-gmro02910030b07d1

Seq. No.

33535

Contig ID

330616 1.R1040

5'-most EST

jC-gmro02910071f02d1

Seq. No.

33536

Contig ID

330631\_1.R1040

5'-most EST

jC-gmro02910030d08d1

Method NCBI GI BLASTX g2346972

BLAST score E value

235

Match length

1.0e-19

Match lengt % identity 97

NCBI Description

(AB006598) ZPT2-11 [Petunia x hybrida]

Seq. No.

33537

Contig ID

330665 1.R1040

5'-most EST

jC-gmro02910030g03a1

Seq. No.

33538

Contig ID

330711 1.R1040

5'-most EST

jC-gmro02910031b04d1

Seq. No.

33539

Contig ID

330764\_1.R1040

5073



5'-most EST jC-gmro02910031f10d1

Method BLASTX
NCBI GI g3122572
BLAST score 209
E value 1.0e-16
Match length 93
% identity 53

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (76 KD MITOCHONDRIAL COMPLEX I

SUBUNIT) >gi\_1084434\_pir\_\_S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi\_758340\_emb\_CAA59818\_ (X85808) 76 kDa mitochondrial

complex I subunit [Solanum tuberosum]

Seq. No. 33540

Contig ID 330842\_1.R1040

5'-most EST jC-gmro02910032e01d1

Method BLASTX
NCBI GI g4417296
BLAST score 219
E value 9.0e-18
Match length 55
% identity 67

NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]

Seq. No. 33541

Contig ID 330978\_1.R1040

5'-most EST jC-gmro02910034e02d1

Seq. No. 33542

Contig ID 330988 1.R1040

5'-most EST jC-gmro02910034e08d1

Method BLASTN
NCBI GI g1370197
BLAST score 55
E value 4.0e-22
Match length 235

Match length 235 % identity 87

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB8E

Seq. No. 33543

Contig ID 330996\_1.R1040

5'-most EST jC-gmro02910034f02d1

Seq. No. 33544

Contig ID 331016 1.R1040

5'-most EST jC-gmro02910034g05d1

Seq. No. 33545

Contig ID 331041 1.R1040

5'-most EST jC-gmro02910071a10d1

Seq. No. 33546

Contig ID 331077\_1.R1040

5'-most EST g4260395 Method BLASTX NCBI GI g4220541



BLAST score E value 2.0e-39 Match length 237 47 % identity

NCBI Description (AL035356) Rab geranylgeranyl transferase like protein

[Arabidopsis thaliana]

Seq. No.

33547 331106 1.R1040 Contig ID

5'-most EST

jC-gmro02910036a10a1

Method NCBI GI BLASTX g2130080

BLAST score E value

338 4.0e-32

Match length % identity

89 73

NCBI Description

Nramp1 protein - rice >gi 1470320 bbs 177441 (S81897)

OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa, indica, cv. IR 36, etiolated shoots, Peptide, 517 aa] [Oryza sativa] >gi\_2231132 (L41217) integral membrane

protein [Oryza sativa]

Seq. No.

33548

Contig ID

331114 1.R1040

5'-most EST

jC-gmro02910036h01d1

Method BLASTX NCBI GI q4490736 BLAST score 149 2.0e-09 E value Match length 50

% identity 60

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No.

33549

Contig ID

331153 1.R1040

5'-most EST

jC-gmro02910036f03a1

Seq. No.

33550

Contig ID

331191 1.R1040

5'-most EST

jC-gmro02910036g07a1

Seq. No.

33551

Contig ID

331310 1.R1040

5'-most EST

jC-gmro02910037f11a1

Method NCBI GI BLASTX g3142295

BLAST score

302

E value Match length 3.0e-27

% identity

122 25

NCBI Description

(AC002411) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. [Arabidopsis

thaliana]

Seq. No.

33552

Contig ID 5'-most EST 331468 1.R1040

jC-gmro02910039b04d1



Contig ID 331526 1.R1040 5'-most EST uC-gmropic057a04b1

Seq. No.

33554

Contig ID

331534\_1.R1040

5'-most EST

jC-gmro02910039e10d1

Seq. No.

33555

Contig ID 5'-most EST 331667 1.R1040 fC-gmro700864430d3

Seq. No.

33556

Contig ID

331711 1.R1040

5'-most EST

jC-gmro02910040h10d1

Method NCBI GI BLASTX g1771160

BLAST score E value

249 3.0e-21

Match length % identity

68 72

NCBI Description

(X98929) SBT1 [Lycopersicon esculentum]

>gi 3687305 emb CAA06999 (AJ006378) subtilisin-like

protease [Lycopersicon esculentum]

Seq. No.

33557

Contig ID

331718 1.R1040

5'-most EST Method

g43966<del>6</del>9 BLASTX

NCBI GI BLAST score g1354510 364

E value Match length

1.0e-34 88

% identity NCBI Description

(U55205) HAL2-like protein [Arabidopsis thaliana]

Seq. No.

33558

Contig ID

331728 1.R1040

5'-most EST

g5057699

Seq. No.

33559

Contig ID

331748 1.R1040

5'-most EST

jC-gmro02910041021a1

Seq. No.

33560

Contig ID

331900 1.R1040

5'-most EST

jC-qmro02910046b11d1

Seq. No.

33561

Contig ID

331913 1.R1040 jC-gmro02910046c07d1

5'-most EST Method

BLASTX

NCBI GI

g2961357

BLAST score

1217

E value

1.0e-134

Match length 322

5076



% identity (AL022140) putative protein [Arabidopsis thaliana] NCBI Description

33562 Seq. No.

332021 1.R1040 Contig ID 5'-most EST jC-gmro02910047a02d1

33563 Seq. No.

332047 1.R1040 Contig ID

5'-most EST jC-gmr002910047g02d1

Seq. No. 33564

332068 1.R1040 Contig ID jC-qmro02910068f04d1 5'-most EST

33565 Seq. No.

332071 1.R1040 Contig ID

jC-gmro02910047e02a1 5'-most EST

BLASTX Method q1888357 NCBI GI 742 BLAST score 7.0e-79E value Match length 200 % identity 69

(X98130) alpha-mannosidase [Arabidopsis thaliana] NCBI Description

>gi 1890154 emb\_CAA72432\_ (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

33566 Seq. No.

332107 1.R1040 Contig ID 5'-most EST jC-gmro02910047h04a1

33567 Seq. No.

332126 1.R1040 Contig ID 5'-most EST uC-gmropic074e11b1

Seq. No. 33568

332170 1.R1040 Contig ID

5'-most EST jC-qmro02910048e03d1

33569 Seq. No.

332193 1.R1040 Contig ID

jC-gmro02910048f09d1 5'-most EST

33570 Seq. No.

332201\_1.R1040 Contig ID

5'-most EST jC-gmro02910048g03d1

Seq. No. 33571

332231 1.R1040 Contig ID

5'-most EST jC-gmro02910049a07d1

33572 Seq. No.

332266 1.R1040 Contig ID

jC-gmst02400031e03d1 5'-most EST

33573 Seq. No.

332280 1.R1040 Contig ID uC-gmrominsoy095b12b1 5'-most EST BLASTX Method g3342798 NCBI GI 268 BLAST score 1.0e-23 E value 70 Match length 73 % identity (AF061240) glutamine cyclotransferase precursor [Carica NCBI Description 33574 Seq. No. 332324 1.R1040 Contig ID jC-gmro02910050b07d1 5'-most EST Method BLASTX q3202038 NCBI GI BLAST score 428 4.0e-42 E value Match length 113 69 % identity (AF069322) permease 1 [Mesembryanthemum crystallinum] NCBI Description Seq. No. 33575 332400 1.R1040 Contig ID jC-qmro02910051b10d1 5'-most EST 33576 Seq. No. 332470 1.R1040 Contig ID jC-gmro02910051f05d1 5'-most EST 33577 Seq. No. 332621 1.R1040 Contig ID fC-gmro700868519d3 5'-most EST 33578 Seq. No. 332631 1.R1040 Contig ID fC-gmro7000764393r1 5'-most EST 33579 Seq. No. 332686 1.R1040 Contig ID jC-gmro02910054g10a1 5'-most EST 33580 Seq. No. 332720 1.R1040 Contig ID 5'-most EST jC-gmro02910056e01a1 33581 Seq. No.

Contig ID 332814\_1.R1040 5'-most EST uC-gmronoir050e02b1

Method BLASTX
NCBI GI g1946371
BLAST score 358
E value 4.0e-34
Match length 101
% identity 68

NCBI Description (U93215) regulatory protein Viviparous-1 isolog

[Arabidopsis thaliana]



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33582
Seq. No.
                   332911 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910060a08d1
                   BLASTN
Method
NCBI GI
                   g1524177
                   94
BLAST score
E value
                   2.0e-45
                   186
Match length
                   88
% identity
NCBI Description M.sativa mRNA for proteasome subunit
                   33583
Seq. No.
                   332916 1.R1040
Contig ID
5'-most EST
                   g42981\overline{2}4
                   BLASTX
Method
                   g2344900
NCBI GI
BLAST score
                   260
                   2.0e-22
E value
                   57
Match length
                   81
% identity
                  (AC002388) EREBP isolog [Arabidopsis thaliana]
NCBI Description
                   33584
Seq. No.
                   333076 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910061c01d1
                   BLASTX
Method
                   g2576363
NCBI GI
                   396
BLAST score
                   2.0e-38
E value
Match length
                   133
                   57
% identity
                   (U39783) amino acid transport protein [Arabidopsis
NCBI Description
                   thaliana]
                   33585
Seq. No.
                   333129 1.R1040
Contig ID
                   uC-gmrominsoy197c12b1
5'-most EST
                   BLASTX
Method
                   g2224931
NCBI GI
BLAST score
                   292
E value
                   3.0e-26
                   108
Match length
                   56
% identity
                   (AF004215) ethylene-insensitive3-like3 [Arabidopsis
NCBI Description
                   thaliana]
                   33586
Seq. No.
                   333553 2.R1040
Contig ID
                   jC-gmst02400020d09a1
5'-most EST
Seq. No.
                   33587
```

Contig ID 333630\_1.R1040

5'-most EST jC-gmro02910065f08d1

Seq. No. 33588

Contig ID 333638\_1.R1040



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jC-gmro02910065g03a1
5'-most EST
                   33589
Seq. No.
                   333639 1.R1040
Contig ID
                   jC-gmro02910065g03d1
5'-most EST
                   BLASTX
Method
                   g4512660
NCBI GI
                   142
BLAST score
                   2.0e-14
E value
                   87
Match length
                   46
% identity
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4544467 gb AAD22374.1 AC006580 6 (AC006580)
                   hypothetical protein [Arabidopsis Thaliana]
                   33590
Seq. No.
                   333749 1.R1040
Contig ID
                   g56668<del>0</del>7
5'-most EST
                   BLASTX
Method
                   g2262117
NCBI GI
BLAST score
                   412
E value
                   7.0e-40
Match length
                   228
                   43
% identity
                   (AC002343) auxin inducible protein isolog [Arabidopsis
NCBI Description
                   thaliana]
                   33591
Seq. No.
                   333788 1.R1040
Contig ID
                   jC-gmro02910067b07d1
5'-most EST
Seq. No.
                   33592
                   333841 1.R1040
Contig ID
                   jC-gmst02400055g02a1
5'-most EST
                   33593
Seq. No.
                   333841 2.R1040
Contig ID
                   jC-gmro02910067d05d1
5'-most EST
                   33594
Seq. No.
                   333882 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910067f07a1
                   33595
Seq. No.
                   333965 1.R1040
Contig ID
                   iC-gmro02910068c02a1
5'-most EST
Method
                   BLASTX
                   q2673916
NCBI GI
BLAST score
                   188
                   6.0e-14
E value
                   51
Match length
```

% identity 73

(AC002561) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 33596 Contig ID

334010 1.R1040 5'-most EST jC-qmro02910068f02a1



```
Method BLASTX
NCBI GI g4006856
BLAST score 442
E value 1.0e-43
Match length 163
% identity 30
```

NCBI Description (Z99707) receptor kinase-like protein [Arabidopsis

thaliana]

Seq. No. 33597

Contig ID 334082\_1.R1040 5'-most EST fC-gmle700555604r2

Seq. No. 33598

Contig ID 334096\_1.R1040 5'-most EST jC-gmro02910069d07a1

Seq. No. 33599

Contig ID 334123\_1.R1040 5'-most EST jC-gmro02910069f07a1

Method BLASTN
NCBI GI g3510347
BLAST score 52
E value 4.0e-20
Match length 92
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No. 33600

Contig ID 334151 1.R1040 5'-most EST jC-gmr002910069h10d1

Method BLASTX
NCBI GI g1491617
BLAST score 270
E value 1.0e-23
Match length 82
% identity 67

NCBI Description (X99952) peroxidase [Arabidopsis thaliana]

Seq. No. 33601

Contig ID 334213\_1.R1040 5'-most EST jC-gmro02910071h04a1

Seq. No. 33602

Contig ID 334269\_1.R1040 5'-most EST jC-gmro02910071a12d1

Method BLASTX
NCBI GI g2262111
BLAST score 194
E value 9.0e-15
Match length 76
% identity 50

NCBI Description (AC002343) ribitol dehydrogenase isolog [Arabidopsis

thaliana]

Seq. No. 33603



```
334274 1.R1040
Contig ID
                   jC-qmro02910071c04a1
5'-most EST
                  BLASTX
Method
                   g3367587
NCBI GI
BLAST score
                   281
                   6.0e-25
E value
                  152
Match length
                   40
% identity
                   (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
                   33604
Seq. No.
                   334327 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910071d12d1
Method
                   BLASTX
                  g2827623
NCBI GI
BLAST score
                   667
                   6.0e-70
E value
                   142
Match length
                   89
% identity
                   (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   33605
                   334376 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910071g05a1
                   33606
Seq. No.
                   334483 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400009a04d1
Seq. No.
                   33607
                   334621_1.R1040
Contig ID
5'-most EST
                   jC-gmro02910074c02d1
                   BLASTX
Method
NCBI GI
                   q4218113
BLAST score
                   144
                   7.0e-14
E value
Match length
                   56
% identity
                   80
                   (AL035353) xyloglucan endotransglycosylase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   33608
Seq. No.
                   334751 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400063h10d1
Seq. No.
                   33609
Contig ID
                   334858 1.R1040
5'-most EST
                   jC-qmst02400001a09d1
Method
                   BLASTX
NCBI GI
                   g2191135
BLAST score
```

234 E value 2.0e-19 Match length 117 % identity 39

NCBI Description (AF007269) A IG002N01.14 gene product [Arabidopsis

thaliana]



Seq. No. Contig ID

334879 1.R1040 jC-gmst02400001b12a1 5'-most EST

Seq. No.

334883 1.R1040 Contig ID

jC-gmst02400001c02a1 5'-most EST

33612 Seq. No.

334968 1.R1040 Contig ID

jC-qmst02400001h10a1 5'-most EST

Method BLASTN NCBI GI q169048 BLAST score 147 9.0e-77 E value Match length 387 85 % identity

NCBI Description Pea farnesyltransferase beta-subunit mRNA, complete cds

33613 Seq. No.

335005 1.R1040 Contig ID

5'-most EST uC-gmrominsoy309a11b1

Seq. No. 33614

335024 1.R1040 Contig ID

jC-qmst02400002d08d1 5'-most EST

Seq. No. 33615

335055 1.R1040 Contig ID

jC-gmst02400002g02a1 5'-most EST

Seq. No. 33616

335073 1.R1040 Contig ID

jC-gmst02400002h10d1 5'-most EST

33617 Seq. No.

335174 1.R1040 Contig ID

jC-qmst02400004b09d1 5'-most EST

33618 Seq. No.

335284 1.R1040 Contig ID

5'-most EST jC-gmst02400005c07a1

33619 Seq. No.

335386 1.R1040 Contig ID

jC-gmst02400006c05a1 5'-most EST

Seq. No. 33620

335403 1.R1040 Contig ID

jC-gmst02400006d08d1 5'-most EST

BLASTX Method NCBI GI g2462781 217 BLAST score 2.0e-17 E value Match length 51

75 % identity

NCBI Description (U73175) carbamoyl phosphate synthetase small subunit



## [Arabidopsis thaliana]

Seq. No. 33621 Contig ID 335427 1.R1040

5'-most EST jC-gmst02400020db06d1

Seq. No. 33622

Contig ID 335428\_1.R1040

5'-most EST jC-gmst02400006g01a1

Seq. No. 33623

Contig ID 335429\_1.R1040

5'-most EST jC-gmst02400006g01d1

Seq. No. 33624

Contig ID 335484\_1.R1040

5'-most EST jC-gmst02400007b09d1

Method BLASTX
NCBI GI g3256035
BLAST score 202
E value 1.0e-15
Match length 77
% identity 49

NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum

bicolor]

Seq. No. 33625

Contig ID 335487\_1.R1040 5'-most EST fC-gmro700566572d3

Seq. No. 33626

Contig ID 335507 1.R1040

5'-most EST jC-gmst02400007d07d1

Seq. No. 33627

Contig ID 335541\_1.R1040

5'-most EST jC-gmst02400007f07a1

Seq. No. 33628

Contig ID 335557 1.R1040

5'-most EST jC-gmst02400007g09d1

Seq. No. 33629

Contig ID 335564\_1.R1040

5'-most EST jC-gms\(\overline{t}\)02400007h05d1

Method BLASTX
NCBI GI g2098575
BLAST score 185
E value 1.0e-13
Match length 44
% identity 75

NCBI Description (AC002115) F25451\_2 [Homo sapiens]

Seq. No. 33630

Contig ID 335572 1.R1040

5'-most EST jC-gmst02400077e05d1



Seq. No. 33631

Contig ID 335630\_1.R1040

5'-most EST jC-gmst02400008d04d1

Seq. No. 33632

Contig ID 335732\_1.R1040

5'-most EST jC-gmst02400009b03d1

Method BLASTX
NCBI GI g3080433
BLAST score 290
E value 5.0e-26
Match length 140
% identity 46

NCBI Description (AL022605) putative gamma-glutamyltransferase [Arabidopsis

thaliana]

Seq. No. 33633

Contig ID 335810 1.R1040 5'-most EST jC-gmst02400017c11a1

Seq. No. 33634

Contig ID 335885\_1.R1040

5'-most EST jC-gmst02400011a08d1

Seq. No. 33635

Contig ID 336036\_1.R1040

5'-most EST jC-gmst02400027h05d1

Seq. No. 33636

Contig ID 336078\_1.R1040

5'-most EST jC-gmst02400014b11a1

Seq. No. 33637

Contig ID 336162\_1.R1040

5'-most EST uC-gmrominsoy299f04b1

Method BLASTX
NCBI GI g2598575
BLAST score 354
E value 8.0e-34
Match length 98

% identity 65

NCBI Description (Y15293) MtN21 [Medicago truncatula]

Seq. No. 33638

Contig ID 336172\_1.R1040

5'-most EST jC-gmst02400014g03a1

Method BLASTX
NCBI GI g3341687
BLAST score 170
E value 8.0e-12
Match length 66
% identity 53

NCBI Description (AC003672) putative ras protein [Arabidopsis thaliana]

Seq. No. 33639

Contig ID 336203\_1.R1040 5'-most EST jC-gmst02400014h07a1



Seq. No. 33640

Contig ID 336206\_1.R1040 5'-most EST jC-gmst02400014h09a1

Method BLASTX
NCBI GI g1621463
BLAST score 545
E value 8.0e-56
Match length 104
% identity 89

NCBI Description (U73104) laccase [Liriodendron tulipifera]

Seq. No. 33641

Contig ID 336219\_1.R1040 5'-most EST jC-gmst02400015a11a1

Method BLASTX
NCBI GI g3033391
BLAST score 265
E value 4.0e-23
Match length 138
% identity 38

NCBI Description (AC004238) putative amino acid transporter [Arabidopsis

thaliana]

Seq. No. 33642

Contig ID 336220\_1.R1040

5'-most EST jC-gmst02400015a11d1

Seq. No. 33643

Contig ID 336276 1.R1040

5'-most EST jC-gmst02400015e04a1

Seq. No. 33644

Contig ID 336476 1.R1040

5'-most EST jC-gmst02400017b12a1

Seq. No. 33645

Contig ID 336483\_1.R1040

Method BLASTX
NCBI GI g4099090
BLAST score 379
E value 2.0e-36
Match length 101
% identity 70

NCBI Description (U83178) unknown [Arabidopsis thaliana]

Seq. No. 33646

Contig ID 336508 1.R1040

5'-most EST  $q57528\overline{5}3$ 

Seq. No. 33647

Contig ID 336536\_1.R1040 5'-most EST fC-gmle7000786711d1

Method BLASTX
NCBI GI g3805845
BLAST score 230



E value 5.0e-19 Match length 64

% identity 60

NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 33648

Contig ID 336562 1.R1040

5'-most EST jC-gmst02400068f05d1

Seq. No. 33649

Contig ID 336593\_1.R1040

Seq. No. 33650

Contig ID 336627\_2.R1040

5'-most EST jC-gmst02400018c09a1

Seq. No. 33651

Contig ID 336637\_1.R1040 5'-most EST uC-gmronoir008c11b1

Seq. No. 33652

Contig ID 336699\_1.R1040

5'-most EST jC-gmst02400045e10a1

Method BLASTX
NCBI GI g2980790
BLAST score 156
E value 3.0e-10
Match length 101

% identity 44

NCBI Description (AL022197) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33653

Contig ID 336781 1.R1040

5'-most EST jC-gmst02400020de04d1

Seq. No. 33654

Contig ID 336789\_1.R1040

5'-most EST jC-gmst02400020f02a1

Seq. No. 33655

Contig ID 336855 1.R1040

5'-most EST g5752695

Seq. No. 33656

Contig ID 336859 1.R1040

5'-most EST jC-gmst02400045g09d1

Seq. No. 33657

Contig ID 336900 1.R1040

5'-most EST jC-gmst02400023d09d1

Seq. No. 33658

Contig ID 336944\_1.R1040

5'-most EST jC-qmst02400023f03a1

Method BLASTX NCBI GI g4454056



BLAST score E value 5.0e-27 Match length 66 85 % identity

NCBI Description (AJ000930) ClpP [Arabidopsis thaliana]

Seq. No. 33659

336970 1.R1040 Contig ID 5'-most EST jC-gmst02400033d11d1

Method BLASTX NCBI GI g3451065 BLAST score 175 1.0e-12 E value Match length 32 % identity

NCBI Description (AL031326) water channel - like protein [Arabidopsis

thaliana]

33660 Seq. No.

Contig ID 337003 1.R1040

5'-most EST jC-gmst02400023h12d1

Seq. No. 33661

337171 1.R1040 Contig ID

5'-most EST jC-qmst02400026b05a1

Method BLASTX NCBI GI g3522938 BLAST score 188 E value 5.0e-23 Match length 132 % identity 63

NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 33662

Contig ID 337195 1.R1040

5'-most EST jC-gmst02400026c06a1

Seq. No. 33663

Contig ID 337251 1.R1040 5'-most EST jC-gmst02400026f01a1

Seq. No. 33664

Contig ID 337289 1.R1040

5'-most EST jC-qmst02400026h06a1

Method BLASTX NCBI GI q2244878 BLAST score 489 E value 4.0e-49 Match length 193 % identity 57

NCBI Description (Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33665

337337 1.R1040 Contig ID 5'-most EST jC-gmst02400027b11a1

33666 Seq. No.



Contig ID 337441 1.R1040

5'-most EST uC-gmrominsoy093h12b1

Method BLASTX
NCBI GI g3298544
BLAST score 452
E value 8.0e-45
Match length 201
% identity 57

NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]

Seq. No. 33667

Contig ID 337446 1.R1040

5'-most EST jC-gmst02400027h03a1

Seq. No. 33668

Contig ID 337465 1.R1040

5'-most EST jC-gmst02400028b05a1

Seq. No. 33669

Contig ID 337503 1.R1040

5'-most EST jC-gmst02400028d10a1

Method BLASTX
NCBI GI g3702340
BLAST score 375
E value 9.0e-36
Match length 215
% identity 39

NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33670

Contig ID 337613 1.R1040

5'-most EST jC-gmst02400029e01a1

Method BLASTX
NCBI GI g3776559
BLAST score 699
E value 6.0e-74
Match length 165
% identity 77

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi\_3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb AC003970. ESTs gb Z35332 and gb F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 33671

Contig ID 337662 1.R1040

5'-most EST g5677286

Seq. No. 33672

Contig ID 337706 1.R1040

5'-most EST jC-gmst02400030a12a1

Seq. No. 33673

Contig ID 337708\_1.R1040

5'-most EST jC-gmst02400030b01a1

Seq. No. 33674

Contig ID 337710 1.R1040



```
5'-most EST
                  jC-qmst02400030b02a1
Seq. No.
                  33675
Contig ID
                  337737 1.R1040
5'-most EST
                  jC-qmst02400030f06a1
                  33676
Seq. No.
                  337763 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400030g04d1
Seq. No.
                  33677
                  337777 1.R1040
Contig ID
5'-most EST
                  jC-qmst02400030h04d1
Method
                  BLASTN
NCBI GI
                  g747979
BLAST score
                  35
E value
                  5.0e-10
Match length
                  47
% identity
                  94
NCBI Description
                  Nicotiana tabacum UMP synthase (pyr5-6) mRNA, partial cds
Seq. No.
                  33678
Contig ID
                  337788 1.R1040
5'-most EST
                  jC-gmst02400031a02d1
Seq. No.
                  33679
                  337951 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400032b03d1
Method
                  BLASTX
NCBI GI
                  g3047089
BLAST score
                  207
E value
                  3.0e-16
                  97
Match length
% identity
                  47
                  (AF058826) contains similarity to pseudouridylate
NCBI Description
                  synthases [Arabidopsis thaliana]
Seq. No.
                  33680
Contig ID
                  338030 1.R1040
5'-most EST
                  jC-gmst02400032f08d1
Seq. No.
                  33681
Contig ID
                  338060 1.R1040
5'-most EST
                  jC-qmst02400032h07d1
```

Seq. No. 33682

Contig ID 338065 1.R1040

5'-most EST jC-qmst02400032h12d1

Seq. No. 33683

Contig ID 338082 1.R1040

5'-most EST jC-gmst02400033a08d1

Seq. No. 33684

Contig ID 338091 1.R1040

5'-most EST jC-gmst02400033b03d1



Seq.	No.	33685

Contig ID 338112 1.R1040 5'-most EST jC-gmst02400033c05d1

Seq. No. 33686

Contig ID 338180 1.R1040

5'-most EST jC-gmst02400033g03d1

Seq. No. 33687

Contig ID 338188 1.R1040

5'-most EST jC-gmst02400033g08d1

Seq. No. 33688

Contig ID 338192 1.R1040

5'-most EST jC-gmst02400033g12d1

Method BLASTN
NCBI GI g499067
BLAST score 265
E value 1.0e-147
Match length 301

% identity 97

NCBI Description G.max gmr2 gene

Seq. No. 33689

Contig ID 338204\_1.R1040 5'-most EST jC-gmst02400033h08a1

Seq. No. 33690

Contig ID 338269 1.R1040

5'-most EST jC-gmst02400036a11d2

Seq. No. 33691

Contig ID 338281\_1.R1040

5'-most EST jC-gmst02400036b11d2

Seq. No. 33692

Contig ID 338526\_1.R1040

5'-most EST jC-gmst02400040b12a1

Seq. No. 33693

Contig ID 338748\_1.R1040

5'-most EST jC-gmst02400049e08d1

Seq. No. 33694

Contig ID 338812\_1.R1040

5'-most EST  $jC-gms\overline{t}02400043h05d1$ 

Seq. No. 33695

Contig ID 338830 1.R1040

5'-most EST jC-gmst02400044a06a1

Seq. No. 33696

Contig ID 338831 1.R1040

5'-most EST jC-gmsT02400044a06d1

Seq. No. 33697

Contig ID 338843\_1.R1040



5'-most EST jC-qmst02400044b04d1 Seq. No. 33698 Contig ID 338896 1.R1040 jC-qmst02400044f01d1

Method BLASTX q3063445 NCBI GI 118 BLAST score E value 2.0e-14104 Match length 37 % identity

5'-most EST

(AC003981) F22013.7 [Arabidopsis thaliana] NCBI Description

Seq. No. 33699

338929 1.R1040 Contig ID 5'-most EST jC-gmst02400044h02d1

Seq. No. 33700

339048 1.R1040 Contig ID 5'-most EST jC-gmst02400046a03d1

Seq. No. 33701

339074\_1.R1040 Contig ID

5'-most EST  $q43050\overline{2}0$ BLASTX Method NCBI GI g3169178 BLAST score 523 5.0e-53 E value 259 Match length 41 % identity

NCBI Description (AC004401) hypothetical protein [Arabidopsis thaliana]

33702 Seq. No.

339079 1.R1040 Contig ID

5'-most EST jC-gmst02400046c08d1

33703 Seq. No.

Contig ID 339257 1.R1040 5'-most EST jC-gmst02400047g03d1

Seq. No. 33704

Contig ID 339262 1.R1040 5'-most EST jC-qmst02400047h05a1

Seq. No. 33705

Contig ID 339265 1.R1040

5'-most EST jC-qmst02400047h07a1

Seq. No. 33706

Contig ID 339302 1.R1040

5'-most EST jC-gmst02400048b10a1

Method BLASTX NCBI GI g3582340 BLAST score 146 2.0e-09 E value Match length 90 % identity 41



## NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 33707
Contig ID 339552 1.R1040

5'-most EST uC-gmronoir046g03b1

Method BLASTX
NCBI GI 94512705
BLAST score 820
E value 2.0e-93
Match length 203
% identity 88

NCBI Description (AC006569) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 33708

Contig ID 339613\_1.R1040

5'-most EST jC-gmst02400050g11a1

Method BLASTX
NCBI GI 94455275
BLAST score 266
E value 3.0e-23
Match length 121
% identity 48

NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 33709

Contig ID 339617\_1.R1040

5'-most EST jC-gmst02400071f06d1

Seq. No. 33710

Contig ID 339656\_1.R1040

5'-most EST jC-gmst02400051b09d1

Seq. No. 33711

Contig ID 339670 1.R1040

5'-most EST uC-gmflminsoy008g11b1

Method BLASTX
NCBI GI g4457221
BLAST score 237
E value 2.0e-19
Match length 88
% identity 55

NCBI Description (AF127797) putative bZIP DNA-binding protein [Capsicum

chinense]

Seq. No. 33712

Contig ID 339684\_1.R1040 5'-most EST jC-gmst02400051c12a1

Seq. No. 33713

Contig ID 339986\_1.R1040

5'-most EST jC-gmst02400053f06a1

Seq. No. 33714

Contig ID 340111\_1.R1040 5'-most EST jC-gmst02400054e06d1

Method BLASTX

NCBI GI g3335339 BLAST score 161 E value 8.0e-11 Match length 106 % identity 36

NCBI Description (AC004512) Contains similarity to MADS-box protein AGL3

gb U81369 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 33715

Contig ID 340137\_1.R1040 5'-most EST uC-gmropic008e06b1

Method BLASTN
NCBI GI g2598656
BLAST score 52

E value 3.0e-20 Match length 100 % identity 93

NCBI Description Vicia faba mRNA for elongation factor 1-alpha (EF1-a)

Seq. No. 33716

Contig ID 340162\_1.R1040 5'-most EST g4396083

Seq. No. 33717

Contig ID 340366\_1.R1040 5'-most EST g5509055

Seq. No. 33718

Contig ID 340398\_1.R1040

5'-most EST jC-gmst02400056f04a1

Method BLASTX
NCBI GI g818849
BLAST score 599
E value 4.0e-62
Match length 161
% identity 67

NCBI Description (U25430) nucleotide pyrophosphatase precursor [Oryza

sativa]

Seq. No. 33719

Contig ID 340450\_1.R1040 5'-most EST jC-gmst02400057a05d1

Seq. No. 33720

Contig ID 340520 1.R1040

5'-most EST jC-gmst02400057d11d1

Seq. No. 33721

Contig ID 340629\_1.R1040

5'-most EST jC-gmst02400058b05a1

Method BLASTN
NCBI GI g4567193
BLAST score 39
E value 1.0e-12
Match length 202
% identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC T26C19 genomic



## sequence, complete sequence

 Seq. No.
 33722

 Contig ID
 340648\_1.R1040

 5'-most EST
 fC-gmse700754614d2

Seq. No. 33723

Contig ID 340682\_1.R1040

5'-most EST jC-gmst02400058e06d1

Method BLASTX
NCBI GI g3023721
BLAST score 196
E value 8.0e-15
Match length 114
% identity 39

NCBI Description FLOWERING TIME CONTROL PROTEIN FCA

>gi\_2204095\_emb\_CAB05391\_ (Z82992) FCA gamma [Arabidopsis

thaliana]

Seq. No. 33724

Contig ID 340719 1.R1040

5'-most EST jC-gmst02400058h01a1

Method BLASTX
NCBI GI g112717
BLAST score 155
E value 4.0e-10
Match length 53
% identity 62

NCBI Description 21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi\_82050\_pir\_\_S10911

hypothetical protein precursor - carrot

>gi 18312 emb CAA36642 (X52395) precursor polypeptide (AA

-22 to 171) [Daucus carota]

Seq. No. 33725

Contig ID 340790\_1.R1040

5'-most EST jC-gmst02400060b05d1

Seq. No. 33726

Contig ID 340944 1.R1040

5'-most EST jC-gmst02400061c10d1

Seq. No. 33727

Contig ID 341021\_1.R1040 5'-most EST fC-gmst700892334r4

Seq. No. 33728

Contig ID 341035 1.R1040

5'-most EST jC-gmst02400062a10d1

Seq. No. 33729

Contig ID 341095\_1.R1040

5'-most EST jC-gmst02400062e10d1

Seq. No. 33730

Contig ID 341111\_1.R1040

5'-most EST jC-gmst02400062f10a1



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Seq. No.
                  341174 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400063b01d1
                  33732
Seq. No.
                  341201 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400063c06a1
```

33733 Seq. No. 341299 1.R1040 Contig ID 5'-most EST jC-gmst02400063h08a1 BLASTN Method q4567259 NCBI GI 40 BLAST score

5.0e-13 E value Match length 68 90 % identity

Arabidopsis thaliana chromosome II BAC F3K23 genomic NCBI Description

sequence, complete sequence

33734 Seq. No.

341349 1.R1040 Contig ID jC-gmst02400064d10d1 5'-most EST

BLASTX Method q4049344 NCBI GI 172 BLAST score 3.0e-12 E value 56 Match length 66 % identity

(AL034567) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 33735

341396 1.R1040 Contig ID

5'-most EST jC-gmst02400065a07a2

33736 Seq. No.

341417 1.R1040 Contig ID

jC-qmst02400065b09a2 5'-most EST

BLASTX Method NCBI GI g2062174 BLAST score 253 1.0e-21 E value Match length 53 87 % identity

(ACO01645) transcription factor (TINY) isolog [Arabidopsis NCBI Description

thalianal

Seq. No. 33737

341444 1.R1040 Contig ID

jC-gmst02400065d01d1 5'-most EST

BLASTX Method NCBI GI q1076531 BLAST score 325 E value 6.0e-30 Match length 64 % identity 89

NCBI Description hypothetical protein, pollen allergen homolog - garden pea



>gi\_2129891\_pir\_\_S65056 pollen allergen homolog precursor
(clone PPA1) - garden pea >gi\_732905\_emb\_CAA59470\_ (X85187)
homology with pollen allergens [Pisum sativum]

Seq. No. 33738 Contig ID 341479 1.R1040

5'-most EST jC-gmst02400078a08a1

Seq. No. 33739

Contig ID 341662\_1.R1040

5'-most EST jC-gmst02400066g09a2

Seq. No. 33740

Contig ID 341694 1.R1040

5'-most EST jC-gmst02400067a03d1

Method BLASTX
NCBI GI g3668088
BLAST score 409
E value 5.0e-40
Match length 93
% identity 76

NCBI Description (AC004667) G9a-like protein [Arabidopsis thaliana]

Seq. No. 33741

Contig ID 341752\_1.R1040

5'-most EST jC-gmst02400067e03a1

Seq. No. 33742

Contig ID 341893 1.R1040

5'-most EST jC-gmst02400069a03a1

Seq. No. 33743

Contig ID 341918 1.R1040

5'-most EST jC-gmst02400069c10a1

Seq. No. 33744

Contig ID 341962 1.R1040

5'-most EST jC-gmst02400069g07a1

Method BLASTX
NCBI GI g2191152
BLAST score 745
E value 5.0e-79
Match length 223
% identity 64

NCBI Description (AF007269) A IG002N01.31 gene product [Arabidopsis

thaliana]

Seq. No. 33745

Contig ID 341981\_1.R1040

5'-most EST jC-gms\(\overline{t}\)02400070a07d1

Seq. No. 33746

Contig ID 341983 1.R1040

5'-most EST jC-gmst02400070b09a1

Seq. No. 33747

Contig ID 341996 1.R1040



```
jC-qmst02400070b09d1
5'-most EST
                   33748
Seq. No.
                   342045 1.R1040
Contig ID
                   jC-gmst02400070e11d1
5'-most EST
Seq. No.
                   33749
                   342118 1.R1040
Contig ID
                   uC-gmropic061h07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3176726
BLAST score
                   864
E value
                   4.0e-93
Match length
                   220
% identity
                   (AC002392) putative serine proteinase [Arabidopsis
NCBI Description
                   thaliana]
                   33750
Seq. No.
                   342120 1.R1040
Contig ID
5'-most EST
                   g5677163
                   BLASTX
Method
NCBI GI
                   g3004564
                   153
BLAST score
                   6.0e-10
E value
Match length
                   89
                   40
% identity
                   (AC003673) putative receptor Ser/Thr protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   33751
                   342159 1.R1040
Contig ID
                   jC-gmst02400071e01a1
5'-most EST
Seq. No.
                   33752
                   342173 1.R1040
Contig ID
                   jC-gmst02400071e11d1
5'-most EST
                   BLASTX
Method
                   g3860273
NCBI GI
                   451
BLAST score
                   6.0e-45
E value
                   108
Match length
                   71
% identity
                   (AC005824) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4314398_gb_AAD15608_ (AC006232) hypothetical protein
                   [Arabidopsis thaliana]
                   33753
Seq. No.
                   342224 1.R1040
Contiq ID
                   jC-gmst02400071h08d1
5'-most EST
                   33754
Seq. No.
                   342557 1.R1040
Contig ID
                   jC-gms\overline{t}02400074b08d1
5'-most EST
                   BLASTX
Method
                   g3201656
NCBI GI
```

181

BLAST score



E value 6.0e-13 Match length 131 % identity 37

NCBI Description (AF005933) galactokinase [Lactobacillus casei]

Seq. No. 33755

Contig ID 342668\_1.R1040 5'-most EST jC-gmst02400074h03a1

Method BLASTX
NCBI GI g3445238
BLAST score 437
E value 4.0e-43
Match length 193
% identity 48

NCBI Description (AL022347) putative protein [Arabidopsis thaliana]

>gi 3451059 emb CAA20455.1\_ (AL031326) putative protein

[Arabidopsis thaliana]

Seq. No. 33756

Contig ID 342679 1.R1040

5'-most EST jC-gmst02400074h09a1

Method BLASTX
NCBI GI g4206197
BLAST score 534
E value 1.0e-54
Match length 130
% identity 43

NCBI Description (AF071527) putative pre-mRNA splicing factor [Arabidopsis

thaliana]

Seq. No.

33757

Contig ID 342775\_1.R1040

5'-most EST uC-gmrominsoy116b09b1

Seq. No. 33758

Contig ID 342824\_1.R1040

5'-most EST jC-gmst02400076f02a1

Seq. No. 33759

Contig ID 342843\_1.R1040

5'-most EST jC-gmst02400076g03d1

Seq. No. 33760

Contig ID 342956\_1.R1040

5'-most EST jC-gmst02400077e06d1

Seq. No. 33761

Contig ID 343146\_1.R1040 5'-most EST fC-gmst700652684a1

Method BLASTX
NCBI GI g520582
BLAST score 237
E value 7.0e-20
Match length 67
% identity 69

NCBI Description (D37796) Ids3 [Hordeum vulgare]



Seq. No. 33762

Contig ID 343160\_1.R1040 5'-most EST fC-gmf1700862926r4

Seq. No. 33763

Contig ID 343179\_1.R1040 5'-most EST fC-gmse700862729r4

Seq. No. 33764

Contig ID 343192\_1.R1040 5'-most EST fC-gmf1700863558r3

Seq. No. 33765

Contig ID 343228\_1.R1040 5'-most EST fC-gmle700874601r1

Method BLASTX
NCBI GI g282881
BLAST score 385
E value 4.0e-37
Match length 130
% identity 55

NCBI Description receptor-like protein kinase precursor - Arabidopsis

thaliana >gi 166846 (M84658) receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 33766

Contig ID 343337\_1.R1040 5'-most EST fC-gmf1700902285r4

Seq. No. 33767

Contig ID 343351\_1.R1040 5'-most EST fC-gmf1700906289r2

Seq. No. 33768

Contig ID 343351\_4.R1040 5'-most EST fC-gmro700744539r3

Seq. No. 33769

Contig ID 343439\_1.R1040 5'-most EST fC-gmf1700904235d2

Seq. No. 33770

Contig ID 343537\_1.R1040 5'-most EST fC-gmse700669533r3

Seq. No. 33771

Contig ID 343562 1.R1040

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDN11, complete sequence [Arabidopsis thaliana]



Seq. No. 33772

Contig ID 343566\_1.R1040 5'-most EST fC-gmf1700904815r2

Seq. No. 33773

Contig ID 343839\_1.R1040 5'-most EST fC-gmro700867181r5

Seq. No. 33774

Contig ID 343856 1.R1040 5'-most EST fC-gmf1700906093r5

Seq. No. 33775

Contig ID 343870\_1.R1040 5'-most EST fC-gmf1700906121r2

Seq. No. 33776

Contig ID 343881\_1.R1040 5'-most EST fC-gmf1700906134r2

Seq. No. 33777

Contig ID 343895\_1.R1040 5'-most EST fC-gmf1700906171r2

Seq. No. 33778

Contig ID 343916\_1.R1040 5'-most EST fC-gmfl700906377r2

Seq. No. 33779

Contig ID 343927\_1.R1040 5'-most EST fC-gmfl700906435r2

Seq. No. 33780

Contig ID 343938\_1.R1040 5'-most EST fC-gmf1700906442r6

Seq. No. 33781

Contig ID 344084\_1.R1040 5'-most EST fC-gmle7000740015d1

Seq. No. 33782

Contig ID 344112\_1.R1040 5'-most EST fC-gmle7000740866r1

Method BLASTX
NCBI GI g4115914
BLAST score 389
E value 2.0e-37
Match length 109
% identity 64

NCBI Description (AF118222) contains similarity to Iron/Ascorbate family of

oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85, N=1) [Arabidopsis thaliana] >gi\_4539410\_emb\_CAB40043.1\_ (AL049524) putative Fe(II)/ascorbate oxidase [Arabidopsis

thaliana]

Seq. No. 33783

Contig ID 344116 1.R1040

```
5'-most EST
                  fC-qmle7000740910r1
                  33784
Seq. No.
                  344144 1.R1040
Contig ID
                  fC-gmle7000741294r1
5'-most EST
                  33785
Seq. No.
                  344207 1.R1040
Contig ID
                  fC-gmse700758907a2
5'-most EST
                  BLASTX
Method
                  q2569940
NCBI GI
                  302
BLAST score
                  2.0e-27
E value
                  132
Match length
                  49
% identity
                  (Y15194) GRS protein [Arabidopsis thaliana]
NCBI Description
                  33786
Seq. No.
                  344281 1.R1040
Contig ID
                  fC-gmle700763807d4
5'-most EST
                  33787
Seq. No.
                  344285_1.R1040
Contig ID
5'-most EST
                  fC-qmle7000763827r1
Method
                  BLASTX
NCBI GI
                  q3192042
                   283
BLAST score
                  3.0e-25
E value
                  111
Match length
                   55
% identity
NCBI Description (AL023796) phosphoglucomutase [Schizosaccharomyces pombe]
                   33788
Seq. No.
                   344313 1.R1040
Contig ID
                   fC-qmle700786228d4
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1076269
                   182
BLAST score
                   3.0e-13
E value
Match length
                   56
% identity
                   57
NCBI Description pullulanase - spinach >gi_634093_emb_CAA58803_ (X83969)
                   pullulanase [Spinacia oleracea]
Seq. No.
                   33789
                   344347 1.R1040
Contig ID
5'-most EST
                   fC-gmro700567008r2
                   BLASTX
Method
```

Method BLASTX
NCBI GI g1155255
BLAST score 340
E value 8.0e-32
Match length 119
% identity 57

NCBI Description (U39228) beta-glucosidase [Prunus avium]

Seq. No. 33790

Contig ID 344362\_1.R1040



5'-most EST fC-gmle700553715d4

Method BLASTX
NCBI GI g3885336
BLAST score 219
E value 1.0e-17
Match length 97
% identity 44

NCBI Description (AC005623) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 33791

Contig ID 344373\_1.R1040 5'-most EST fC-gmle700553863r4

Seq. No. 33792

Contig ID 344466\_1.R1040 5'-most EST fC-gmle700555826d3

Seq. No. 33793

Contig ID 344470\_1.R1040 5'-most EST fC-gmle700555866r2

Seq. No. 33794

Contig ID 344517\_1.R1040 5'-most EST fC-gmle700557003d3

Seq. No. 33795

Contig ID 344577\_1.R1040 5'-most EST fC-gmle700557575d3

Seq. No. 33796

Contig ID 344599\_1.R1040 5'-most EST fC-gmle700557833d3

Seq. No. 33797

Contig ID 344756\_1.R1040 5'-most EST fC-gmle700560105b1

Seq. No. 33798

Contig ID 344759\_1.R1040 5'-most EST fC-gmle700560163r2

Seq. No. 33799

Contig ID 344799\_1.R1040 5'-most EST fC-gmle700742959r4

Seq. No. 33800

Contig ID 344808\_1.R1040 5'-most EST fC-gmle700681442r4

Seq. No. 33801

Contig ID 344836\_1.R1040 5'-most EST fC-gmle700684006f1

Method BLASTX
NCBI GI g2129541
BLAST score 623
E value 5.0e-65



Match length % identity NCBI Description

161 73

ATPK19 protein - Arabidopsis thaliana >gi\_914079\_bbs\_160872 ATPK19=ribosomal-protein S6 kinase homolog [Arabidopsis thaliana, Peptide, 471 aa] >gi\_867995\_dbj\_BAA07661\_

(D42061) ribosomal-protein S6 kinase homolog [Arabidopsis

thaliana]

Seq. No. 33802

Contig ID 5'-most EST 344925\_1.R1040 fC-gmle700739091r3

Seq. No. 33803

Contig ID 5'-most EST

344949\_1.R1040 fC-gmle700739616r4

Seq. No. 33804

Contig ID 5'-most EST 344956\_1.R1040 fC-gmle700739771f2

Seq. No. Contig ID

33805 344962\_1.R1040

5'-most EST

fC-gmle700739836r3

Seq. No.
Contig ID
5'-most EST

33806 344967\_1.R1040 fC-gmro700749355f4

Seq. No.
Contig ID
5'-most EST

33807 344968\_1.R1040 fC-gmle700739861r3

Seq. No.
Contig ID
5'-most EST

33808 344993 1.R1040

Seq. No.
Contig ID
5'-most EST

fC-gmle700740186r4
33809

Soc No

345000\_1.R1040 fC-gmle700740303r3

Seq. No.
Contig ID
5'-most EST

33810 345006\_1.R1040 fC-gmle700740321r3

Seq. No.
Contig ID
5'-most EST

33811 345012\_1.R1040 fC-gmle700740331r4

Seq. No.
Contig ID
5'-most EST

33812 345022\_1.R1040 fC-gmle700740544r4

Seq. No.
Contig ID
5'-most EST

33813 345025\_1.R1040 fC-gmle700741257r3

Seq. No.

Contig ID	345030_2.R1040
5'-most EST	fC-gmle700740810r4
Seq. No.	33815
Contig ID	345036_1.R1040
5'-most EST	fC-gmle700740866r4
Seq. No.	33816
Contig ID	345052_1.R1040
5'-most EST	fC-gmle700741226r3
Seq. No. Contig ID 5'-most EST	33817 345063_1.R1040 fC-gmle700741294r3
Seq. No.	33818
Contig ID	345076_1.R1040
5'-most EST	fC-gmle700741539r4
Seq. No.	33819
Contig ID	345085_1.R1040
5'-most EST	fC-gmle700741958r3
Seq. No.	33820
Contig ID	345091_1.R1040
5'-most EST	fC-gmle700741988r4
Seq. No.	33821
Contig ID	345100_1.R1040
5'-most EST	fC-gmle700742139r4
Seq. No.	33822
Contig ID	345109 1.R1040

Seq. No.	33822
	345109_1.R1040
5'-most EST	fC-gmle700742323r4

Seq. No.	33823
Contig ID	345156_1.R1040
5'-most EST	fC-gmle700743339r4

Seq. No.	33824
Contig ID	345165_1.R1040
5'-most EST	fC-qmle700743470r3

Seq. No.	33825
Contig ID	345172_1.R1040
5'-most EST	fC-gmle700743611r4

Seq. No.	33826
Contig ID	345178_1.R1040
5'-most EST	fC-gmle700743613r3

Seq. No.	33827
Contig ID	345185_1.R1040
5'-most EST	fC-gmle700743672r3

Seq. No. 33828 Contig ID 345192\_1.R1040



5'-most EST fC-gmle700743681r3

Seq. No. 33829

Contig ID 345202\_1.R1040 5'-most EST fC-gmle700743719r3

Seq. No. 33830

Contig ID 345214\_1.R1040 5'-most EST fC-gmle700744058r4

Seq. No. 33831

Contig ID 345248\_1.R1040 5'-most EST fC-gmse7000763420d1

Seq. No. 33832

Contig ID 345275\_1.R1040 5'-most EST fC-gmle700787001d6

Method BLASTN
NCBI GI g3334860
BLAST score 125
E value 8.0e-64
Match length 310
% identity 91

NCBI Description Solanum tuberosum chloroplast tRNA-Asn, tRNA-Arg genes

Seq. No. 33833

Contig ID 345286\_1.R1040 5'-most EST fC-gmse700787220d1

Seq. No. 33834

Contig ID 345303\_1.R1040 5'-most EST fC-gmle700788580r2

Seq. No. 33835

Contig ID 345312\_1.R1040 5'-most EST fC-gmst700891395r2

Seq. No. 33836

Contig ID 345314\_1.R1040 5'-most EST fC-gmle700789620d3

Method BLASTX
NCBI GI g3063691
BLAST score 133
E value 4.0e-18
Match length 81
% identity 54

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 33837

Contig ID 345359\_1.R1040 5'-most EST fC-gmst700892015d3

Seq. No. 33838

Contig ID 345412\_1.R1040 5'-most EST fC-gmle700872274d7

Seq. No. 33839



```
345427 2.R1040
Contig ID
                   fC-gmro700746923r3
5'-most EST
                   33840
Seq. No.
                   345436 1.R1040
Contig ID
                   fC-gmle700872632r3
5'-most EST
                   BLASTX
Method
                   g4314378
NCBI GI
                   425
BLAST score
                   1.0e-41
E value
Match length
                   135
% identity
                   56
NCBI Description
```

(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 345540 1.R1040 Contig ID fC-gmst700894542d3 5'-most EST Method BLASTX g3860020 NCBI GI 228 BLAST score

33841

7.0e-19 E value 90 Match length 51 % identity

(AF091091) unknown [Homo sapiens] NCBI Description

33842 Seq. No. 345593 1.R1040 Contig ID fC-gmro7000745012r1 5'-most EST Method BLASTX g1916645 NCBI GI

379 BLAST score 3.0e-36 E value Match length 113 % identity 65

(U71605) desacetoxyvindoline 4-hydroxylase [Catharanthus NCBI Description

roseus]

33843 Seq. No.

345628 1.R1040 Contig ID fC-qmro7000746172r1 5'-most EST

33844 Seq. No.

345671 1.R1040 Contig ID fC-gmro7000746951d1 5'-most EST

33845 Seq. No.

345718 1.R1040 Contig ID fC-gmro7000747614d1 5'-most EST

33846 Seq. No.

345721 1.R1040 Contig ID 5'-most EST fC-gmro7000747701d1

33847 Seq. No.

345732 1.R1040 Contig ID fC-gmro7000748156d1 5'-most EST



Seq. No. 33848

Contig ID 345748\_1.R1040 5'-most EST fC-gmro700748409d3

Method BLASTX
NCBI GI g2335097
BLAST score 167
E value 2.0e-11
Match length 81
% identity 49

% identity 49 NCBI Description (AC002339) putative receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 33849

Contig ID 345752\_1.R1040 5'-most EST fC-gmro7000748459r1

Seq. No. 33850

Contig ID 345754\_1.R1040 5'-most EST fC-gmro700748475d3

Method BLASTX
NCBI GI g1236961
BLAST score 274
E value 4.0e-24
Match length 82
% identity 60

NCBI Description (U50201) prunasin hydrolase precursor [Prunus serotina]

Seq. No. 33851

Contig ID 345824\_1.R1040 5'-most EST fC-gmro7000749638r1

Seq. No. 33852

Contig ID 345881\_1.R1040 5'-most EST fC-gmro7000764345r1

Seq. No. 33853

Contig ID 345885\_1.R1040 5'-most EST fC-gmro700351273g1

Method BLASTX
NCBI GI g2088647
BLAST score 691
E value 9.0e-73
Match length 246
% identity 54

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana] >gi 3158394 (AF036340) LRR-containing F-box protein

[Arabidopsis thaliana]

Seq. No. 33854

Contig ID 345889\_1.R1040 5'-most EST fC-gmro700449492d2

Method BLASTX
NCBI GI g549750
BLAST score 319
E value 6.0e-29
Match length 196
% identity 36



NCBI Description HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION >gi\_539221\_pir\_\_S38045 hypothetical protein YKL207w - yeast

(Saccharomyces cerevisiae) >gi\_486369\_emb\_CAA82052\_ (Z28207) ORF YKL207w [Saccharomyces cerevisiae]

Seq. No. 33855

Contig ID 345904\_1.R1040 5'-most EST fC-gmro700561429d7

Seq. No. 33856

Contig ID 346038\_1.R1040

5'-most EST g5666824

Method BLASTX

NCBI GI g3879918

BLAST score 162

E value 4.0e-11

Match length 62

% identity 50

% identity 50 NCBI Description (Z74043) Similarity to Human beta-galactosidase

(SW:BGAL\_HUMAN) [Caenorhabditis elegans]

Seq. No. 33857

Contig ID 346064\_1.R1040 5'-most EST fC-gmro700565227r2

Seq. No. 33858

Contig ID 346103\_1.R1040 5'-most EST fC-gmro700565834r2

Seq. No. 33859

Contig ID 346127\_1.R1040 5'-most EST fC-gmro700566777r1

Method BLASTN
NCBI GI g971167
BLAST score 164
E value 4.0e-87
Match length 256
% identity 91

NCBI Description Pisum sativum Wando ornithine carbamoyltransferase mRNA,

complete cds

Seq. No. 33860

Contig ID 346207\_1.R1040 5'-most EST fC-gmro700568583g1

Method BLASTX
NCBI GI g4490310
BLAST score 1256
E value 1.0e-143
Match length 313
% identity 82

NCBI Description (AL035678) somatic embryogenesis receptor-like kinase-like

protein [Arabidopsis thaliana]

Seq. No. 33861

Contig ID 346248\_1.R1040 5'-most EST fC-gmro700744202r4



Seq. No.	33862
Contig ID	346254

4 1.R1040 fC-qmro700744240r4 5'-most EST

Seq. No. Contig ID 5'-most EST 33863 346259 1.R1040 fC-gmro700744504r3

Seq. No. Contig ID 5'-most EST 33864 346271 1.R1040 fC-gmro700744905r4

Seq. No. Contig ID 5'-most EST 33865 346277 1.R1040 fC-qmro700744975r4

Seq. No. Contig ID 5'-most EST 33866 346283 1.R1040 fC-gmro700745012r4

Seq. No. Contig ID 5'-most EST 33867 346289 1.R1040 fC-gmro700745310r3

Seq. No. Contig ID 5'-most EST 33868 346293 1.R1040 fC-qmro700745326r3

Seq. No. Contig ID 5'-most EST 33869 346297 1.R1040 fC-gmro700745763r4

Seq. No. Contig ID 5'-most EST 33870 346302\_1.R1040 fC-gmro700745818r4

Seq. No. Contig ID 5'-most EST 33871 346307 1.R1040 fC-gmro700745970r4

Seq. No. Contig ID 5'-most EST 33872 346313 1.R1040 fC-gmro700745995r4

Seq. No. Contig ID 5'-most EST 33873 346318\_1.R1040 fC-gmst700666294r3

Seq. No. Contig ID 5'-most EST 33874 346323 1.R1040 fC-gmro700746124r4

Seq. No. Contig ID 5'-most EST

33875 346334 1.R1040 fC-gmro700746172r3

Seq. No.



Contig	ID
5'-most	EST

346343\_1.R1040 fC-gmro700746240r3

Seq. No.
Contig ID
5'-most EST

33877 346362\_1.R1040 fC-gmro700746472r4

Seq. No.
Contig ID
5'-most EST

33878 346366\_1.R1040 fC-gmro700746535r3

Seq. No. Contig ID 5'-most EST 33879 346372\_1.R1040 fC-gmro700746614r3

Seq. No.
Contig ID
5'-most EST

33880 346378\_1.R1040 fC-gmro700746693r3

Seq. No. Contig ID 5'-most EST 33881 346383\_1.R1040 fC-gmro700746706r3

Seq. No.
Contig ID
5'-most EST

33882 346405\_1.R1040 fC-gmro700746951r3

Seq. No.
Contig ID
5'-most EST

33883 346414\_1.R1040 fC-gmro700747038r4

Seq. No.
Contig ID
5'-most EST

33884 346425\_1.R1040 fC-gmro700747183r3

Seq. No. Contig ID 5'-most EST

33885 346431\_1.R1040 fC-gmro700747276r3

Seq. No.
Contig ID
5'-most EST

33886 346437\_1.R1040 fC-gmro700747310r4

Seq. No.
Contig ID
5'-most EST

33887 346443\_1.R1040 fC-gmro700747348r3

Seq. No. Contig ID 5'-most EST 33888 346448\_1.R1040 fC-gmro700747359r4

Seq. No.
Contig ID
5'-most EST

33889 346458\_1.R1040 fC-gmro700747479r4

Seq. No. Contig ID 33890 346463\_1.R1040



5'-most EST f	EC-gmro700747514r4
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Seq. No.	33891
Contig ID	346468 1.R1040
5'-most EST	fC-gmro700747557r4

Seq. No.	33892
Contig ID	346477 1.R1040
5'-most EST	fC-gmro700747701r3

Seq. No.	33893
Contig ID	346483 1.R1040
5'-most EST	fC-gmro700747711r3

Seq. No.	33894
Contig ID	346494 1.R1040
5'-most EST	fC-gmro700747787r3

Seq. No.	33895
Contig ID	346504 1.R1040
5'-most EST	fC-gmro700748151r4

Seq. No.	33896
Contig ID	346509 1.R1040
5'-most EST	fC-gmro700748156r4

Seq. No.	33897
Contig ID	346513 1.R1040
5'-most EST	fC-gmro700748208r3

Seq. No.	33898
Contig ID	346518 1.R1040
5'-most EST	fC-gmro700748236r4

Seq. No.	33899
Contig ID	346523 1.R1040
5'-most EST	fC-cmro700748271r3

Seq. No.	33900
Contig ID	346528 1.R1040
5'-most EST	fC-gmro700748296r3

Seq. No.	33901
Contig ID	346533 1.R1040
5'-most EST	fC-gmro700748342r4

Seq. No.	33902
Contig ID	346537 1.R1040
5'-most EST	fC-gmro700748409r3

Seq. No.	33903
Contig ID	346552 1.R1040
5'-most EST	fC-gmr0700748540r3

Seq. No.	33904
Contig ID	346558 1.R1040
5'-most EST	fC-gmro700748571r4

Seq. No. Contig ID 5'-most EST	33905 346562_1.R1040 fC-gmro700748591r4
Seq. No. Contig ID 5'-most EST	33906 346571_1.R1040 fC-gmro700748726r3
Seq. No. Contig ID 5'-most EST	33907 346576_1.R1040 fC-gmro700748737r3
Seq. No. Contig ID 5'-most EST	33908 346581_1.R1040 fC-gmro700748836r3
Seq. No. Contig ID 5'-most EST	33909 346587_1.R1040 fC-gmro700748845r3
Seq. No. Contig ID 5'-most EST	33910 346596_1.R1040 fC-gmro700749034r3
Seq. No. Contig ID 5'-most EST	33911 346602_1.R1040 fC-gmro700749069r3
Seq. No. Contig ID 5'-most EST	33912 346612_1.R1040 fC-gmro700749140r3
Seq. No. Contig ID 5'-most EST	33913 346618_1.R1040 fC-gmro700749247r4
Seq. No. Contig ID 5'-most EST	33914 346627_1.R1040 fC-gmro700749265r4

Seq. No. 33915

Contig ID 346632 1.R1040 5'-most EST fC-gmro700749283r4

Seq. No. 33916 Contig ID 346637 1.R1040 fC-gmro700749341r35'-most EST

Seq. No. 33917 Contig ID 5'-most EST 346643 1.R1040 fC-gmro700749381r3

33918 Seq. No. Contig ID 5'-most EST 346648 1.R1040 fC-gmro700749436r3



Seq. No. 3391

Contig ID 346653\_1.R1040 5'-most EST fC-gmro700875829r1

Seq. No. 33920

Contig ID 346657\_1.R1040 5'-most EST fC-gmro700749507r3

Seq. No. 33921

Contig ID 34665\_1.R1040 5'-most EST fC-gmro700749669r3

Seq. No. 33922

Contig ID 346669\_1.R1040 5'-most EST fC-gmro700749762r4

Seq. No. 33923

Contig ID 346673\_1.R1040 5'-most EST fC-gmro700749772r4

Seq. No. 33924

Contig ID 346681\_1.R1040 5'-most EST fC-gmro700749847r3

Seq. No. 33925

Contig ID 346686\_1.R1040 5'-most EST fC-gmro700749944r4

Seq. No. 33926

Contig ID 346691\_1.R1040 5'-most EST fC-gmro700750041r3

Seq. No. 33927

Contig ID 346696\_1.R1040 5'-most EST fC-gmro700750047r4

Seq. No. 33928

Contig ID 346730\_1.R1040 5'-most EST fC-gmse7000758287r1

Method BLASTN
NCBI GI g2108433
BLAST score 41

BLAST score 41 E value 1.0e-13 Match length 161 % identity 86

NCBI Description Phaseolus vulgaris gibberellin 20-oxidase mRNA, complete

cds

Seq. No. 33929

Contig ID 346742 1.R1040 5'-most EST fC-gmro700792501r6

Seq. No. 33930

Contig ID 346742\_2.R1040 5'-most EST fC-gmro700794491r6

Seq. No. 33931



346756 1.R1040 Contig ID 5'-most EST fC-qmro700792724r8

Seq. No. Contig ID 5'-most EST 33932 346787 1.R1040 fC-gmro700795004f1

Seq. No. Contig ID

5'-most EST

33933 346806 1.R1040 fC-qmro700795654r6

Seq. No.

33934

Contig ID 5'-most EST 346878 1.R1040 fC-gmro700834955g1

BLASTX Method NCBI GI BLAST score E value

g3335351 579 1.0e-59

Match length % identity

179 12

NCBI Description

(AC004512) Similar to ERECTA receptor protein kinase

gb D83257 from A. thaliana. ESTs gb T41629 and gb AA586072

come from this gene. [Arabidopsis thaliana]

Seq. No.

33935

Contig ID 5'-most EST 346885 1.R1040 fC-gmro700835567e1

Seq. No.

33936

Contig ID 5'-most EST 347090 1.R1040 fC-gmro700844704d4

BLASTX Method NCBI GI g3096919 721 BLAST score 3.0e-76 E value 206 Match length

% identity NCBI Description

78 (AL023094) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No.

33937

Contig ID 5'-most EST 347220 1.R1040 fC-gmro700865409d3

Seq. No.

33938

Contig ID 5'-most EST

347240 1.R1040 fC-gmro700847173f2

Seq. No.

33939

Contig ID 5'-most EST 347283 1.R1040 fC-gmro700846785r4

Seq. No.

Contig ID 5'-most EST 347315 1.R1040 fC-qmro700847042r7

Seq. No.

33941



Contig ID	347422 1.R1040
5'-most EST	fC-gmro700848272r5

Seq. No.	33942
Contig ID	347579 1.R1040
5'-most EST	fC-gmro700864412r5

Seq. No.	33943
Contig ID	347591 1.R1040
	£0

5'-most EST fC-gmst700791918r2

Seq. No. 33944 Contig ID 347611\_1.R1040 5'-most EST fC-gmro700864858r5

 Seq. No.
 33947

 Contig ID
 348010\_1.R1040

 5'-most EST
 fC-gmst700890071d3

 Method
 BLASTX

 NCBI GI
 g886116

 BLAST score
 180

BLAST score 180
E value 3.0e-13
Match length 43
% identity 72

NCBI Description (U27609) TCH4 protein [Arabidopsis thaliana] >gi\_2952473 (AF051338) xyloglucan endotransglycosylase related protein

[Arabidopsis thaliana]

Seq. No. 33948 Contig ID 348076\_1.R1040 5'-most EST fC-gmro700873716d1

 Seq. No.
 33949

 Contig ID
 348077\_1.R1040

 5'-most EST
 fC-gmro700873747d1

 Seq. No.
 33950

 Contig ID
 348081\_1.R1040

 5'-most EST
 fC-gmst700891472r1

33951 Seq. No. 348300 1.R1040 Contig ID  $\texttt{fC-gms}\overline{\texttt{e}}7000752657\texttt{r1}$ 5'-most EST BLASTX Method NCBI GI g2245131 209 BLAST score 2.0e-16 E value 89 Match length

51

% identity

5116



NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33952

Contig ID 348319\_1.R1040 5'-most EST fC-gmse7000753191f1

Method BLASTX
NCBI GI g232161
BLAST score 284
E value 2.0e-25
Match length 83
% identity 69

NCBI Description 19 KD GLOBULIN PRECURSOR (ALPHA-GLOBULIN)

>gi\_68857\_pir\_\_WMRZ19 19K globulin precursor - rice

>gi\_20159\_emb\_CAA45400\_ (X63990) 19 kDa globulin precursor

[Oryza sativa]

Seq. No. 33953

Contig ID 348339\_1.R1040 5'-most EST fC-gmse700753764a1

Method BLASTX
NCBI GI g3608134
BLAST score 388
E value 3.0e-37
Match length 253
% identity 36

NCBI Description (AC005314) dnaJ-like protein [Arabidopsis thaliana]

Seq. No. 33954

Contig ID 348349\_1.R1040 5'-most EST fC-gmse700754105d2

Seq. No. 33955

Contig ID 348371\_1.R1040 5'-most EST fC-gmse700754553d1

Seq. No. 33956

Contig ID 348455\_1.R1040 5'-most EST fC-gmse700762414d3

Method BLASTX
NCBI GI g4469013
BLAST score 347
E value 1.0e-32
Match length 122
% identity 61

NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33957

Contig ID 348562\_1.R1040 5'-most EST fC-gmse700758907d4

Seq. No. 33958

Contig ID 348674 1.R1040 5'-most EST fC-gmst700649675a3

Method BLASTN
NCBI GI g169752
BLAST score 127
E value 3.0e-65



Match length 223 % identity 89

NCBI Description Rice alpha-amylase mRNA, complete cds, clone pOS103

Seq. No. 33959

Contig ID 348690\_1.R1040 5'-most EST fC-gmse700651322r1

Seq. No. 33960

.Contig ID 348696\_1.R1040 5'-most EST fC-gmst700654319g1

Seq. No. 33961

Contig ID 348858\_1.R1040 5'-most EST fC-gmse700655090d4

Method BLASTX
NCBI GI g1477480
BLAST score 234
E value 2.0e-19
Match length 70
% identity 67

NCBI Description (U40341) carbamoyl phosphate synthetase large chain

[Arabidopsis thaliana]

Seq. No. 33962

Contig ID 349146\_1.R1040 5'-most EST fC-gmst700663510r4

Method BLASTX
NCBI GI g2499613
BLAST score 540
E value 3.0e-55
Match length 130
% identity 77

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG MMK2

>gi 1204129 emb CAA57719 (X82268) protein kinase [Medicago

satīva]

Seq. No. 33963

Contig ID 349151\_1.R1040 5'-most EST fC-gmst700662560y1

Method BLASTX
NCBI GI g1352980
BLAST score 207
E value 4.0e-16
Match length 64
% identity 73

NCBI Description ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR

MTR4) >gi\_1078374\_pir\_\_S56822 SKI2 protein homolog YJL050w

- yeast (Saccharomyces cerevisiae)

>gi\_1008185\_emb\_CAA89341\_ (Z49325) ORF YJL050w

[Saccharomyces cerevisiae]

Seq. No. 33964

Contig ID 349170\_1.R1040 5'-most EST fC-gmse700658520r5

Method BLASTN NCBI GI q2636696



BLAST score 1.0e-74 E value 392 Match length 93 % identity

NCBI Description Mus musculus lysyl oxidase-2 (Lox2) mRNA, partial cds

33965 Seq. No.

349207 1.R1040 Contig ID fC-gmse700658863r5 5'-most EST

33966 Seq. No.

349468 1.R1040 Contig ID 5'-most EST fC-qmst700666737r3

33967 Seq. No.

349483 1.R1040 Contig ID fC-gmse700668119i2 5'-most EST

BLASTX Method q1651934 NCBI GI 260 BLAST score 4.0e-22 E value 175 Match length 35 % identity

(D90901) hypothetical protein [Synechocystis sp.] NCBI Description

33968 Seq. No.

349747 1.R1040 Contig ID fC-qmst700663367r1 5'-most EST

33969 Seq. No.

349855 1.R1040 Contig ID fC-qmse700672209d4 5'-most EST

BLASTX Method NCBI GI q1708971 311 BLAST score E value 4.0e-28 Match length 161 % identity 43

(R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR NCBI Description

(HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)

>gi\_421871\_pir\_\_S32156 mandelonitrile lyase (EC 4.1.2.10) black cherry >gi\_288116\_emb\_CAA51194\_ (X72617)

mandelonitrile lyase [Prunus serotina] >gi\_1730332 (U78814) (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus serotina] >gi\_1090776\_prf\_\_2019441A mandelonitrile lyase

[Prunus serotina]

33970 Seq. No.

349926 1.R1040 Contig ID fC-gmse700670512r3 5'-most EST

33971 Seq. No.

349953 1.R1040 Contig ID fC-gmse700671032g1 5'-most EST

Method BLASTN g575730 NCBI GI 635 BLAST score



E value 0.0e+00
Match length 753
% identity 97

NCBI Description Z.mays mRNA for transmembrane protein

Seq. No. 33972

Contig ID 349985\_1.R1040 5'-most EST fC-gmse700671225d3

Method BLASTX
NCBI GI g3641836
BLAST score 158
E value 1.0e-10
Match length 70
% identity 56

NCBI Description (AL023094) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 33973

Contig ID 349988\_1.R1040 5'-most EST fC-gmse700671225z1

Method BLASTX
NCBI GI g3068705
BLAST score 264
E value 1.0e-22
Match length 176
% identity 35

NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 33974

Contig ID 349995 1.R1040 5'-most EST fC-gmst700664692r1

Seq. No. 33975

Contig ID 350026\_1.R1040 5'-most EST fC-gmse700671753g1

Method BLASTX
NCBI GI g1773287
BLAST score 1386
E value 1.0e-154
Match length 342
% identity 77

NCBI Description (U71080) cinnamate-4-hydroxylase [Arabidopsis thaliana]

Seq. No. 33976

Contig ID 350084\_1.R1040 5'-most EST fC-gmse700672216f2

Method BLASTX
NCBI GI g3643604
BLAST score 407
E value 2.0e-39
Match length 228
% identity 9

NCBI Description (AC005395) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 33977

Contig ID 350085\_1.R1040



5'-most EST fC-qmse700672216d3

Seq. No. 33978

Contig ID 350103\_1.R1040 5'-most EST fC-gmse700672249z1

Seq. No. 33979

Contig ID 350110\_1.R1040 5'-most EST fC-gmst700665136r1

Method BLASTX
NCBI GI g4234955
BLAST score 210
E value 1.0e-16
Match length 80

% identity 51

NCBI Description (AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]

Seq. No. 33980

Contig ID 350113\_1.R1040 5'-most EST fC-gmse700672271z1

Method BLASTN
NCBI GI g168419
BLAST score 670
E value 0.0e+00
Match length 918
% identity 93

NCBI Description Maize (Z.mays) aldolase mRNA, complete cds

Seq. No. 33981

Contig ID 350190\_1.R1040 5'-most EST fC-gmse700672612z1

Seq. No. 33982

Contig ID 350213\_1.R1040 5'-most EST fC-gmse700672781r5

Seq. No. 33983

Contig ID 350257 1.R1040 5'-most EST fC-gmse700673112r3

Seq. No. 33984

Contig ID 350544\_1.R1040 5'-most EST fC-qmse700675307r3

Seq. No. 33985

Contig ID 350661\_1.R1040

5'-most EST g5605669

Seq. No. 33986

Contig ID 350744\_1.R1040 5'-most EST fC-gmse700752365d4

Seq. No. 33987

Contig ID 350780\_1.R1040 5'-most EST fC-qmse700753037d4

Seq. No. 33988



350803 1.R1040 Contig ID fC-qmse700753340d4 5'-most EST

BLASTN Method g1770523 NCBI GI

BLAST score 36

1.0e-10 E value Match length 36 100 % identity

NCBI Description H.sapiens U32 small nucleolar RNA gene

33989 Seq. No.

Contig ID 350818 1.R1040 5'-most EST fC-qmse700753716d5

BLASTX Method q4406761 NCBI GI 323 BLAST score 6.0e - 30E value Match length 78 76 % identity

(AC006836) putative ubiquinone biosynthesis protein NCBI Description

[Arabidopsis thaliana]

33990 Seq. No.

350829 1.R1040 Contig ID 5'-most EST fC-gmse700753825d1

33991 Seq. No.

350849 1.R1040 Contig ID 5'-most EST fC-gmse700754216d2

33992 Seq. No.

350881 1.R1040 Contig ID 5'-most EST fC-qmse700754725d2

Method BLASTN NCBI GI g2598586 BLAST score 221 1.0e-121 E value 473 Match length

% identity 88

NCBI Description Medicago truncatula mRNA for cycloartenol synthase, partial

33993 Seq. No.

350902 1.R1040 Contig ID fC-gmse700755168d4 5'-most EST

33994 Seq. No.

350991 1.R1040 Contig ID fC-gmse700757667d6 5'-most EST

33995 Seq. No.

351263 1.R1040 Contig ID fC-gmst700665357r5 5'-most EST

33996 Seq. No.

351520 1.R1040 Contig ID 5'-most EST fC-gmse700856529r4



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Seq. No.
                  351579 1.R1040
Contig ID
                  fC-gmst700605402f4
5'-most EST
Method
                  BLASTX
                  g1076579
NCBI GI
BLAST score
                  245
                  6.0e-21
E value
                  61
Match length
                  69
% identity
                  alcohol dehydrogenase homolog ADH3a - tomato
NCBI Description
                  33998
Seq. No.
                  351581 1.R1040
```

Contig ID fC-gmst700605413f4 5'-most EST BLASTX Method g1353352 NCBI GI 547 BLAST score

4.0e-56 E value Match length 170 59 % identity

(U31975) alanine aminotransferase [Chlamydomonas NCBI Description

reinhardtii]

33999 Seq. No.

351584 1.R1040 Contig ID fC-gmst700605438a2 5'-most EST

Method BLASTX g3367596 NCBI GI BLAST score 458 9.0e-46 E value Match length 149 % identity 58

(AL031135) putative protein [Arabidopsis thaliana] NCBI Description

34000 Seq. No.

351711 1.R1040 Contig ID 5'-most EST fC-gmst700650943r1

34001 Seq. No.

351723 1.R1040 Contig ID 5'-most EST fC-gmst700650945r6

Method BLASTX NCBI GI g1514597 226 BLAST score 3.0e-18 E value Match length 116 % identity 41

(Y07595) transcription factor TFIIH [Homo sapiens] NCBI Description

>qi 4504201 ref NP 001508.1 pGTF2H4 general transcription

factor IIH, polypeptide 4 (52kD subunit)

Seq. No. 34002

Contig ID 351878 1.R1040 5'-most EST fC-gmst700652684d1

Seq. No. 34003

Contig ID 351906 1.R1040



5'-most EST fC-gmst700651965d7

Seq. No. 34004

Contig ID 352072\_1.R1040 5'-most EST fC-gmst700653543r6

Method BLASTX
NCBI GI g861157
BLAST score 968
E value 1.0e-105
Match length 247
% identity 76

NCBI Description (Z35163) cell wall invertase II; beta-furanofructosidase

[Vicia faba]

Seq. No. 34005

Contig ID 352186\_1.R1040 5'-most EST fC-gmst700653794r7

Seq. No. 34006

Contig ID 352317\_1.R1040 5'-most EST fC-gmst700660827r5

Seq. No. 34007

Contig ID 352327 1.R1040 5'-most EST fC-gmst700660854r5

Seq. No. 34008

Contig ID 352407\_1.R1040 5'-most EST fC-gmst700661765r3

Seq. No. 34009

Contig ID 352411\_1.R1040 5'-most EST fC-gmst700661785d4

Seq. No. 34010

Contig ID 352454\_1.R1040 5'-most EST fC-gmst700662075r5

Seq. No. 34011

Contig ID 352478\_1.R1040 5'-most EST fC-gmst700662785b1

Seq. No. 34012

Contig ID 352518\_1.R1040 5'-most EST fC-gmst700662684d3

Seq. No. 34013

Contig ID 352596\_1.R1040 5'-most EST fC-gmst700663510r3

Seq. No. 34014

Contig ID 352799\_1.R1040 5'-most EST fC-gmst700664577r3

Seq. No. 34015

Contig ID 353012\_1.R1040 5'-most EST fC-gmst700665233r6



Seq. N	0.
Contig	ID
5'-mos	t EST

34016 353023\_1.R1040 fC-gmst700665327r5

Seq. No.
Contig ID
5'-most EST

34017 353059\_1.R1040 fC-gmst700665435r5

Seq. No.
Contig ID
5'-most EST

34018 353076\_1.R1040 fC-gmst700665646r5

Seq. No.
Contig ID
5'-most EST

34019 353119\_1.R1040 fC-gmst700665913r5

Seq. No.
Contig ID
5'-most EST

34020 353141\_1.R1040 fC-gmst700665984r5

Seq. No.
Contig ID
5'-most EST

34021 353182\_1.R1040 fC-gmst700666090r5

Seq. No.
Contig ID
5'-most EST

34022 353196\_1.R1040 fC-gmst700666104r5

Seq. No.
Contig ID
5'-most EST

34023 353211\_1.R1040 fC-gmst700666279r5

Seq. No.
Contig ID
5'-most EST

34024 353258\_1.R1040 fC-gmst700666508r5

Seq. No.
Contig ID
5'-most EST

34025 353319\_1.R1040 fC-gmst700667018r5

Seq. No.
Contig ID
5'-most EST

34026 353440\_1.R1040 fC-gmst700892053r2

Seq. No.
Contig ID
5'-most EST

34027 353656\_1.R1040 fC-gmst700890147y1

Seq. No.
Contig ID
5'-most EST

34028 353906\_1.R1040 uC-gmflminsoy001b10b1

Seq. No. 34029

Contig ID 5'-most EST 354050\_1.R1040

uC-gmflminsoy082d09b1



Seq. No. 34030

Contig ID 354245\_1.R1040

5'-most EST uC-gmflminsoy008b08b1

Seq. No. 34031

Contig ID 354262\_1.R1040

5'-most EST uC-gmflminsoy008d08b1

Seq. No. 34032

Contig ID 354264\_1.R1040 5'-most EST uC-gmropic025a05b1

Method BLASTX
NCBI GI g4220462
BLAST score 561
E value 2.0e-57
Match length 121
% identity 88

NCBI Description (AC006216) Strong similarity to gb\_Z50851 HD-zip (athb-8)

gene from Arabidopsis thaliana containing Homeobox PF\_00046

and bZIP PF 00170 domains. [Arabidopsis thaliana]

Seq. No. 34033

Contig ID 354297 1.R1040

5'-most EST uC-gmflminsoy010a08b1

Seq. No. 34034

Contig ID 354314 1.R1040

5'-most EST uC-gmflminsoy010c06b1

Seq. No. 34035

Contig ID 354316 1.R1040

5'-most EST uC-gmflminsoy041c10b1

Method BLASTX
NCBI GI g3367520
BLAST score 141
E value 1.0e-08
Match length 70
% identity 47

NCBI Description (AC004392) Similar to protein kinase APK1A,

tyrosine-serine-threonine kinase gb\_D12522 from A.

thaliana. [Arabidopsis thaliana]

Seq. No. 34036

Contig ID 354362\_1.R1040

5'-most EST uC-gmflminsoy010h02b1

Seq. No. 34037

Contig ID 354384 1.R1040

5'-most EST uC-gmflminsoy011b03b1

Method BLASTX
NCBI GI g1786136
BLAST score 316
E value 7.0e-29
Match length 210
% identity 36

NCBI Description (AB000452) PEThy; ZPT2-6 [Petunia x hybrida]

```
Seq. No.
                  354418 1.R1040
Contig ID
5'-most EST
                  g4302953
                  34039
Seq. No.
                  354536 1.R1040
Contig ID
                  uC-gmflminsoy014b10b1
5'-most EST
                  34040
Seq. No.
                  354555 1.R1040
Contig ID
                  uC-gmrominsoy250c10b1
5'-most EST
Method
                  BLASTX
                  g2244971
NCBI GI
                   625
BLAST score
                  3.0e-65
E value
                   143
Match length
% identity
                   87
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   34041
Seq. No.
```

5'-most EST uC-gmrominsoy0001h10b1 Method BLASTX g4406820 NCBI GI 572 BLAST score 4.0e-59 E value Match length 136 % identity 77

Contig ID

(AC006201) putative ras superfamily member [Arabidopsis NCBI Description

thaliana]

354595 1.R1040

34042 Seq. No.

354599 1.R1040 Contig ID

5'-most EST uC-gmflminsoy015c06b1

BLASTX Method g3522943 NCBI GI BLAST score 717 E value 5.0e-76 177 Match length 38 % identity

NCBI Description (AC004411) putative p-glycoprotein [Arabidopsis thaliana]

34043 Seq. No.

354617 1.R1040 Contig ID

uC-gmflminsoy016d06b1 5'-most EST

34044 Seq. No.

354659 1.R1040 Contig ID uC-gmropic096e06b1 5'-most EST

Method BLASTX g3947735 NCBI GI BLAST score 313 1.0e-28 E value Match length 139 % identity

NCBI Description (AJ009720) NL27 [Solanum tuberosum]



Seq. No. 34045

Contig ID 354744 1.R1040

5'-most EST uC-gmflminsoy018g10b1

Method BLASTN
NCBI GI g4220645
BLAST score 36
E value 1.0e-10
Match length 171
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYA6, complete sequence [Arabidopsis thaliana]

Seq. No. 34046

Contig ID 354833 1.R1040

5'-most EST g4396975
Method BLASTX
NCBI GI g1673366
BLAST score 739
E value 1.0e-78
Match length 149
% identity 89

NCBI Description (Z22673) cytosolic tRNA-Ala synthetase [Arabidopsis

thaliana]

Seq. No. 34047

Contig ID 354847 1.R1040

5'-most EST uC-qmflminsoy020e04b1

Method BLASTX
NCBI GI g2853073
BLAST score 198
E value 1.0e-26
Match length 153
% identity 48

NCBI Description (AL021768) putative protein [Arabidopsis thaliana]

Seq. No. 34048

Contig ID 355313\_1.R1040

5'-most EST uC-qmflminsoy026d04b1

Method BLASTX
NCBI GI g2224663
BLAST score 764
E value 3.0e-81
Match length 294
% identity 55

NCBI Description (AB002359) KIAA0361 [Homo sapiens]

Seq. No. 34049

Contig ID 355483 1.R1040

5'-most EST g5606799
Method BLASTN
NCBI GI g471307
BLAST score 34
E value 2.0e-09
Match length 52
% identity 94

NCBI Description G.max gene for cyclin



```
Seq. No.
                  355602 1.R1040
Contig ID
                  uC-gmflminsoy029h03b1
5'-most EST
Method
                  BLASTX
                  g4559333
NCBI GI
                  148
BLAST score
                  2.0e-09
E value
                  79
Match length
                  44
% identity
                  (AC007087) unknown protein [Arabidopsis thaliana]
NCBI Description
                  34051
Seq. No.
                  355684 1.R1040
Contig ID
                  uC-gmflminsoy030g12b1
5'-most EST
                  BLASTX
Method
                   g3935179
NCBI GI
                   139
BLAST score
                   2.0e-11
E value
                   113
Match length
                   38
% identity
                  (AC004557) F17L21.22 [Arabidopsis thaliana]
NCBI Description
                   34052
Seq. No.
                   355704 1.R1040
Contig ID
                   q5666621
5'-most EST
                   BLASTX
Method
                   g1653953
NCBI GI
                   171
BLAST score
                   5.0e-12
E value
                   110
Match length
                   30
% identity
                  (D90917) hypothetical protein [Synechocystis sp.]
NCBI Description
                   34053
Seq. No.
                   355735 1.R1040
Contig ID
                   uC-gmflminsoy036d05b1
5'-most EST
                   34054
Seq. No.
                   355786 1.R1040
Contig ID
                   uC-gmflminsoy062f06b1
5'-most EST
                   34055
Seq. No.
                   355814 1.R1040
Contig ID
                   uC-gmflminsoy032f09b1
5'-most EST
                   BLASTN
Method
                   q1419035
NCBI GI
BLAST score
                   244
                   1.0e-135
E value
                   388
Match length
                   91
% identity
NCBI Description M.sativa mRNA for delta-1-pyrroline-5-carboxylate synthase,
                   P5CS-1
```

34056 Seq. No.

355869 1.R1040 Contig ID

5'-most EST uC-gmflminsoy078g06b1

BLASTX Method



```
g3176707
NCBI GI
                  146
BLAST score
                   2.0e-09
E value
                   44
Match length
% identity
                   64
                   (AC002392) putative proline-rich protein APG [Arabidopsis
NCBI Description
                   thaliana]
                   34057
Seq. No.
```

355923\_1.R1040 Contig ID uC-gmflminsoy035e10b1 5'-most EST

Method BLASTX q126722 NCBI GI 154 BLAST score 3.0e-10 E value Match length 85 35 % identity

ALPHA-MANNOSIDASE II (MANNOSYL-OLIGOSACCHARIDE NCBI Description

1,3-1,6-ALPHA-MANNOSIDASE) (MAN II) (GOLGI ALPHA-MANNOSIDASE II) >gi\_110673\_pir\_\_A41641

mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase (EC 3.2.1.114) - mouse >gi 49944 emb CAA43480\_ (X61172) mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase [Mus

musculus]

34058 Seq. No.

355995 1.R1040 Contig ID

5'-most EST uC-qmrominsoy194g07b1

34059 Seq. No.

355999 1.R1040 Contig ID

g4396410 5'-most EST Method BLASTX g2232354 NCBI GI 243 BLAST score 3.0e-25 E value Match length 112 55 % identity

(AF006081) UDPG glucosyltransferase [Solanum berthaultii] NCBI Description

34060 Seq. No.

356041 1.R1040 Contig ID

uC-gmflminsoy065c06b1 5'-most EST

BLASTN Method g3367637 NCBI GI 36 BLAST score 8.0e-11 E value 48 Match length % identity

Arabidopsis thaliana mRNA for monogalactosyldiacylglycerol NCBI Description

synthase

34061

Seq. No.

356063 1.R1040 Contig ID

5'-most EST uC-gmflminsoy037d09b1

34062 Seq. No.



Contig ID 356152 1.R1040

5'-most EST uC-gmflminsoy040f09b1

Method BLASTX
NCBI GI g1076545
BLAST score 458
E value 1.0e-57
Match length 162
% identity 71

NCBI Description guanine nucleotide regulatory protein - fava bean

>gi\_547478\_emb\_CAA85733\_ (Z37503) guanine nucleotide
regulatory protein [Vicia faba] >gi\_1098297\_prf\_\_2115367E

small GTP-binding protein [Vicia faba]

Seq. No. 34063

Contig ID 356212 1.R1040

5'-most EST uC-gmflminsoy041e09b1

Seq. No. 34064

Contig ID 356238\_1.R1040 5'-most EST uC-gmropic067a12b1

Method BLASTX
NCBI GI g4544473
BLAST score 393
E value 3.0e-38
Match length 124
% identity 31

NCBI Description (AC006580) putative mei2 protein [Arabidopsis thaliana]

Seq. No. 34065

Contig ID 356254 1.R1040

5'-most EST uC-gmflminsoy042b10b1

Method BLASTX
NCBI GI g1369852
BLAST score 567
E value 2.0e-58
Match length 146
% identity 73

NCBI Description (L46702) kinesin heavy chain-like protein [Solanum

tuberosum]

Seq. No. 34066

Contig ID 356278\_1.R1040

5'-most EST uC-gmflminsoy044h01b1

Seq. No. 34067

Contig ID 356297\_1.R1040

5'-most EST uC-gmflminsoy042g02b1

Method BLASTX
NCBI GI g417308
BLAST score 301
E value 3.0e-27
Match length 160
% identity 39

NCBI Description PROBABLE HELICASE MOT1 >gi\_283205\_pir\_\_S22775 MOT1 protein

- yeast (Saccharomyces cerevisiae) >gi\_171965 (M83224) Mot1
[Saccharomyces cerevisiae] >gi\_1147612 (U41849) LPF4c;
Mot1p is a probable helicase essential for vegetative



growth on rich glucose medium at 30 degree C: Swiss-Prot Accession number P32333; similar to S. cerevisiae RAD26 gene product: Swiss-Prot Accession number P40352 [Saccharo

Seq. No. 34068

Contig ID 356307 1.R1040 5'-most EST g4396674

Method BLASTX
NCBI GI g4522004
BLAST score 525
E value 2.0e-53
Match length 189

% identity 63

NCBI Description (AC007069) putative histidine kinase, sensory transduction

[Arabidopsis thaliana]

Seq. No. 34069

Contig ID 356309 1.R1040

5'-most EST uC-gmflminsoy042h04b1

Seq. No. 34070

Contig ID 356334\_1.R1040

5'-most EST uC-gmrominsoy177h07b1

Seq. No. 34071

Contig ID 356337 1.R1040

5'-most EST uC-gmflminsoy043b12b1

Seq. No. 34072

Contig ID 356375\_1.R1040

5'-most EST uC-gmflminsoy100b12b1

Seq. No. 34073

Contig ID 356401\_1.R1040

5'-most EST q5688034

Seq. No. 34074

Contig ID 356429 1.R1040

5'-most EST uC-gmflminsoy044c10b1

Method BLASTX
NCBI GI g3402687
BLAST score 346
E value 1.0e-32
Match length 91
% identity 71

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 34075

Contig ID 356450 1.R1040

5'-most EST uC-gmflminsoy053e01b1

Seq. No. 34076

Contig ID 356518\_1.R1040

5'-most EST uC-gmrominsoy180a08b1

Method BLASTN NCBI GI g1326160

BLAST score 54



2.0e-21 E value 88 Match length 97 % identity

Phaseolus vulgaris dehydrin mRNA, complete cds NCBI Description

Seq. No. Contig ID 34077

356556 1.R1040

5'-most EST

g5605939

Seq. No.

34078

Contig ID

356709 1.R1040

5'-most EST

uC-gmflminsoy047h01b1

Seq. No.

34079

Contig ID

356715 1.R1040

5'-most EST

uC-gmflminsoy047h08b1

Seq. No.

34080

Contig ID

356770 1.R1040

5'-most EST Method

 $942867\overline{2}1$ BLASTX

NCBI GI

BLAST score

g1362112 469

E value Match length

3.0e-65 169

% identity NCBI Description 76 protein kinase NPK2 (EC 2.7.1.-) - common tobacco

>gi\_862342\_dbj\_BAA06731\_ (D31964) NPK2 [Nicotiana tabacum]

Seq. No.

34081

Contig ID 5'-most EST

356863 1.R1040 uC-gmropic092e11b1

Method

 ${\tt BLASTX}$ 

NCBI GI

g3068704

BLAST score

535

E value

2.0e-54

Match length

232 49

% identity

NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No.

34082

Contig ID

356872 1.R1040

5'-most EST

uC-gmflminsoy053f11b1

Method NCBI GI BLASTX g2245036

BLAST score

304

E value

2.0e-27

Match length

174

% identity

NCBI Description

(Z97342) triacylglycerol lipase homolog [Arabidopsis

thaliana]

Seq. No.

34083

Contig ID 5'-most EST 356943 1.R1040

uC-gmflminsoy054e08b1

Seq. No.

34084



Contig ID 356947 1.R1040

5'-most EST uC-gmflminsoy054e12b1

Seq. No. 34085

Contig ID 356949\_1.R1040

5'-most EST uC-gmflminsoy054f02b1

Seq. No. 34086

Contig ID 357074\_1.R1040 5'-most EST uC-gmropic050f10b1

Seq. No. 34087

Contig ID 357107 1.R1040

5'-most EST uC-gmflminsoy056f07b1

Method BLASTX
NCBI GI g3941448
BLAST score 582
E value 4.0e-60
Match length 116
% identity 88

% identity 88
NCBI Description (AF062878) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 34088

Contig ID 357154 1.R1040

5'-most EST uC-gmflminsoy057c04b1

Seq. No. 34089

Contig ID 357197 1.R1040

5'-most EST uC-gmflminsoy057g02b1

Method BLASTX
NCBI GI g2342682
BLAST score 221
E value 7.0e-23
Match length 81
% identity 62

NCBI Description (AC000106) Contains similarity to Rattus AMP-activated

protein kinase (gb\_X95577). [Arabidopsis thaliana]

Seq. No. 34090

Contig ID 357236 1.R1040

5'-most EST uC-gmflminsoy058b11b1

Method BLASTX
NCBI GI g4176557
BLAST score 419
E value 3.0e-41
Match length 132
% identity 58

NCBI Description (AL035259) conserved hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 34091

Contig ID 357404\_1.R1040

5'-most EST uC-gmrominsoy263b11b1

Method BLASTX
NCBI GI g3201617
BLAST score 376



4.0e-36 E value Match length 66 % identity

(AC004669) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 34092

357499 1.R1040 Contig ID uC-gmropic105e10b1 5'-most EST

Method BLASTX NCBI GI g728905 257 BLAST score E value 3.0e-27 Match length 128 50 % identity

PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC NCBI Description

RETICULUM CA2+-ATPASE) >gi\_1078206 pir S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae)

>gi\_171114 (L01795) ATPase [Saccharomyces cerevisiae] >gi\_595560 (U12980) Drs2p: Membrane spanning

Ca-ATPase(P-type), member of the cation transport(E1-E2)

ATPase [Saccharomyces cerevisiae]

Seq. No. 34093

358040 1.R1040 Contig ID 5'-most EST uC-gmropic087b10b1

Method BLASTX NCBI GI q3687246 BLAST score 241 2.0e-20 E value Match length 61 % identity 79

(AC005169) putative suppressor protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 34094

358071 1.R1040 Contig ID

uC-gmflminsoy109f01b1 5'-most EST

BLASTX Method q3450842 NCBI GI 506 BLAST score 3.0e-51E value 136 Match length % identity

(AF080436) mitogen activated protein kinase kinase [Oryza NCBI Description

sativa]

34095 Seq. No.

358140 1.R1040 Contig ID

5'-most EST uC-gmflminsoy079a04b1

Method BLASTX NCBI GI g3510251 BLAST score 190 2.0e-14 E value 70 Match length % identity

NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]



```
Seq. No. 3409
```

Contig ID 358221\_1.R1040

5'-most EST uC-gmflminsoy074e07b1

Method BLASTX
NCBI GI g3004555
BLAST score 221
E value 5.0e-18
Match length 140

% identity 4
NCBI Description (AC003673) similar to salt inducible protein [Arabidopsis

thaliana]

Seq. No. 34097

Contig ID 358345\_1.R1040

5'-most EST uC-gmrominsoy273a10b1

Method BLASTX
NCBI GI g3292826
BLAST score 655
E value 2.0e-68
Match length 137
% identity 80

NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34098

Contig ID 358380\_1.R1040

5'-most EST uC-gmflminsoy076d06b1

Seq. No. 34099

Contig ID 358447\_1.R1040

5'-most EST uC-gmflminsoy077c01b1

Method BLASTX
NCBI GI g3152598
BLAST score 348
E value 7.0e-33
Match length 116
% identity 57

NCBI Description (AC002986) Contains similarity to C2-HC type zinc finger

protein C.e-MyT1 gb\_U67079 from C. elegans and to

hypersensitivity-related gene 201 isolog T28M21.14 from A.

thaliana BAC gb AF002109. [Arabidopsis thaliana]

Seq. No. 34100

Contig ID 358648\_1.R1040

5'-most EST uC-gmronoir0001f05b1

Seq. No. 34101

Contig ID 358685\_1.R1040

5'-most EST uC-gmflminsoy080b09b1

Method BLASTX
NCBI GI 94455232
BLAST score 617
E value 3.0e-64
Match length 190
% identity 61

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 34102



```
358703 1.R1040
Contig ID
                   uC-gmflminsoy080d03b1
5'-most EST
                   BLASTX
Method
                   g2149640
NCBI GI
                   697
BLAST score
                   1.0e-73
E value
                   156
Match length
                   84
% identity
```

(U91995) Argonaute protein [Arabidopsis thaliana] NCBI Description

34103 Seq. No.

358725 1.R1040 Contig ID

uC-gmflminsoy080g08b1 5'-most EST

Seq. No. 34104

358731 1.R1040 Contig ID 5'-most EST uC-gmronoir045a03b1

BLASTX Method g1351676 NCBI GI 185 BLAST score 3.0e - 30E value Match length 153 % identity 43

PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C21E11.05C NCBI Description

>gi\_2130307\_pir\_\_S62590 hypothetical protein SPAC21E11.05c

- fission yeast (Schizosaccharomyces pombe)

>gi 1067221 emb CAA91964 (Z67999) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]

34105 Seq. No.

358867 1.R1040 Contig ID

5'-most EST uC-gmflminsoy082f08b1

BLASTX Method g3283026 NCBI GI 343 BLAST score 4.0e-32 E value 173 Match length 36 % identity

NCBI Description (AF051562) putative transposase [Arabidopsis thaliana]

34106 Seq. No.

358885 1.R1040 Contig ID

5'-most EST g5607084

Seq. No. 34107

358918 1.R1040 Contig ID 5'-most EST uC-gmropic097g07b1

Method BLASTX NCBI GI g3482972 159 BLAST score 1.0e-10 E value Match length 124 % identity

(AL031369) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 34108

358964 1.R1040 Contig ID



```
uC-qmflminsoy084e07b1
5'-most EST
                  BLASTX
Method
                  q1825766
NCBI GI
BLAST score
                  182
                  3.0e-13
E value
                  138
Match length
                   33
% identity
                  (U88314) similar to flavin-containing monooxygenases
NCBI Description
                   [Caenorhabditis elegans]
                   34109
Seq. No.
                   359431 1.R1040
Contig ID
                  uC-gmropic005e04b1
5'-most EST
                   34110
Seq. No.
                   359487 1.R1040
Contig ID
5'-most EST
                   uC-gmropic065f05b1
                   34111
Seq. No.
                   359935 1.R1040
Contig ID
                   uC-gmrominsoy0001a08a1
5'-most EST
                   BLASTX
Method
                   q4512698
NCBI GI
BLAST score
                   180
                   4.0e-13
E value
                   53
Match length
                   64
% identity
NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]
                   34112
Seq. No.
                   359960 1.R1040
Contig ID
5'-most EST
                   g51266<del>5</del>3
Seq. No.
                   34113
                   360036 1.R1040
Contig ID
                   uC-gmrominsoy025f05b1
5'-most EST
                   34114
Seq. No.
                   360042 1.R1040
Contig ID
                   uC-gmrominsoy055h08b1
5'-most EST
                   BLASTN
Method
                   g1235973
NCBI GI
BLAST score
                   153
E value
                   2.0e-80
Match length
                   381
                   80
```

% identity

NCBI Description G.pallida mRNA for collagen

Seq. No.

34115

360049 1.R1040 Contig ID

5'-most EST

uC-gmrominsoy026a01b1

Seq. No.

34116

360160 1.R1040 Contig ID uC-gmropic042b09b1 5'-most EST

BLASTX Method g3415117 NCBI GI



BLAST score 355 E value 1.0e-33 Match length 83 % identity 39

NCBI Description (AF081203) villin 3 [Arabidopsis thaliana]

Seq. No. 34117

Contig ID 360252\_1.R1040

5'-most EST uC-gmrominsoy030e09b1

Method BLASTX
NCBI GI g400042
BLAST score 303
E value 1.0e-27
Match length 100
% identity 20

NCBI Description TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521

>gi\_539700\_pir\_\_A38093 transformation-sensitive protein IEF

£.

SSP 3521 - human >gi 184565 (M86752)

transformation-sensitive protein [Homo sapiens]

Seq. No. 34118

Contig ID 360262\_1.R1040

5'-most EST uC-gmrominsoy030g02b1

Seq. No. 34119

Contig ID 360279 1.R1040

5'-most EST uC-gmrominsoy031b07b1

Method BLASTX
NCBI GI g1184072
BLAST score 353
E value 2.0e-33
Match length 97
% identity 75

NCBI Description (U40766) COL-1 [Meloidogyne incognita]

Seq. No. 34120

Contig ID 360304\_1.R1040 5'-most EST uC-gmropic096c09b1

Seq. No. 34121

Contig ID 360433 1.R1040

5'-most EST uC-gmrominsoy038b12b1

Seq. No. 34122

Contig ID 360436\_1.R1040

5'-most EST uC-gmrominsoy035b05b1

Method BLASTX
NCBI GI g3881546
BLAST score 177
E value 6.0e-13
Match length 72
% identity 43

NCBI Description (Z69904) Similarity to Human RAD23 protein homolog2 (PIR Acc. No. S44443); cDNA EST EMBL:D71787 comes from this gene; cDNA EST EMBL:D72299 comes from this gene; cDNA EST

EMBL: D72362 comes from this gene; cDNA EST EMBL: D72820 co



Seq. No. 34123

Contig ID 360643 1.R1040

5'-most EST uC-gmrominsoy169d02b1

Method BLASTN
NCBI GI g4220637
BLAST score 38
E value 8.0e-12

Match length 66 % identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MIE1, complete sequence [Arabidopsis thaliana]

Seq. No. 34124

Contig ID 360732\_1.R1040

5'-most EST uC-gmrominsoy302b03b1

Method BLASTX
NCBI GI g563237
BLAST score 240
E value 3.0e-20
Match length 80
% identity 56

NCBI Description (U16030) cuticular collagen Bmcol-2 [Brugia malayi]

Seq. No. 34125

Contig ID 360773 1.R1040

5'-most EST uC-gmrominsoy046h09b1

Seq. No. 34126

Contig ID 360795 1.R1040

5'-most EST uC-gmrominsoy158b08b1

Seq. No. 34127

Contig ID 360835\_1.R1040

5'-most EST uC-gmrominsoy048c04b1

Seq. No. 34128

Contig ID 360866 1.R1040

5'-most EST uC-gmrominsoy049a05b1

Method BLASTX
NCBI GI g731834
BLAST score 204
E value 5.0e-16
Match length 74
% identity 54

NCBI Description HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION

>gi\_1077790\_pir\_\_S49797 hypothetical protein YIL083c yeast (Saccharomyces cerevisiae) >gi 577131 emb CAA86711.1

(Z46728) YI9910.13c, unknown orf, len: 365, CAI: 0.17

[Saccharomyces cerevisiae]

Seq. No. 34129

Contig ID 360892 1.R1040

5'-most EST uC-gmrominsoy049f09b1

Seq. No. 34130

Contig ID 360936 1.R1040

5'-most EST uC-gmrominsoy052g10b1



Method q3600038 NCBI GI BLAST score 733 6.0e-78 E value 160 Match length 86 % identity (AF080119) similar to Saccharomyces cerevisiae NCBI Description transcription regulator SPO8 (SW:P41833) [Arabidopsis thaliana] 34131 Seq. No. 361015 1.R1040 Contig ID 5'-most EST uC-gmronoir007e08b1 34132 Seq. No. 361051 1.R1040 Contig ID 5'-most EST uC-gmrominsoy094b01b1 BLASTX Method g2459587 NCBI GI BLAST score 227 1.0e-18 E value Match length 118 31 % identity (U77675) 22 upper [Onchocerca volvulus] NCBI Description Seq. No. 34133 361135 1.R1040 Contig ID 5'-most EST uC-gmrominsoy060a01b1 34134 Seq. No. Contig ID 361145 1.R1040 5'-most EST uC-gmronoir043g06b1 BLASTX Method g1707276 NCBI GI 509 BLAST score 1.0e-51 E value Match length 118 % identity 44 (U80931) similar to ADP/ATP translocase [Caenorhabditis NCBI Description elegans] 34135 Seq. No. Contig ID 361161 1.R1040 uC-gmrominsoy060e06b1 5'-most EST 34136 Seq. No. Contig ID 361211 1.R1040

uC-qmrominsoy061f12b1 5'-most EST

BLASTX Method NCBI GI g627424 BLAST score 300 E value 2.0e-27 Match length 85 66 % identity

dolichyl-diphosphooligosaccharide--protein glycotransferase NCBI Description (EC 2.4.1.119) 50kD subunit - human >gi 2135018 pir S66254

dolichyl-diphosphooligosaccharide--protein glycotransferase



## (EC 2.4.1.119) 50K chain - human

34137 Seq. No. 361222 1.R1040 Contig ID uC-gmrominsoy062a10b1 5'-most EST Method BLASTX g1184072 NCBI GI 370 BLAST score 1.0e-35 E value Match length 82 % identity 88 (U40766) COL-1 [Meloidogyne incognita] NCBI Description

Seq. No. 34138

Contig ID 361236 1.R1040

5'-most EST uC-gmrominsoy062c03b1

Seq. No. 34139

Contig ID 361259 1.R1040

5'-most EST uC-gmrominsoy090g08b1

Seq. No. 34140

Contig ID 361289\_1.R1040

5'-most EST uC-gmrominsoy064b09b1

Method BLASTX
NCBI GI g547837
BLAST score 259
E value 2.0e-22
Match length 136
% identity 38

NCBI Description L-LACTATE DEHYDROGENASE >gi\_480440\_pir\_\_S36863 L-lactate

dehydrogenase (EC 1.1.1.27) - Thermotoga maritima

>gi\_396281\_emb\_CAA52355\_ (X74302) L-lactate dehydrogenase

[Thermotoga maritima]

Seq. No. 34141

Contig ID 361298 1.R1040

5'-most EST uC-gmrominsoy174d09b1

Seq. No. 34142

Contig ID 361446\_1.R1040

5'-most EST uC-gmrominsoy069b09b1

Method BLASTX
NCBI GI g2129698
BLAST score 168
E value 9.0e-12
Match length 59
% identity 53

NCBI Description protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana

>gi 1054633 emb CAA63387 (X92728) protein kinase

[Arabidopsis thaliana]

Seq. No. 34143

Contig ID 361485\_1.R1040

5'-most EST uC-gmrominsoy071f10b1

Method BLASTX NCBI GI g3860249

5142



BLAST score 273 E value 5.0e-24 Match length 129 % identity 50

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 34144

Contig ID 361506\_1.R1040

5'-most EST uC-gmrominsoy071b11b1

Method BLASTX
NCBI GI g630594
BLAST score 269
E value 2.0e-23
Match length 161
% identity 40

NCBI Description DNA topoisomerase II - Caenorhabditis elegans >gi\_156413

(L07144) DNA topoisomerase II [Caenorhabditis elegans]

Seq. No. 34145

Contig ID 361526 1.R1040

5'-most EST uC-gmrominsoy265e06b1

Method BLASTX
NCBI GI g2144165
BLAST score 159
E value 9.0e-11
Match length 99
% identity 40

NCBI Description aspartic proteinase (EC 3.4.23.-) - dog hookworm

(Ancylostoma caninum) (fragment) >gi\_1507725 (U34888)

aspartic protease [Ancylostoma caninum]

Seq. No. 34146

Contig ID 361682\_1.R1040

5'-most EST uC-gmrominsoy079h11b1

Seq. No. 34147

Contig ID 361687 1.R1040

5'-most EST uC-gmrominsoy080h10b1

Seq. No. 34148

Contig ID 361748 1.R1040

5'-most EST uC-gmrominsoy081c06b1

Method BLASTX
NCBI GI g3928008
BLAST score 618
E value 2.0e-64
Match length 140
% identity 86

NCBI Description (AJ130877) heat shock protein 60 (HSP60) [Plectus

acuminatus]

Seq. No. 34149

Contig ID 361773\_1.R1040

5'-most EST uC-gmrominsoy081h05b1

Method BLASTX NCBI GI g2129820 BLAST score 494



E value 6.0e-50 Match length 130 % identity 67

NCBI Description chitinase (EC 3.2.1.14) class II - peanut

>gi\_1237025\_emb\_CAA57773\_ (X82329) chitinase (class II)

[Arachis hypogaea]

Seq. No. 34150

Contig ID 361998\_1.R1040

5'-most EST uC-gmrominsoy090c07b1

Method BLASTX
NCBI GI g1125763
BLAST score 161
E value 6.0e-11
Match length 141
% identity 25

NCBI Description (U42835) C. elegans vitellogenin 5 precursor, vit-5 (Spieth

et al., NAR 13:7129-7138(1985)) [Caenorhabditis elegans]

Seq. No. 34151

Contig ID 362227 1.R1040

5'-most EST uC-gmrominsoy096e04b1

Method BLASTX
NCBI GI g3879811
BLAST score 305
E value 8.0e-28
Match length 140
% identity 49

NCBI Description (Z66524) Homology with Squid retinal-binding protein (PIR

Acc. No. A53057) [Caenorhabditis elegans]

Seq. No. 34152

Contig ID 362292\_1.R1040

5'-most EST uC-gmrominsoy307h02b1

Method BLASTX
NCBI GI g4006915
BLAST score 314
E value 7.0e-29
Match length 138
% identity 51

NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34153

Contig ID 362380\_1.R1040 5'-most EST uC-gmropic032c08b1

Method BLASTX
NCBI GI g123637
BLAST score 539
E value 3.0e-55
Match length 114
% identity 89

NCBI Description HEAT SHOCK 70 KD PROTEIN A >gi\_72214\_pir\_\_HHKW7A heat shock

protein 70 A - Caenorhabditis elegans >gi\_156352 (M18540)

heat shock protein 70A [Caenorhabditis elegans]

Seq. No. 34154

Contig ID 362556\_1.R1040



```
uC-gmropic107h01b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4454567
                  408
BLAST score
                  2.0e-39
E value
                  246
Match length
% identity
                  (AF128407) lipase homolog [Arabidopsis thaliana]
NCBI Description
                  34155
Seq. No.
                  362579 1.R1040
Contig ID
                  uC-gmrominsoy105e11b1
5'-most EST
                   34156
Seq. No.
                   362817 1.R1040
Contig ID
                  uC-gmrominsoy111e03b1
5'-most EST
```

34157 Seq. No. 362915 1.R1040 Contig ID uC-gmrominsoy114b03b1 5'-most EST

BLASTX Method NCBI GI g1311386 BLAST score 667 4.0e-70 E value 166 Match length 72 % identity

Cyanogenic Beta-Glucosidase Mol\_id: 1; Molecule: Cyanogenic NCBI Description

Beta-Glucosidase; Chain: Null;  $\overline{E}c: 3.2.1.21$ 

34158 Seq. No.

363034 1.R1040 Contig ID

5'-most EST uC-gmrominsoy116g04b1

Seq. No. 34159

363100 1.R1040 Contig ID

5'-most EST  $g55101\overline{7}3$ 

Seq. No. 34160

363117 1.R1040 Contig ID

uC-gmrominsoy263f02b1 5'-most EST

BLASTX Method NCBI GI q4558666 BLAST score 148 1.0e-09 E value Match length 92 % identity 33

(AC007063) putative Na/H antiporter isolog [Arabidopsis NCBI Description

thaliana]

34161 Seq. No.

363212 1.R1040 Contig ID

5'-most EST uC-gmrominsoy124h12b1

Seq. No. 34162

Contig ID 363220 1.R1040

uC-gmrominsoy122d11b1 5'-most EST



Seq. No. 34163

Contig ID 363348\_1.R1040 5'-most EST uC-gmropic050c10b1

Method BLASTX
NCBI GI g4263818
BLAST score 275
E value 2.0e-24
Match length 99
% identity 54

NCBI Description (AC006067) unknown protein [Arabidopsis thaliana]

Seq. No. 34164

Contig ID 363645 1.R1040

5'-most EST uC-gmrominsoy136a12b1

Seq. No. 34165

Contig ID 363693\_1.R1040

5'-most EST g5057607
Method BLASTX
NCBI GI g3004552
BLAST score 542
E value 2.0e-55
Match length 197
% identity 57

NCBI Description (AC003673) unknown protein [Arabidopsis thaliana]

Seq. No. 34166

Contig ID 363719 1.R1040

5'-most EST uC-gmrominsoy138d09b1

Seq. No. 34167

Contig ID 363809 1.R1040

5'-most EST uC-gmrominsoy141g09b1

Method BLASTX
NCBI GI g4530126
BLAST score 356
E value 8.0e-34
Match length 130
% identity 51

NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1

[Phaseolus vulgaris]

Seq. No. 34168

Contig ID 363820\_1.R1040

5'-most EST uC-gmrominsoy142a09b1

Seq. No. 34169

Contig ID 363992\_1.R1040

5'-most EST uC-gmrominsoy188e05b1

Seq. No. 34170

Contig ID 363995 1.R1040

5'-most EST uC-gmrominsoy214g07b1

Method BLASTX
NCBI GI g1703018
BLAST score 461
E value 4.0e-46



Match length 73 % identity

6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING NCBI Description

>gi\_984325 (U30255) phosphogluconate dehydrogenase [Homo sapiens] >gi\_4505759\_ref\_NP\_002622.1\_pPGD\_ phosphogluconate

dehydrogenase

Seq. No.

34171

Contig ID

364106 1.R1040

5'-most EST

uC-gmrominsoy158g04b1

Method NCBI GI BLASTX g1293848

BLAST score

206

E value Match length % identity

6.0e-16 205 26

NCBI Description (U56966) vitellogenin [Caenorhabditis elegans]

Seq. No.

34172

Contig ID

364110 1.R1040

5'-most EST

uC-gmropic0001d12b1

Seq. No.

34173

Contig ID

364172 1.R1040

5'-most EST

uC-gmrominsoy164g04b1

Seq. No.

34174

Contig ID

364175 1.R1040

5'-most EST

uC-qmrominsoy164h06b1

Method NCBI GI BLAST score BLASTX g730683 699

E value

8.0e-74

Match length % identity

189 69

NCBI Description

40S RIBOSOMAL PROTEIN SA (P40) (34/67 KD LAMININ BINDING

PROTEIN) >gi 476088 (U02370) 34/67 kD laminin binding

protein [Urechis caupo]

Seq. No.

34175

Contig ID

364334 1.R1040

5'-most EST

g56881<del>6</del>7

Seq. No.

34176

Contig ID

364364 1.R1040

5'-most EST

uC-gmronoir007a07b1 BLASTX

Method NCBI GI

g1236781

BLAST score

272

E value

6.0e-24

Match length

82

% identity

68

NCBI Description

(X96732) cuticular collagen [Ostertagia circumcincta]

Seq. No.

34177

Contig ID

364537 1.R1040

5'-most EST

uC-gmrominsoy213a06b1



```
Method
                  BLASTX
                  g1184072
NCBI GI
                   329
BLAST score
                   1.0e-30
E value
Match length
                   141
                   52
% identity
                  (U40766) COL-1 [Meloidogyne incognita]
NCBI Description
                   34178
Seq. No.
                   364634 1.R1040
Contig ID
                   uC-gmrominsoy179b05b1
5'-most EST
Seq. No.
                   34179
                   364656 1.R1040
Contig ID
                   uC-gmrominsoy179f10b1
5'-most EST
                   34180
Seq. No.
                   364678 1.R1040
Contig ID
5'-most EST
                   uC-gmropic098a08b1
                   34181
Seq. No.
                   364764 1.R1040
Contig ID
5'-most EST
                   uC-qmrominsoy182h10b1
                   34182
Seq. No.
                   364773 1.R1040
Contig ID
5'-most EST
                   uC-qmropic088c05b1
Method
                   BLASTN
NCBI GI
                   g2618599
BLAST score
                   35
                   4.0e-10
E value
Match length
                   151
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MBD2, complete sequence [Arabidopsis thaliana]
                   34183
Seq. No.
                   364787 1.R1040
Contig ID
5'-most EST
                   uC-qmrominsoy183e12b1
                   34184
Seq. No.
                   364861 1.R1040
Contig ID
                   uC-gmrominsoy186g09b1
5'-most EST
                   34185
Seq. No.
                   364988 1.R1040
Contig ID
                   uC-gmrominsoy192a01b1
5'-most EST
                   BLASTX
Method
                   g730692
NCBI GI
                   225
BLAST score
```

2.0e-18 E value 121 Match length

44 % identity

RUBISCO-ASSOCIATED PROTEIN >gi\_454179 (L28804) putative NCBI Description [Glycine max] >qi 1090839 prf 2019481A RuBisCO complex

protein [Glycine max]



```
Seq. No.
                  365032 1.R1040
Contig ID
                  uC-gmrominsoy193a03b1
5'-most EST
                  BLASTN
Method
                  g1235973
NCBI GI
                  97
BLAST score
                  4.0e-47
E value
                  269
Match length
% identity
NCBI Description G.pallida mRNA for collagen
Seq. No.
                  34187
                  365078 1.R1040
Contig ID
                  uC-qmrominsoy194f11b1
5'-most EST
                   34188
Seq. No.
                   365190 1.R1040
Contig ID
                   uC-gmrominsoy198a01b1
5'-most EST
                   34189
Seq. No.
                   365195 1.R1040
Contig ID
                   uC-gmronoir010a05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4406777
                   254
BLAST score
                   1.0e-21
E value
Match length
                   56
                   89
% identity
                   (AC006532) putative zinc-finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   34190
Seq. No.
                   365282 1.R1040
Contig ID
                   uC-gmrominsoy200g01b1
5'-most EST
                   {\tt BLASTX}
Method
                   g625982
NCBI GI
                   274
BLAST score
                   5.0e-24
E value
                   116
Match length
                   55
% identity
                   S-locus-specific glycoprotein S12 precursor - field mustard
NCBI Description
                   >gi 547238 bbs 149323 (S70937) S-glycoprotein [Brassica
                   campestris, S12S12 homozygotes, stigmas, Peptide, 436 aa]
                   [Brassica rapa] >gi_743639_prf__2013216A S glycoprotein
                   [Brassica rapa]
                   34191
Seq. No.
                   365373 1.R1040
Contig ID
                   uC-gmrominsoy204a05b1
5'-most EST
                   BLASTX
Method
                   g4220481
NCBI GI
```

BLAST score 236
E value 1.0e-19
Match length 89
% identity 57

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

```
Seq. No.
                   365383 1.R1040
Contig ID
                   uC-gmrominsoy204c02b1
5'-most EST
                   BLASTX
Method
                   g2464932
NCBI GI
                   191
BLAST score
E value
                   2.0e-14
                   62
Match length
% identity
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                   34193
Seq. No.
                   365387 1.R1040
Contig ID
                   uC-qmrominsoy204c06b1
5'-most EST
                   34194
Seq. No.
                   365418 1.R1040
Contig ID
                   uC-gmrominsoy205c02b1
5'-most EST
                   34195
Seq. No.
                   365446 1.R1040
Contig ID
                   uC-gmrominsoy206a12b1
5'-most EST
Seq. No.
                   34196
                   365486 1.R1040
Contig ID
                   uC-gmropic117b11b1
5'-most EST
                   BLASTX
Method
                   q2827637
NCBI GI
BLAST score
                   184
                   1.0e-13
E value
```

103 Match length 38 % identity

(AL021636) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 34197 365585 1.R1040 Contig ID uC-gmrominsoy210d06b1 5'-most EST

34198 Seq. No. 365586 1.R1040 Contig ID

uC-gmrominsoy210d08b1 5'-most EST

34199 Seq. No. 365667 1.R1040 Contig ID uC-gmronoir008c01b1 5'-most EST BLASTX Method g4206787 NCBI GI 239 BLAST score 4.0e-20 E value 117 Match length

% identity (AF112863) syntaxin-related protein Nt-syr1 [Nicotiana NCBI Description tabacum]

34200 Seq. No.

365851 1.R1040 Contig ID

uC-gmrominsoy217f08b1 5'-most EST



```
BLASTX
Method
                  q1480453
NCBI GI
                  258
BLAST score
                  2.0e-22
E value
Match length
                  104
                  47
% identity
                  (U41853) 150 kDa oxygen regulated protein [Rattus
NCBI Description
                  norvegicus]
Seq. No.
                   34201
                   365886 1.R1040
Contig ID
5'-most EST
                   uC-gmropic026e11b1
                   34202
Seq. No.
                   365946 1.R1040
Contig ID
                   uC-qmrominsoy220b01b1
5'-most EST
                   34203
Seq. No.
                   366080 1.R1040
Contig ID
                   uC-qmrominsoy224e08b1
5'-most EST
                   34204
Seq. No.
                   366146 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy227g11b1
                   34205
Seq. No.
                   366224 1.R1040
Contig ID
                   uC-gmrominsoy229a12b1
5'-most EST
                   34206
Seq. No.
                   366281 1.R1040
Contig ID
                   uC-gmrominsoy230d04b1
5'-most EST
                   BLASTX
Method
                   q1235974
NCBI GI
BLAST score
                   356
                   8.0e-34
E value
                   92
Match length
                   70
% identity
                   (X96713) collagen [Globodera pallida]
NCBI Description
                   34207
Seq. No.
                   366326 1.R1040
Contig ID
                   uC-gmrominsoy231f04b1
 5'-most EST
                   BLASTX
Method
                   g3702340
NCBI GI
                   374
BLAST score
                   5.0e-36
E value
Match length
                   122
```

% identity

(AC005397) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

34208

Contig ID

366534 1.R1040

uC-gmrominsoy237a11b1 5'-most EST

Seq. No.

34209

Contig ID

366537 1.R1040



```
5'-most EST
                  uC-qmrominsoy238b04b1
                  34210
Seq. No.
                  366539 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy238b07b1
                   34211
Seq. No.
                  366553 1.R1040
Contig ID
                  uC-gmrominsoy237e03b1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g2258315
BLAST score
                   174
                   2.0e-12
E value
Match length
                   103
                   44
% identity
                   (AF004878) resistance complex protein I2C-1 [Lycopersicon
NCBI Description
                   esculentum]
Seq. No.
                   34212
Contig ID
                   366561 1.R1040
                   uC-gmrominsoy237g01b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3136056
BLAST score
                   164
                   2.0e-11
E value
Match length
                   125
                   34
% identity
                  (AL023592) RanBP7/importin-beta/Cselp superfamily protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   34213
Seq. No.
                   366826 1.R1040
Contig ID
                   uC-gmrominsoy263c07b1
5'-most EST
Method
                   BLASTX
                   q2384956
NCBI GI
BLAST score
                   284
E value
                   1.0e-25
                   85
Match length
% identity
                   (AF022985) No definition line found [Caenorhabditis
NCBI Description
                   elegans]
                   34214
Seq. No.
                   367470 1.R1040
Contig ID
5'-most EST
                   uC-qmrominsoy275f10b1
                   BLASTX
Method
                   g2213600
NCBI GI
BLAST score
                   223
E value
                   3.0e-18
Match length
                   114
% identity
                   (AC000348) T7N9.20 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34215
                   367543 1.R1040
Contig ID
```

 $g56058\overline{5}1$ 

BLASTX

5'-most EST

Method



NCBI GI g1086586 BLAST score 243 E value 3.0e-20 Match length 187 % identity 30

NCBI Description (U41007) similar to G beta repeats (PROSITE:PS00670)

[Caenorhabditis elegans]

يا رني

Seq. No. 34216

Contig ID 367587\_1.R1040

5'-most EST uC-gmrominsoy275d12b1

Seq. No. 34217

Contig ID 367653 1.R1040

5'-most EST uC-gmrominsoy276b03b1

Seq. No. 34218

Contig ID 367674 1.R1040

5'-most EST uC-gmrominsoy276f01b1

Method BLASTX
NCBI GI g1458286
BLAST score 376
E value 4.0e-36
Match length 121
% identity 65

% identity 65
NCBI Description (U64842) partial CDS, [Caenorhabditis elegans]

Seq. No. 34219

Contig ID 367833\_1.R1040

5'-most EST uC-gmrominsoy283g03b1

Seq. No. 34220

Contig ID 368031\_1.R1040

5'-most EST uC-gmrominsoy298h11b1

Method BLASTX
NCBI GI g3378491
BLAST score 181
E value 2.0e-13
Match length 53
% identity 60

NCBI Description (AJ007578) pRIB5 protein [Ribes nigrum]

Seq. No.

Contig ID 368122\_1.R1040

5'-most EST uC-gmrominsoy304b01b1

34221

Method BLASTX
NCBI GI g3879463
BLAST score 581
E value 3.0e-60
Match length 137
% identity 78

NCBI Description (Z68751) predicted using Genefinder; Similarity to Dog

endoplasmin precursor GRP94 (SW:ENPL\_CANFA); cDNA EST EMBL:D27273 comes from this gene; cDNA EST EMBL:D27275 comes from this gene; cDNA EST EMBL:D27274 comes from this

gene



Seq. No. 34222

Contig ID 368125 1.R1040

5'-most EST uC-gmrominsoy302c02b1

Seq. No. 34223

Contig ID 368201\_1.R1040

5'-most EST uC-gmrominsoy306g09b1

Seq. No. 34224

Contig ID 368247 1.R1040

5'-most EST uC-gmrominsoy306c10b1

Seq. No. 34225

Contig ID 368305\_1.R1040 5'-most EST uC-gmropic006h03b1

Seq. No. 34226

Contig ID 368305 2.R1040

5'-most EST uC-gmrominsoy308b01b1

Seq. No. 34227

Contig ID 368454\_1.R1040

5'-most EST uC-gmrominsoy312a05b1

Method BLASTX
NCBI GI g477280
BLAST score 277
E value 2.0e-24
Match length 74

Match length 74 % identity 68

NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) 55K

protein precursor - potato >gi\_410633\_bbs\_136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,

534 aa]

Seq. No. 34228

Contig ID 368472\_1.R1040 5'-most EST uC-gmropic034g02b1

Method BLASTX
NCBI GI g233489
BLAST score 158
E value 1.0e-10
Match length 100
% identity 34

% identity 34
NCBI Description coagulation factor IX/factor X-binding protein A chain
[Trimeresurus flavoviridis, venom, Peptide, 129 aa]
>gi 3212543 pdb 1IXX\_A Chain A, Crystal Structure Of

Coagulation Factors IxX-Binding Protein (IxX-Bp) From Venom Of Habu Snake With A Heterodimer Of C-Type Lectin Domains

>gi\_3212545\_pdb\_1IXX\_C Chain C, Crystal Structure Of
Coagulation Factors IxX-Binding Protein (IxX-Bp) From Venom

Of Habu Snake With A Heterodimer Of C-Type Lectin Domains >gi 3212547 pdb 1IXX\_E Chain E, Crystal Structure Of

Coagulation Factors IxX-Binding Protein (IxX-Bp) From Venom Of Habu Snake With A Heterodimer Of C-Type Lectin Domains

Seq. No. 34229



```
368656 1.R1040
Contig ID
                   uC-gmrominsoy317b11b1
5'-most EST
                   34230
Seq. No.
                   368700 1.R1040
Contig ID
```

5'-most EST Method BLASTN g16185 NCBI GI 235 BLAST score 1.0e-129 E value Match length 356

92 % identity A.thaliana atpgpl gene for P-glycoprotein, homologous to NCBI Description

uC-gmrominsoy318c12b1

mammalian mdr genes

368716 1.R1040 Contig ID uC-gmrominsoy318e06b1 5'-most EST BLASTN Method q3738275 NCBI GI 504 BLAST score E value 0.0e + 00

34231

Match length 516 % identity

Seq. No.

Arabidopsis thaliana chromosome II BAC F17A22 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

34232 Seq. No.

368730 1.R1040 Contig ID

uC-gmrominsoy318g09b1 5'-most EST

BLASTN Method g4006885 NCBI GI BLAST score 336 0.0e + 00E value 372 Match length 98 % identity

Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig NCBI Description

fragment No

34233 Seq. No.

368731 1.R1040 Contig ID

uC-gmrominsoy318h12b1 5'-most EST

BLASTN Method g2244950 NCBI GI 520 BLAST score 0.0e+00E value Match length 536 99 % identity

Arabidopsis thaliana DNA chromosome 4, ESSA I contig NCBI Description

fragment No

34234 Seq. No.

368740 1.R1040 Contig ID

uC-gmrominsoy318h09b1 5'-most EST

BLASTN Method g16473 NCBI GI BLAST score 507



E value 0.0e+00
Match length 519
% identity 56

NCBI Description Arabidopsis thaliana 25S-18S ribosomal DNA spacer

Seq. No. 34235

Contig ID 368757\_1.R1040

5'-most EST uC-gmrominsoy319c02b1

Method BLASTX
NCBI GI g2959759
BLAST score 163
E value 3.0e-11
Match length 80
% identity 38

NCBI Description (Y14704) galactokinase [Candida parapsilosis]

Seq. No. 34236

Contig ID 368930\_1.R1040 5'-most EST uC-gmronoir031b03b1

Seq. No. 34237

Contig ID 369042\_1.R1040 5'-most EST uC-gmronoir005b08b1

Seq. No. 34238

Contig ID 369046\_1.R1040 5'-most EST uC-gmronoir034b12b1

Method BLASTX
NCBI GI g3287946
BLAST score 515
E value 2.0e-52
Match length 130
% identity 75

NCBI Description PUTATIVE HELICASE C6F12.16 IN CHROMOSOME I

>gi\_2330862\_emb\_CAB11099\_ (Z98533) putative rna helicase

[Schizosaccharomyces pombe]

Seq. No. 34239

Contig ID 369048\_1.R1040 5'-most EST uC-gmronoir034c03b1

Seq. No. 34240

Contig ID 369129\_1.R1040 5'-most EST uC-gmronoir059f03b1

Seq. No. 34241

Contig ID 369142\_1.R1040 5'-most EST uC-gmronoir007g02b1

Method BLASTX
NCBI GI g3157932
BLAST score 353
E value 5.0e-68
Match length 222
% identity 62

NCBI Description (AC002131) Similar to hypothetical protein HYP1 gb Z97338

from A. thaliana. [Arabidopsis thaliana]



```
Seq. No.
                  369144 1.R1040
Contig ID
                  uC-gmronoir007g05b1
5'-most EST
                  BLASTX
Method
                  q2597972
NCBI GI
BLAST score
                   513
                   3.0e-52
E value
                   124
Match length
% identity
                   (AJ001621) RAL-1 protein [Litomosoides sigmodontis]
NCBI Description
                   34243
Seq. No.
                   369169 1.R1040
Contig ID
                   uC-gmronoir043b10b1
5'-most EST
                   BLASTX
Method
                   q1236781
NCBI GI
BLAST score
                   308
                   2.0e-28
E value
                   95
Match length
                   65
% identity
                  (X96732) cuticular collagen [Ostertagia circumcincta]
NCBI Description
                   34244
Seq. No.
                   369195 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir057h07b1
                   34245
Seq. No.
                   369200 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir009b06b1
                   34246
Seq. No.
                   369208 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir054b12b1
                   34247
Seq. No.
                   369215 1.R1040
Contig ID
                   uC-gmronoir009e06b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2982452
                   247
BLAST score
                   5.0e-21
E value
                   147
Match length
 % identity
                   (AL022223) receptor protein kinase-like protein
NCBI Description
                   [Arabidopsis thaliana]
 Seq. No.
                   34248
                   369217 1.R1040
 Contig ID
                   uC-gmronoir035g05b1
 5'-most EST
Method
                   BLASTX
                   g2500025
 NCBI GI
                   318
 BLAST score
                   2.0e-29
 E value
```

127 Match length 46 % identity

PROBABLE ADENYLOSUCCINATE SYNTHETASE (IMP--ASPARTATE NCBI Description LIGASE) >gi\_1825781 (U88315) Similar to adenylosuccinate



synthetase; coded for by C. elegans cDNA yk104b12.3; coded for by C. elegans cDNA yk121e6.3; coded for by C. elegans cDNA yk117a11.3; coded for by C. elegans cDNA yk19c6.3; coded for by C. elegans cDNA yk

Seq. No. 34249

Contig ID 369219\_1.R1040 5'-most EST uC-gmronoir054f03b1

Seq. No. 34250

Contig ID 369222 1.R1040 5'-most EST uC-gmronoir057g11b1

Method BLASTX
NCBI GI g3096951
BLAST score 471
E value 2.0e-47
Match length 103
% identity 90

NCBI Description (AJ005784) heat shock protein 90 [Brugia pahangi]

Seq. No. 34251

Contig ID 369307\_1.R1040 5'-most EST uC-gmronoir033e09b1

Seq. No. 34252

Contig ID 369326\_1.R1040 5'-most EST uC-gmronoir012h12b1

Method BLASTX
NCBI GI g1706582
BLAST score 747
E value 1.0e-79
Match length 149
% identity 95

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi\_1072161 (U40935)

elongation-factor 1-alpha [Caenorhabditis  $\overline{e}$ legans]

>gi\_1255296 (U51994) coded for by C. elegans cDNA CEESE09R; coded for by C. elegans cDNA CEESH59F; coded for by C. elegans cDNA CESAE06F; coded for by C. elegans cDNA

ykldll.3; coded for by C. elegans cDNA ykldll.5; coded for

by C. elegans cDNA yk17e7.3

Seq. No. 34253

Contig ID 369366\_1.R1040 5'-most EST uC-gmronoir014a01b1

Seq. No. 34254

Contig ID 369430\_1.R1040 5'-most EST uC-gmronoir040b12b1

Seq. No. 34255

Contig ID 369514\_1.R1040 5'-most EST uC-gmronoir040d07b1

Seq. No. 34256

Contig ID 369567\_1.R1040 5'-most EST uC-gmronoir052b03b1



Seq. No. 34257

Contig ID 369663\_1.R1040 5'-most EST uC-gmronoir026a08b1

Seq. No. 34258

Contig ID 369689\_1.R1040 5'-most EST uC-gmronoir054c09b1

Seq. No. 34259

Contig ID 369719\_1.R1040 5'-most EST uC-gmronoir054c11b1

Method BLASTX
NCBI GI g3877452
BLAST score 219
E value 7.0e-18
Match length 84
% identity 45

NCBI Description (Z81086) predicted using Genefinder; Similarity to Human

platelet-endothelial tetraspan antigen (SWLPET3\_HUMAN)

[Caenorhabditis elegans]

Seq. No. 34260

Contig ID 369770\_1.R1040 5'-most EST uC-gmronoir030c08b1

Seq. No. 34261

Contig ID 369777\_1.R1040 5'-most EST uC-gmronoir030d11b1

Seq. No. 34262

Contig ID 369791\_1.R1040 5'-most EST uC-gmronoir052h02b1

Seq. No. 34263

Contig ID 370067\_1.R1040 5'-most EST uC-gmronoir038e06b1

Seq. No. 34264

Contig ID 370069\_1.R1040 5'-most EST uC-gmronoir038f03b1

Seq. No. 34265

Contig ID 370078\_1.R1040 5'-most EST uC-gmronoir038h03b1

Method BLASTX
NCBI GI g1817584
BLAST score 267
E value 2.0e-23
Match length 137
% identity 44

NCBI Description (Y08991) adaptor protein [Homo sapiens]

Seq. No. 34266

Contig ID 370163\_1.R1040

5'-most EST g5688101

Seq. No. 34267



Contig ID	370363 1.R1040
5'-most EST	uC-gmropic075b08b1

Seq. No.	34268
Contig ID	370443 1.R104
51-most FST	uC-cmronoir05

5'-most EST uC-gmronoir050c02b1

0

Seq. No. 34269

Contig ID 370734\_1.R1040 5'-most EST uC-gmronoir059a02b1

Seq. No. 34270

Contig ID 371053\_1.R1040 5'-most EST uC-gmronoir070e12b1

Seq. No. 34271

Contig ID 371095\_1.R1040 5'-most EST uC-gmronoir073c02b1

Seq. No. 34272

Contig ID 371263\_1.R1040 5'-most EST uC-gmropic0001h09a1

Seq. No. 34273

Contig ID 371706\_1.R1040 5'-most EST uC-gmropic014c01b1

Seq. No. 34274

Contig ID 371818\_1.R1040 5'-most EST uC-gmropic106g05b1

Seq. No. 34275

Contig ID 372045\_1.R1040 5'-most EST uC-gmropic015c03b1

Seq. No. 34276

Contig ID 372149\_1.R1040 5'-most EST uC-gmropic016g08b1

Method BLASTX
NCBI GI g1707017
BLAST score 533
E value 1.0e-54
Match length 115
% identity 90

NCBI Description (U78721) RNA helicase isolog [Arabidopsis thaliana]

Seq. No. 34277

Contig ID 372556\_1.R1040 5'-most EST uC-gmropic022f01b1

Seq. No. 34278

Contig ID 373030\_1.R1040 5'-most EST uC-gmropic028g01b1

Method BLASTX
NCBI GI g3953471
BLAST score 563
E value 4.0e-58



Match length 122 % identity 83

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 34279

Contig ID 373180\_1.R1040 5'-most EST uC-gmropic065g01b1

Method BLASTX
NCBI GI g4467124
BLAST score 201
E value 2.0e-15
Match length 222
% identity 29

NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34280

Contig ID 373469\_1.R1040 5'-most EST uC-gmropic034b01b1

Seq. No. 34281

Contig ID 373646\_1.R1040 5'-most EST uC-gmropic036d03b1

Seq. No. 34282

Contig ID 373888\_1.R1040 5'-most EST uC-gmropic039e06b1

Seq. No. 34283

Contig ID 374364\_1.R1040 5'-most EST uC-gmropic101f01b1

Method BLASTX
NCBI GI g2465925
BLAST score 397
E value 1.0e-38
Match length 135
% identity 57

NCBI Description (AF024649) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. 34284

Contig ID 375029\_1.R1040 5'-most EST uC-gmropic059f08b1

Seq. No. 34285

Contig ID 375324\_1.R1040 5'-most EST uC-gmropic063c06b1

Method BLASTX
NCBI GI g4139038
BLAST score 148
E value 2.0e-09
Match length 74
% identity 11

NCBI Description (AF072272) resistance protein candidate RGC2K [Lactuca

sativa]

Seq. No. 34286

Contig ID 375970\_1.R1040



5'-most EST uC-gmropic073a01b1

Seq. No. 34287

Contig ID 375993\_1.R1040 5'-most EST uC-gmropic096c05b1

Seq. No. 34288

Contig ID 376035\_1.R1040 5'-most EST uC-gmropic073g03b1

Method BLASTX
NCBI GI g2959320
BLAST score 271
E value 9.0e-24
Match length 59
% identity 90

NCBI Description (Z97057) ANR1 , MADS-box protein [Arabidopsis thaliana]

Seq. No. 34289

Contig ID 376073\_1.R1040 5'-most EST uC-gmropic074b06b1

Seq. No. 34290

Contig ID 376082\_1.R1040

5'-most EST  $g95740\overline{9}$ 

Seq. No. 34291

Contig ID 376231\_1.R1040 5'-most EST uC-gmropic078f04b1

Seq. No. 34292

Contig ID 376326\_1.R1040

5'-most EST  $g50577\overline{8}3$ 

Seq. No. 34293

Contig ID 376588\_1.R1040 5'-most EST uC-gmropic090c06b1

Method BLASTX
NCBI GI g4371296
BLAST score 318
E value 3.0e-29
Match length 141
% identity 46

NCBI Description (AC006260) putative receptor protein kinase [Arabidopsis

thalianal

Seq. No. 34294

Contig ID 376624\_1.R1040 5'-most EST uC-gmropic090h02b1

Seq. No. 34295

Contig ID 376989\_1.R1040 5'-most EST uC-gmropic099b02b1

Seq. No. 34296

Contig ID 377209\_1.R1040 5'-most EST uC-gmropic102b02b1

Method BLASTX



NCBI GI g4469024 BLAST score 817 E value 1.0e-87 Match length 222 % identity 66

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 34297

Contig ID 377858\_1.R1040 5'-most EST uC-gmropic111c07b1

Seq. No. 34298

Contig ID 378085\_1.R1040 5'-most EST uC-gmropic114g03b1

Method BLASTX
NCBI GI 94530126
BLAST score 218
E value 1.0e-17
Match length 153
% identity 33

NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1

[Phaseolus vulgaris]

Seq. No. 34299

Contig ID 378116\_1.R1040 5'-most EST uC-gmropic115g05b1

Method BLASTN
NCBI GI g47594
BLAST score 359
E value 0.0e+00
Match length 424
% identity 96

NCBI Description Synechocystis sp. ndhE gene (partial), psaC gene for

photosystem I iron-sulfur protein and ndhD-like ORF

Seq. No. 34300

Contig ID 378324\_1.R1040

5'-most EST  $g42600\overline{0}5$ 

Seq. No. 34301

Contig ID 378379\_1.R1040

5'-most EST g4260076

Seq. No. 34302

Contig ID 378384 1.R1040

NCBI Description (AF042195) auxin response factor 7 [Arabidopsis thaliana]

Seq. No. 34303

Contig ID 378427\_1.R1040

5'-most EST g4260128



```
BLASTX
Method
                   q1495804
NCBI GI
BLAST score
                   442
                   4.0e-44
E value
                   110
Match length
% identity
                   75
NCBI Description (X96406) 13-lipoxygenase [Solanum tuberosum]
Seq. No.
                   34304
                   378666 1.R1040
Contig ID
                   g4260450
5'-most EST
Seq. No.
                   34305
                   378715 1.R1040
Contig ID
5'-most EST
                   q4277028
                   34306
Seq. No.
                   379005 1.R1040
Contig ID
5'-most EST
                   g4292087
Method
                   BLASTX
NCBI GI
                   g3549691
BLAST score
                   1112
E value
                   1.0e-122
Match length
                   209
% identity
                   89
                  (AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]
NCBI Description
Seq. No.
                   34307
                   379147 1.R1040
Contig ID
                   g5508921
5'-most EST
Method
                   BLASTX
                   q1170601
NCBI GI
BLAST score
                   169
                   6.0e-12
E value
Match length
                   119
                   42
% identity
                   FRUIT PROTEIN PKIWI502 >gi 1085869 pir S48036 hypothetical
NCBI Description
                   protein - kiwi fruit >gi_450237 (L\overline{27}809) pKIWI502
                   [Actinidia deliciosa]
                   34308
Seq. No.
                   379387 1.R1040
Contig ID
5'-most EST
                   942906\overline{5}6
                   34309
Seq. No.
                   379614 1.R1040
Contig ID
5'-most EST
                   g4284382
                   BLASTX
Method
                   g4580470
NCBI GI
BLAST score
                   172
                   9.0e-12
E value
```

141 Match length

(AC006081) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

% identity

34310

38

Contig ID

380046\_1.R1040

NCBI Description

```
q4405639
5'-most EST
                  BLASTX
Method
                  q4415942
NCBI GI
                   178
BLAST score
                   7.0e-13
E value
Match length
                   92
% identity
                   41
                  (AC006418) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34311
                   380240 1.R1040
Contig ID
5'-most EST
                   g4295003
Method
                   BLASTX
NCBI GI
                   q431154
BLAST score
                   229
E value
                   6.0e-21
Match length
                   159
% identity
                   35
                  (D21813) ORF [Lilium longiflorum]
NCBI Description
                   34312
Seq. No.
Contig ID
                   380280 1.R1040
5'-most EST
                   q4313610
Method
                   BLASTX
                   q4220482
NCBI GI
BLAST score
                   431
E value
                   2.0e-42
Match length
                   188
% identity
                   48
                   (AC006069) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   34313
Seq. No.
Contig ID
                   380619 1.R1040
                   q4292476
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2864615
BLAST score
                   389
                   1.0e-37
E value
Match length
                   141
                   60
% identity
                   (AL021811) putative protein [Arabidopsis thaliana]
NCBI Description
                   34314
Seq. No.
                   380785 1.R1040
Contig ID
5'-most EST
                   g4293267
Seq. No.
                   34315
                   381119 1.R1040
Contig ID
5'-most EST
                   g4295745
Method
                   BLASTX
                   q3738293
NCBI GI
                   362
BLAST score
                   2.0e-40
E value
Match length
                   129
% identity
                   68
                   (AC005309) putative CCAAT-binding transcription factor
```

subunit A (CBF-A) [Arabidopsis thaliana]

E value

Match length

2.0e-12

84



```
34316
Seq. No.
                  381329 1.R1040
Contig ID
                  g4297292
5'-most EST
Method
                  BLASTN
NCBI GI
                  g508560
BLAST score
                  118
                   3.0e-60
E value
                  126
Match length
% identity
                  98
                  Solanum tubersum mitochondrial 26S ribosomal RNA (rrn26)
NCBI Description
                   34317
Seq. No.
                   381636 1.R1040
Contig ID
5'-most EST
                   q4299653
Method
                  BLASTN
                   g312886
NCBI GI
BLAST score
                   368
                   0.0e+00
E value
Match length
                   509
                   95
% identity
NCBI Description T.reesei tefl gene for translation elongation factor la
                   34318
Seq. No.
                   381672 1.R1040
Contig ID
5'-most EST
                   q4305559
Method
                   BLASTX
                   g123544
NCBI GI
                   209
BLAST score
                   1.0e-16
E value
                   91
Match length
% identity
                   45
                   18.5 KD CLASS I HEAT SHOCK PROTEIN (HSP 18.5)
NCBI Description
                   >gi 81788 pir S00646 heat shock protein 18.5-C - soybean
                   >gi 18654 emb CAA30154 (X07160) hsp18.5-C protein (AA 1 -
                   161) [Glycine max]
                   34319
Seq. No.
                   381710 1.R1040
Contig ID
5'-most EST
                   g4303261
                   BLASTN
Method
NCBI GI
                   g310575
                   161
BLAST score
                   2.0e-85
E value
                   293
Match length
                   91
% identity
                  Glycine max nodulin-26 mRNA, complete cds
NCBI Description
                   34320
Seq. No.
                   381934 1.R1040
Contig ID
5'-most EST
                   g4301890
Method
                   BLASTX
                   g2499773
NCBI GI
BLAST score
                   134
```



% identity 49

NCBI Description 46 KD FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL

CIS-TRANS ISOMERASE) (PPIASE) >gi\_1079010\_pir\_\_A55320 immunophilin FKBP46 - fall armyworm >gi\_595845 (U15038)

immunophilin FKBP46 [Spodoptera frugiperda]

Seq. No. 34321

Contig ID 381949 1.R1040

5'-most EST g4307437

Method BLASTX

NCBI GI g3929383

BLAST score 152

E value 7.0e-10

Match length 71 % identity 45

NCBI Description SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR

SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN)

>gi\_1405747\_emb\_CAA67134\_ (X98511) PR264/SC35 [Mus

musculus]

Seq. No. 34322

Contig ID 381980\_1.R1040

5'-most EST g4302233

Method BLASTX

NCBİ GI g2500047

BLAST score 221

E value 6.0e-18

Match length 50 % identity 82

NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE

PHOSPHO-HYDROLASE) (PPASE) >gi\_534916\_emb\_CAA85362\_ (Z36894) soluble inorganic pyrophosphatase [Solanum

tuberosum]

Seq. No. 34323

Contig ID 382296\_1.R1040

NCBI Description (AC006081) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 34324

Contig ID 382950\_1.R1040

5'-most EST  $g43134\overline{9}3$ 

Seq. No. 34325

Contig ID 383013 1.R1040

5'-most EST  $g56057\overline{3}1$ 

Seq. No. 34326

Contig ID 383813\_1.R1040

5'-most EST  $g55102\overline{3}7$ 



```
Seq. No.
                  34327
                  384008 1.R1040
Contig ID
5'-most EST
                  g5509051
                  34328
Seq. No.
                  384210 1.R1040
Contig ID
                  g43963<u>1</u>7
5'-most EST
                  BLASTX
Method
                  q3876615
NCBI GI
BLAST score
                  348
                  1.0e-32
E value
                  134
Match length
                  50
% identity
                   (Z74031) Similarity to Yeast D-lactate dehydrogenase
NCBI Description
                   (SW:DLD1 YEAST); cDNA EST EMBL:C12235 comes from this gene;
                   cDNA EST EMBL:C12916 comes from this gene; cDNA EST
                  EMBL:C10532 comes from this gene; cDNA EST EMBL:C10979
                  comes f
                   34329
Seq. No.
Contig ID
                  384227 1.R1040
                   g4396334
5'-most EST
                  BLASTX
Method
                  g2760326
NCBI GI
                   225
BLAST score
                   7.0e-19
E value
                   145
Match length
                   43
% identity
                  (AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34330
                   384574 1.R1040
Contig ID
5'-most EST
                   g4396695
                   34331
Seq. No.
                   384885 1.R1040
Contig ID
5'-most EST
                   g4397027
Seq. No.
                   34332
                   385189 1.R1040
Contig ID
5'-most EST
                   g4397355
                   BLASTN
Method
NCBI GI
                   g556899
BLAST score
                   57
                   4.0e-23
E value
Match length
                   121
                   87
% identity
                  L.esculentum (cv. Rentita) mRNA for 54-kD signal
NCBI Description
                   recognition particle (SRP) specific protein
```

Seq. No. 34333

Contig ID 385852\_1.R1040 5'-most EST g4437084

Seq. No. 34334

Contig ID 386922\_1.R1040



```
q5058552
5'-most EST
                   BLASTN
Method
                   g1055367
NCBI GI
BLAST score
                   68
                   1.0e-29
E value
                   236
Match length
                   83
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   34335
Seq. No.
                   387116 1.R1040
Contig ID
                   q56059\overline{2}3
5'-most EST
                   BLASTX
Method
                   g480997
NCBI GI
                   434
BLAST score
                   7.0e-43
E value
                   164
Match length
                   54
% identity
                   beta-fructofuranosidase (EC 3.2.1.26) class 1 - carrot
NCBI Description
                   >gi 407055 emb CAA53097 (X75351) beta-fructofuranosidase
                   [Daucus carota] >gi 4454117_emb_CAA77267_ (Y18707)
                   beta-fructofuranosidase, isoform I [Daucus carota]
                   34336
Seq. No.
                   387221 1.R1040
Contig ID
5'-most EST
                   q5606037
                   34337
Seq. No.
                   388056 1.R1040
Contig ID
5'-most EST
                   g5509015
Method
                   BLASTX
                   g2828285
NCBI GI
                   273
BLAST score
                   3.0e-24
E value
                   62
Match length
                   79
% identity
                   (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                   34338
Seq. No.
                   388187 1.R1040
Contig ID
5'-most EST
                   g5509057
                   BLASTX
Method
                   g629858
NCBI GI
BLAST score
                   175
                   8.0e-13
E value
Match length
                   34
% identity
                   82
NCBI Description protein kinase C inhibitor - maize
                   34339
Seq. No.
Contig ID
                   388197 1.R1040
                   q55090<del>6</del>7
5'-most EST
```

9.0e-24 E value

231

BLASTX

g3421413

Method NCBI GI

BLAST score



Match length 57 % identity NCBI Description

(AF081922) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] >gi\_3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

34340 Seq. No.

388215 1.R1040 Contig ID

5'-most EST g5509087

Seq. No. 34341

388218 1.R1040 Contig ID

5'-most EST g5509090

34342 Seq. No.

388357 1.R1040 Contig ID

5'-most EST g5509242

34343 Seq. No.

388363 1.R1040 Contiq ID

5'-most EST g5509248

Seq. No. 34344

388387 1.R1040 Contig ID

5'-most EST q5509272

Seq. No. 34345

388419 1.R1040 Contig ID

5'-most EST g5509308

34346 Seq. No.

388436 1.R1040 Contig ID

5'-most EST g5509327

Seq. No.

34347

388884 1.R1040 Contig ID 5'-most EST q5677195

Method BLASTX g285636 NCBI GI 407 BLAST score 2.0e-39 E value

165 Match length 55 % identity

(D14161) ORF [Hordeum vulgare] NCBI Description

Seq. No. 34348

388936 1.R1040 Contig ID

g5666960 5'-most EST BLASTX Method g2826820 NCBI GI

BLAST score 527 9.0e-54 E value Match length 167 % identity 62

(Y15171) ribosomal protein L7a [Fugu rubripes] NCBI Description

34349 Seq. No.

Match length

NCBI Description

% identity

155

38



```
389018 1.R1040
Contig ID
5'-most EST
                  q5126360
                  34350
Seq. No.
                  389061 1.R1040
Contig ID
5'-most EST
                  g5126514
Seq. No.
                  34351
                  389140 1.R1040
Contig ID
                  g5126480
5'-most EST
                  34352
Seq. No.
Contig ID
                  389171 1.R1040
5'-most EST
                  g5126513
                  BLASTX
Method
NCBI GI
                  g4539293
BLAST score
                  220
                  6.0e-37
E value
Match length
                  129
                  65
% identity
                  (AL049480) putative membrane transporter [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  34353
                  389354_1.R1040
Contig ID
5'-most EST
                  g5126676
                  34354
Seq. No.
Contig ID
                  389381 1.R1040
5'-most EST
                  q5126692
                   34355
Seq. No.
                   389420 1.R1040
Contig ID
5'-most EST
                  g5126727
Seq. No.
                   34356
Contig ID
                   389578 1.R1040
                   g5126845
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3451074
BLAST score
                   599
                   1.0e-100
E value
Match length
                   208
                   83
% identity
                  (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                   34357
Seq. No.
Contig ID
                   389721 1.R1040
5'-most EST
                   q5126901
Method
                   BLASTX
                   g2829910
NCBI GI
BLAST score
                   254
E value
                   1.0e-24
```

5171

(AC002291) Unknown protein, contains regulator of

chromosome condensation motifs [Arabidopsis thaliana]



Seq. No. 34358 389736 1.R1040 Contig ID 5'-most EST q5126906

Seq. No. 34359 390118 1.R1040 Contig ID

5'-most EST q5607175

34360 Seq. No.

390135 1.R1040 Contig ID 5'-most EST g5607195 Method BLASTX NCBI GI q3176664 BLAST score 489

E value 4.0e-49 147 Match length % identity 61

(AC004393) Contains similarity to beta scruin gb\_Z47541 NCBI Description from Limulus polyphemus. ESTs gb T04493 and gb\_AA585955

come from this gene. [Arabidopsis thaliana]

Seq. No. 34361

390140 1.R1040 Contig ID

5'-most EST g5607200

34362 Seq. No.

390196 1.R1040 Contig ID 5'-most EST q5752876

34363 Seq. No. 390256 1.R1040 Contig ID

5'-most EST g5752967

Seq. No. 34364 390386 1.R1040 Contig ID

5'-most EST g5509519

Seq. No. 34365 390429 1.R1040 Contig ID 5'-most EST g5342384

34366 Seq. No.

390578\_1.R1040 Contig ID 5'-most EST g5509632

34367 Seq. No. 390581 1.R1040 Contig ID 5'-most EST g5509635

34368 Seq. No. 390634 1.R1040 Contig ID

5'-most EST g55101<del>9</del>0

34369 Seq. No. 390646 1.R1040 Contig ID g55096<del>5</del>0 5'-most EST



```
Seq. No.
                  34370
                  390674 1.R1040
Contig ID
5'-most EST
                  q5753183
                   34371
Seq. No.
                  390745 1.R1040
Contig ID
                  q55097\overline{2}4
5'-most EST
                  BLASTX
Method
                  g3335366
NCBI GI
BLAST score
                   327
                   4.0e-30
E value
Match length
                   105
% identity
                   58
NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.
                   34372
                   390815 1.R1040
Contig ID
5'-most EST
                   q5509742
                   34373
Seq. No.
                   390845_1.R1040
Contig ID
5'-most EST
                   g5509799
Method
                   BLASTX
                   g2979551
NCBI GI
                   147
BLAST score
                   3.0e-09
E value
Match length
                   82
                   48
% identity
                   (AC003680) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   34374
Seq. No.
Contig ID
                   390904 1.R1040
5'-most EST
                   g5510258
Seq. No.
                   34375
                   390916 1.R1040
Contig ID
5'-most EST
                   q5509800
Method
                   BLASTN
NCBI GI
                   q13154
BLAST score
                   293
                   1.0e-164
E value
Match length
                   444
% identity
                   91
NCBI Description Nicotiana tabacum mitochondrial DNA for ORF
Seq. No.
                   34376
                   390940 1.R1040
Contig ID
5'-most EST
                   g5510293
```

Seq. No. 34377

Contig ID

5'-most EST  $g56770\overline{5}6$ 

Seq. No. 34378

Contig ID 391040\_1.R1040

391025\_1.R1040

Method

NCBI GI

BLASTX

g3688284



```
5'-most EST
                   q5510310
                   34379
Seq. No.
                   391062 1.R1040
Contig ID
5'-most EST
                   g5509851
                   34380
Seq. No.
                   391100 1.R1040
Contig ID
5'-most EST
                   g5510049
Seq. No.
                   34381
                   391112 1.R1040
Contig ID
5'-most EST
                   q5677115
Method
                   BLASTX
                   q2245026
NCBI GI
BLAST score
                   223
E value
                   3.0e-18
Match length
                   62
% identity
                   66
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   34382
                   391131 1.R1040
Contig ID
5'-most EST
                   q5676954
                   34383
Seq. No.
                   391165 1.R1040
Contig ID
5'-most EST
                   q5510362
                   34384
Seq. No.
                   391177 1.R1040
Contig ID
                   g55103<del>6</del>6
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1304226
BLAST score
                   54
                   1.0e-21
E value
                   98
Match length
                   89
% identity
NCBI Description Soybean mRNA for epoxide hydrolase, complete cds
                   34385
Seq. No.
                   391178 1.R1040
Contig ID
5'-most EST
                   g55100<del>6</del>9
                   34386
Seq. No.
                   391205 1.R1040
Contig ID
5'-most EST
                   g5510395
                   34387
Seq. No.
                   391259 1.R1040
Contig ID
5'-most EST
                   q5676991
Seq. No.
                   34388
                   391956 1.R1040
Contig ID
5'-most EST
                   g53423<del>9</del>2
```



```
BLAST score
                   2.0e-10
E value
Match length
                   38
                   79
% identity
                   (AJ011567) lanatoside 15'-O-acetylesterase [Digitalis
NCBI Description
                   34389
Seq. No.
                   392276 1.R1040
Contig ID
5'-most EST
                   g56774\overline{4}8
Seq. No.
                   34390
                   392704 1.R1040
Contig ID
5'-most EST
                   q5677731
                   34391
Seq. No.
                   392824 1.R1040
Contig ID
5'-most EST
                   q56781\overline{5}6
                   BLASTN
Method
                   g2943791
NCBI GI
BLAST score
                   34
                   1.0e-09
E value
Match length
                   70
% identity
                   87
NCBI Description Cucurbita sp. mRNA for PV72, complete cds
                   34392
Seq. No.
Contig ID
                   392855 1.R1040
5'-most EST
                   q5342437
Method
                   BLASTX
NCBI GI
                   g3482913
BLAST score
                   560
E value
                   1.0e-57
Match length
                   171
% identity
                   58
                   (AC003970) Similar to MtN21, gi 2598575, Megicago
NCBI Description
                   truncatula nodulation induced gene [Arabidopsis thaliana]
Seq. No.
                   34393
                   393033 1.R1040
Contig ID
5'-most EST
                   g5342645
                   34394
Seq. No.
                   393085 1.R1040
Contig ID
5'-most EST
                   g5342660
Seq. No.
                   34395
                   393712 1.R1040
Contig ID
5'-most EST
                   g5175420
                   34396
Seq. No.
                   394354 1.R1040
Contig ID
```

5'-most EST g5752568

Seq. No. Seq. ID

34397

2DA-01-Q1-B1-A4

Method BLASTX



```
NCBI GI
                   q1155090
BLAST score
                   231
E value
                   2.0e-19
                   67
Match length
                   61
% identity
                  (X94986) beta glucosidase [Manihot esculenta]
NCBI Description
                   34398
Seq. No.
                   2DA-01-Q1-B1-B2
Seq. ID
Method
                   BLASTN
                   g2264316
NCBI GI
BLAST score
                   51
E value
                   4.0e-20
Match length
                   82
                   72
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MRO11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   34399
                   2DA-01-Q1-B1-D3
Seq. ID
Method
                   BLASTX
                   q4539395
NCBI GI
BLAST score
                   415
                   6.0e-41
E value
Match length
                   112
% identity
                   71
                   (AL035526) putative protein [Arabidopsis thaliana]
NCBI Description
                   34400
Seq. No.
                   2DA-01-Q1-B1-D5
Seq. ID
                   BLASTX
Method
                   g1495366
NCBI GI
                   207
BLAST score
E value
                   1.0e-16
                   99
Match length
                   38
% identity
                   (Z69370) nitrite transporter [Cucumis sativus]
NCBI Description
Seq. No.
                   34401
Seq. ID
                   2DA-01-Q1-B1-G11
Method
                   BLASTX
NCBI GI
                   g4322421
BLAST score
                   250
E value
                   2.0e-21
Match length
                   66
                   74
% identity
                   (AF085230) cadmium resistance factor 1 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   34402
                   2DA-01-Q1-B1-G2
Seq. ID
Method
                   BLASTN
                   g986968
NCBI GI
                   180
BLAST score
                   1.0e-96
E value
                   242
Match length
```

94

% identity



NCBI Description Glycine max TGACG-motif binding protein (STGA1) mRNA, complete cds

Seq. No. 34403

Seq. ID 2DA-02-Q1-B1-A10

Method BLASTX
NCBI GI g2146742
BLAST score 495
E value 3.0e-50
Match length 129
% identity 74

NCBI Description pattern-formation protein GNOM - Arabidopsis thaliana

>gi 1209631 (U36432) GNOM gene product [Arabidopsis

thaliana]

Seq. No. 34404

Seq. ID 2DA-02-Q1-B1-A12

Method BLASTX
NCBI GI g4539386
BLAST score 203
E value 6.0e-16
Match length 85
% identity 64

NCBI Description (AL035526) extensin-like protein [Arabidopsis thaliana]

Seq. No. 34405

Seq. ID 2DA-02-Q1-B1-B1

Method BLASTX
NCBI GI g3970652
BLAST score 109
E value 8.0e-13
Match length 120
% identity 42

NCBI Description (X77499) amino acid permease [Arabidopsis thaliana]

Seq. No. 34406

Seq. ID 2DA-02-Q1-B1-C11

Method BLASTN
NCBI GI g1335998
BLAST score 36
E value 4.0e-11
Match length 132
% identity 83

NCBI Description Arabidopsis thaliana EMB30 gene, complete cds

Seq. No. 34407

Seq. ID 2DA-02-Q1-B1-F4

Method BLASTN
NCBI GI g296442
BLAST score 37
E value 2.0e-11
Match length 93
% identity 90

NCBI Description G.max ADR11 mRNA

Seq. No. 34408

Seq. ID 2DA-02-Q1-B1-H8

BLAST score

E value

328 5.0e-42



```
BLASTN
Method
                   g1143321
NCBI GI
                   53
BLAST score
                   3.0e-21
E value
Match length
                   151
                   89
% identity
                   Glycine max alfa-carboxyltransferase (accA-2) precursor
NCBI Description
                   mRNA, complete cds
Seq. No.
                   34409
                   2DC-01-Q1-B1-E8
Seq. ID
Method
                   BLASTN
NCBI GI
                   q310575
BLAST score
                   109
                   2.0e-54
E value
                   309
Match length
                   86
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                   34410
Seq. No.
Seq. ID
                   2DC-01-Q1-E1-A1
Method
                   BLASTX
NCBI GI
                   g3426039
BLAST score
                   177
                   6.0e-13
E value
                   60
Match length
                   57
% identity
                   (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34411
                   2DC-01-Q1-E1-B9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3452136
                   214
BLAST score
E value
                   1.0e-117
Match length
                   256
                   96
% identity
                   Glycine max mRNA for glucose-6-phosphate-dehydrogenase,
NCBI Description
                   partial
                   34412
Seq. No.
Seq. ID
                   2DC-02-Q1-B1-A9
                   BLASTX
Method
NCBI GI
                   g3402686
BLAST score
                   326
                   2.0e-30
E value
                   115
Match length
                   57
% identity
                   (AC004697) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   34413
Seq. No.
                   2DC-02-Q1-B1-B8
Seq. ID
                   BLASTX
Method
                   g3688600
NCBI GI
```



Match length 129 % identity 66 NCBI Description (AB009030) beta-Amyrin Synthase [Panax ginseng]

Seq. No. 34414 Seq. ID 2DC-02-Q1-B1-D10

Method BLASTN
NCBI GI g609224
BLAST score 156
E value 2.0e-82
Match length 296
% identity 88

NCBI Description P.sativum mRNA for SAMS-2 >gi\_609558\_gb\_L36681\_PEADENSYNB Pisum sativum S-adenosylmethionine synthase mRNA, complete

cds

Seq. No. 34415

Seq. ID 2DC-02-Q1-B1-D2

Method BLASTX
NCBI GI g1711618
BLAST score 375
E value 3.0e-36
Match length 107
% identity 68

NCBI Description LOW AFFINITY SULPHATE TRANSPORTER 3 >gi\_1085993\_pir\_\_S51765

low affinity sulphate transporter - Stylosanthes hamata >gi\_607188 emb\_CAA57831\_ (X82454) low affinity sulphate

transporter [Stylosanthes hamata]

Seq. No. 34416

Seq. ID 2DC-02-Q1-B1-F11

Method BLASTX
NCBI GI g2832682
BLAST score 200
E value 1.0e-15
Match length 69
% identity 59

NCBI Description (AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34417

Seq. ID 2DC-02-Q1-B1-F4

Method BLASTN
NCBI GI g3790440
BLAST score 134
E value 3.0e-69
Match length 382
% identity 84

NCBI Description Canavalia lineata chaperonin 60 alpha subunit mRNA, nuclear

gene encoding chloroplast protein, complete cds

Seq. No. 34418

Seq. ID 2DC-02-Q1-B1-H12

Method BLASTX
NCBI GI g3355476
BLAST score 174
E value 1.0e-12
Match length 68



```
% identity
NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]
                  34419
Seq. No.
                  2DC-02-Q1-B1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q457569
                  50
BLAST score
                  2.0e-19
E value
Match length
                  114
% identity
NCBI Description Soybean mRNA for endo-xyloglucan transferase, partial cds
                  34420
Seq. No.
                  6HA-01-Q1-B1-A10
Seq. ID
                  BLASTN
Method
                  q18764
NCBI GI
BLAST score
                  366
                  0.0e + 00
E value
                  366
Match length
                  100
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
Seq. No.
                   34421
                   6HA-01-Q1-B1-B11
Seq. ID
Method
                  BLASTX
                   q2129844
NCBI GI
                   170
BLAST score
E value
                   1.0e-23
                   94
Match length
                   65
% identity
NCBI Description stress-induced protein stil - soybean
                   34422
Seq. No.
                   6HA-01-Q1-B1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4510342
                   550
BLAST score
                   1.0e-56
E value
Match length
                   117
                   85
% identity
                   (AC006921) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   34423
Seq. ID
                   6HA-01-Q1-B1-D12
Method
                   BLASTX
NCBI GI
                   g3738153
                   201
BLAST score
                   9.0e-16
```

E value

112 Match length 37 % identity

NCBI Description

(AL031852) putative cleavage and polyadenylation specificity factor [Schizosaccharomyces pombe]

34424 Seq. No.

6HA-01-Q1-B1-G9 Seq. ID

Method

NCBI GI

BLAST score

```
Method
NCBI GI
                  a2781355
                  306
BLAST score
                  5.0e-28
E value
                  122
Match length
                  58
% identity
                  (AC003113) F2401.11 [Arabidopsis thaliana]
NCBI Description
                  34425
Seq. No.
                  6HA-01-Q1-B1-H1
Seq. ID
                  BLASTX
Method
                  g3914667
NCBI GI
BLAST score
                   235
                  1.0e-19
E value
                   94
Match length
                   55
% identity
                  50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_2459427 (AC002332) putative chloroplast 50S ribosomal
                   protein L28 [Arabidopsis thaliana]
                   34426
Seq. No.
                   6HA-01-Q1-B1-H11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2656003
BLAST score
                   231
                  2.0e-19
E value
                   63
Match length
                   68
% identity
                   (Z98980) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                   34427
Seq. No.
                   6HA-01-Q1-E1-A9
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2588608
                   189
BLAST score
E value
                   1.0e-102
Match length
                   193
                   99
% identity
                   Human BAC clone RG385F02 from 7p15, complete sequence [Homo
NCBI Description
                   sapiens]
                   34428
Seq. No.
Seq. ID
                   6HA-01-Q1-E1-B9
                   BLASTN
Method
NCBI GI
                   q392590
                   106
BLAST score
                   2.0e-52
E value
                   296
Match length
 % identity
                   Human immunoglobulin heavy chain variable region (clone
NCBI Description
                   Amu1d4-3) mRNA, partial cds
                   34429
 Seq. No.
                    6HA-01-Q1-E1-D12
 Seq. ID
                   BLASTN
```

g392865

397



```
0.0e + 00
E value
Match length
                  424
% identity
                   98
NCBI Description
                  Human neutrophil oxidase factor (NCF2) gene, exon 16
                  34430
Seq. No.
                   6HA-01-Q1-E1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g457569
                  138
BLAST score
                  1.0e-71
E value
                  214
Match length
% identity
                  92
NCBI Description
                  Soybean mRNA for endo-xyloglucan transferase, partial cds
                   34431
Seq. No.
                   6HA-01-Q1-E1-E10
Seq. ID
Method
                  BLASTN
                   g37495
NCBI GI
BLAST score
                   389
                   0.0e + 00
E value
Match length
                   413
% identity
                   99
NCBI Description
                  Human mRNA for translationally controlled tumor protein
                   >gi_4507668_ref_NM_003295.1_TPT1_ Homo sapiens tumor
                  protein, translationally-controlled 1 (TPT1) mRNA
Seq. No.
                   34432
Seq. ID
                   6HA-01-Q1-E1-E11
                   BLASTN
Method
NCBI GI
                   g3900847
BLAST score
                   263
E value
                   1.0e-146
                   371
Match length
                   50
% identity
                  Homo sapiens BAC clone GS421I03 from Xq25-q26, complete
NCBI Description
                   sequence [Homo sapiens]
Seq. No.
                   34433
                   6HA-01-Q1-E1-E12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q736399
BLAST score
                   322
E value
                   0.0e + 00
Match length
                   377
% identity
                   95
NCBI Description Human cofilin mRNA, partial cds
                   34434
Seq. No.
                   6HA-01-Q1-E1-E9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3282242
BLAST score
                   198
E value
                   1.0e-107
```

NCBI Description Human alpha enolase like 1 (ENO1L1) mRNA, partial cds

273

93

Match length % identity

NCBI Description



```
34435
Seq. No.
Seq. ID
                   6HA-01-Q1-E1-F10
Method
                   BLASTN
NCBI GI
                   q187237
BLAST score
                   405
                   0.0e+00
E value
Match length
                   416
                  99
% identity
NCBI Description
                  Human lymphocyte-specific protein 1 (LSP1) mRNA, complete
Seq. No.
                   34436
                   6HA-01-Q1-E1-G12
Seq. ID
Method
                   BLASTN
                   q1764087
NCBI GI
BLAST score
                   411
E value
                   0.0e + 00
Match length
                   426
                   99
% identity
NCBI Description
                  Human cosmid LL12NC01-15A4, ETV6 gene, exon 1A and partial
Seq. No.
                   34437
Seq. ID
                   6HA-01-Q1-E1-H10
Method
                   BLASTN
NCBI GI
                   g2393735
BLAST score
                   33
                   6.0e-09
E value
Match length
                   37
                   97
% identity
NCBI Description
                   Human BAC clone RG043K06 from 7q21-q22, complete sequence
                   [Homo sapiens]
                   34438
Seq. No.
                   6HA-01-Q1-E1-H3
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1161251
BLAST score
                   98
E value
                   7.0e-48
Match length
                   254
% identity
                   86
                   Glycine max nucleosome assembly protein 1 (SNAP-1) mRNA,
NCBI Description
                   complete cds
                   34439
Seq. No.
                   6HA-01-Q1-E1-H9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g177899
BLAST score
                   338
E value
                   0.0e + 00
Match length
                   413
% identity
```

(PLP2) mRNA

Homo sapiens differentiation-dependent A4 protein mRNA, complete cds. >gi\_4505892\_ref\_NM\_002668.1\_PLP2\_ Homo

sapiens proteolipid protein 2 (colonic epithelium-enriched)



```
Seq. No.
                  34440
Seq. ID
                  6HA-02-Q1-B1-A5
Method
                  BLASTX
NCBI GI
                  g1865677
BLAST score
                  329
E value
                  5.0e-31
Match length
                  84
% identity
                  (Y08568) trehalose-6-phosphate synthase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  34441
Seq. ID
                  6HA-02-Q1-B1-A6
Method
                  BLASTX
NCBI GI
                  g4038055
BLAST score
                  172
E value
                  2.0e-12
Match length
                  102
% identity
                  38
                  (AC005897) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  >gi_4557077_gb_AAD22516.1_AC007045_16 (AC007045) putative
                  cytochrome p450 [Arabidopsis thaliana]
Seq. No.
                  34442
Seq. ID
                  6HA-02-Q1-B1-A8
Method
                  BLASTX
NCBI GI
                  q4455274
BLAST score
                  438
E value
                  2.0e-43
Match length
                  111
                  78
% identity
NCBI Description
                   (AL035527) spliceosome associated protein-like [Arabidopsis
                  thaliana]
Seq. No.
                  34443
                  6HA-02-Q1-B1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2388577
BLAST score
                  392
E value
                  4.0e-38
Match length
                  128
% identity
                  60
                  (AC000098) Similar to Arabidopsis putative ion-channel
NCBI Description
                  PID:g2262157 (gb AC002329). [Arabidopsis thaliana]
                  34444
Seq. No.
                  6HA-02-Q1-B1-C11
Seq. ID
Method
                  BLASTX
                  g3242708
NCBI GI
BLAST score
                  141
E value
                  1.0e-08
```

Match length 90 % identity 33

NCBI Description (AC003040) putative serine/threonine protein kinase

[Arabidopsis thaliana]



```
34445
Seq. No.
                   6HA-02-Q1-B1-D3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3337367
BLAST score
                   268
E value
                   1.0e-23
Match length
                   109
                   48
% identity
```

(AC004481) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 34446 6HA-02-Q1-B1-D6 Seq. ID Method BLASTX NCBI GI q3024021 BLAST score 165 E value 1.0e-14 Match length 81 57

% identity INITIATION FACTOR 5A-4 (EIF-5A) (EIF-4D) NCBI Description

>gi 2225883 dbj BAA20878 (AB004825) eukaryotic initiation

factor 5A4 [Solanum tuberosum]

Seq. No. 34447 Seq. ID

6HA-02-Q1-B1-E2

Method BLASTX g1657615 NCBI GI BLAST score 381 8.0e-37 E value Match length 87 82 % identity

(U72502) Glp [Arabidopsis thaliana] >gi 3068706 (AF049236) NCBI Description putative transmembrane protein Glp [Arabidopsis thaliana]

34448 Seq. No.

Seq. ID 6HA-02-Q1-B1-F6

BLASTX Method g3176686 NCBI GI BLAST score 240 2.0e-20 E value Match length 65 % identity

(AC003671) Similar to high affinity potassium transporter, NCBI Description

HAK1 protein gb U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 34449

6HA-02-Q1-B1-G11 Seq. ID

Method BLASTX NCBI GI g2252843 BLAST score 207 E value 2.0e-16 Match length 109 % identity

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 34450

6HA-02-Q1-B1-H6 Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g99741
BLAST score
                  268
                  1.0e-23
E value
Match length
                  91
% identity
                  62
                  P-glycoprotein pgp1 - Arabidopsis thaliana
NCBI Description
Seq. No.
                  34451
Seq. ID
                  6HA-02-Q1-E1-A5
Method
                  BLASTX
NCBI GI
                  g1865677
BLAST score
                  187
                  4.0e-14
E value
Match length
                  49
                  73
% identity
NCBI Description
                  (Y08568) trehalose-6-phosphate synthase [Arabidopsis
                  thaliana]
                  34452
Seq. No.
                  6HA-02-Q1-E1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2388577
BLAST score
                  170
                  5.0e-12
E value
Match length
                  94
% identity
                  46
NCBI Description
                  (AC000098) Similar to Arabidopsis putative ion-channel
                  PID:g2262157 (gb AC002329). [Arabidopsis thaliana]
Seq. No.
                  34453
Seq. ID
                  6HA-02-Q1-E1-E1
                  BLASTX
Method
NCBI GI
                  g2465015
BLAST score
                  180
E value
                  3.0e-13
Match length
                  97
                  39
% identity
NCBI Description
                  (AJ001449) ripening-induced protein [Fragaria vesca]
Seq. No.
                  34454
Seq. ID
                  6HA-02-Q1-E1-F1
Method
                  BLASTX
NCBI GI
                  g123554
BLAST score
                  288
E value
                  6.0e-26
Match length
                  64
% identity
                  86
                  18.1 KD CLASS I HEAT SHOCK PROTEIN >gi 99978 pir_S16248
NCBI Description
                  heat shock protein 18 (clone pMsHsp18.1) - alfalfa
                  (fragment) >gi_19616_emb_CAA41546_ (X58710) heat shock
                  protein [Medicago sativa]
```

Seq. ID 6HA-02-Q1-E1-H6

Method BLASTX NCBI GI g419760



BLAST score 360 E value 2.0e-34 Match length 82 % identity 49

NCBI Description P-glycoprotein atpgp1 - Arabidopsis thaliana

>gi 3849833 emb CAA43646 (X61370) P-glycoprotein

[Arabidopsis thaliana]

Seq. No. 34456

Seq. ID 6HC-01-Q1-B1-B10

Method BLASTX
NCBI GI g282899
BLAST score 188
E value 1.0e-26
Match length 131
% identity 11

NCBI Description embryonic abundant protein, 59K - soybean >gi\_170010

(M80664) maturation polypeptide [Glycine max]

>gi\_384333\_prf\_\_1905420A late embryogenesis abundant

protein [Glycine max]

Seq. No. 34457

Seq. ID 6HC-01-Q1-B1-B7

Method BLASTX
NCBI GI g4336436
BLAST score 186
E value 3.0e-14
Match length 89
% identity 39

NCBI Description (AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No. 34458

Seq. ID 6HC-01-Q1-B1-D1

Method BLASTN
NCBI GI g1022364
BLAST score 201
E value 1.0e-109
Match length 349
% identity 89

NCBI Description V.faba mRNA for sucrose phosphate synthase

Seq. No. 34459

Seq. ID 6HC-01-Q1-B1-E10

Method BLASTX
NCBI GI g2119848
BLAST score 163
E value 2.0e-11
Match length 80
% identity 47

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 -

Arabidopsis thaliana >gi\_16366\_emb\_CAA45789\_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi\_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi\_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]



```
Seq. No.
                  34460
Seq. ID
                  6HC-01-Q1-B1-G7
Method
                  BLASTN
NCBI GI
                  g166421
BLAST score
                  61
E value
                  1.0e-25
                  181
Match length
% identity
                  Medicago sativa ubiquitin carrier protein mRNA, complete
NCBI Description
Seq. No.
                  34461
Seq. ID
                  6HC-01-Q1-E1-A3
                  BLASTX
Method
NCBI GI
                  g549637
BLAST score
                  161
E value
                  4.0e-11
                  92
Match length
                  40
% identity
                  HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION
NCBI Description
                  >gi_539278_pir__S38156 hypothetical protein YKR079c - yeast
                   (Saccharomyces cerevisiae) >gi_486557_emb_CAA82158_
                   (Z28304) ORF YKR079c [Saccharomyces cerevisiae]
Seq. No.
                   34462
                   6HC-01-Q1-E1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1432056
                   272
BLAST score
E value
                   3.0e-24
Match length
                   61
% identity
NCBI Description (U56834) WRKY3 [Petroselinum crispum]
Seq. No.
                   34463
                   6HC-02-Q1-B1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538939
                   139
BLAST score
                   5.0e-09
E value
                   53
Match length
                   51
% identity
                   (AL049483) Col-O casein kinase I-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   34464
Seq. ID
                   6HC-02-Q1-B1-B8
                  BLASTN
Method
NCBI GI
                   g2661020
                   89
BLAST score
                   1.0e-42
E value
                   201
Match length
% identity
                   86
```

5188

NCBI Description Glycine max catalase (cat4) mRNA, complete cds

Seq. ID

Method

34470

BLASTN

ASG32442DA-02-Q1-E1-A8



```
Seq. ID
                   ASG32442DA-01-Q1-E1-A11
Method
                   BLASTN
NCBI GI
                   q169936
BLAST score
                   134
E value
                   2.0e-69
Match length
                   221
% identity
NCBI Description Glycine max chalcone synthase (chs7) gene, complete cds
Seq. No.
                   34466
Seq. ID
                   ASG32442DA-01-Q1-E1-C10
Method
                   BLASTX
NCBI GI
                   g1076283
BLAST score
                   193
                   7.0e-15
E value
                   56
Match length
% identity
NCBI Description
                   adenylylsulfate kinase (EC 2.7.1.25) precursor -
                   Arabidopsis thaliana >gi_414737_emb_CAA53426_ (X75782) APS
                   kinase [Arabidopsis thaliana] >gi_450235 (U05238) APS kinase [Arabidopsis thaliana] >gi_1575322 (U59759) APS
                   kinase [Arabidopsis thaliana] >gi_3252812 (AC004705) APS
                   kinase [Arabidopsis thaliana]
Seq. No.
                   34467
                   ASG32442DA-01-Q1-E1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539395
BLAST score
                   143
E value
                   4.0e-09
Match length
                   36
                   75
% identity
NCBI Description
                   (AL035526) putative protein [Arabidopsis thaliana]
Seq. No.
                   34468
Seq. ID
                   ASG32442DA-01-Q1-E1-E7
Method
                   BLASTX
NCBI GI
                   g1621539
BLAST score
                   223
                   3.0e-18
E value
Match length
                   55
                   78
% identity
                   (U28415) annexin-like protein [Arabidopsis thaliana]
NCBI Description
                   34469
Seq. No.
                   ASG32442DA-01-Q1-E1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3461848
BLAST score
                   206
E value
                   2.0e-16
Match length
                   65
% identity
                   63
                   (AC005315) putative ATPase [Arabidopsis thaliana]
NCBI Description
```

BLAST score

E value

67 3.0e-29



```
g56539
NCBI GI
BLAST score
                  76
                  1.0e-34
E value
                  265
Match length
% identity
                  92
                  R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                  >gi 206360 gb J00764_RATPRLHR5 Rat (hooded) prolactin gene
                  : exon v and flanks
                  34471
Seq. No.
                  ASG32442DA-02-Q1-E1-F2
Seq. ID
                  BLASTX
Method
                  q2282586
NCBI GI
BLAST score
                  253
                  7.0e-22
E value
Match length
                  73
% identity
                  (U82011) methyltransferase [Prunus armeniaca]
NCBI Description
                  34472
Seq. No.
                  ASG32442DA-02-Q1-E1-G8
Seq. ID
Method
                  BLASTN
                  g169069
NCBI GI
                  38
BLAST score
                   5.0e-12
E value
                  70
Match length
% identity
NCBI Description Pea Cu-Zn superoxide dismutase mRNA, complete cds
Seq. No.
                   34473
                   ASG3244V4L-01-Q1-E1-G1
Seq. ID
Method
                   BLASTX
                   g4115939
NCBI GI
BLAST score
                   163
                   6.0e-12
E value
Match length
                   47
% identity
                   40
                   (AF118223) contains similarity to Methanobacterium
NCBI Description
                   thermoautotrophicum transcriptional regulator (GB:AE000850)
                   [Arabidopsis thaliana]
Seq. No.
                   34474
                   ASG3244V4R-02-Q1-E1-A8
Seq. ID
                   BLASTN
Method
                   g3776081
NCBI GI
                   77
BLAST score
                   3.0e-35
E value
                   179
Match length
                   91
% identity
                   Medicago truncatula mRNA for MtN30 gene, partial
NCBI Description
Seq. No.
                   34475
                   LIB3027-001-Q1-B1-D7
Seq. ID
                   BLASTN
Method
NCBI GI
                   q18628
```



316 Match length 85 % identity

Soybean mRNA for A5A4B3 subunits of glycinin NCBI Description

>gi\_2170692\_dbj\_E02461\_E02461 cDNA encoding glycinine

subunit A5A4B3 precursor

34476 Seq. No.

LIB3027-001-Q1-B1-E4 Seq. ID

BLASTN Method NCBI GI g206371 103 BLAST score 8.0e-51 E value 140 Match length 100 % identity

NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks

Seq. No.

34477 LIB3027-001-Q1-B1-E6 Seq. ID

Method BLASTN g2305019 NCBI GI BLAST score 219 1.0e-120 E value Match length 291 94 % identity

NCBI Description Glycine max 2S albumin pre-propeptide mRNA, complete cds

34478 Seq. No.

LIB3027-001-Q1-B1-G4 Seq. ID

BLASTN Method q169962 NCBI GI 92 BLAST score 3.0e-44E value 96 Match length 99 % identity

Soybean 16 kDa seed maturation protein (gGmpm9) gene exons NCBI Description

1-2, complete cds

34479 Seq. No.

LIB3027-001-Q1-B1-H4 Seq. ID

BLASTX Method g138364 NCBI GI 280 BLAST score 2.0e-43 E value 128 Match length 73 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi\_75639\_pir\_\_GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi\_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No.

34480

LIB3027-002-Q1-B1-D1 Seq. ID

BLASTN Method q56539 NCBI GI BLAST score 3.0e - 35E value Match length 307



% identity 89

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi 206360 gb\_J00764 RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 34481

Seq. ID LIB3027-002-Q1-B1-D2

Method BLASTN
NCBI GI g2920665
BLAST score 300
E value 1.0e-168
Match length 304
% identity 100

NCBI Description Glycine max 2,4-D inducible glutathione S-transferase

(GSTa) mRNA, complete cds

Seq. No. 34482

Seq. ID LIB3027-003-Q1-B1-A4

Method BLASTX
NCBI GI g3249066
BLAST score 148
E value 1.0e-09
Match length 103
% identity 37

NCBI Description (AC004473) Similar to S. cerevisiae SIK1P protein

gb 984964. ESTs gb F15433 and gb AA395158 come from this

gene. [Arabidopsis thaliana]

Seq. No. 34483

Seq. ID LIB3027-003-Q1-B1-B7

Method BLASTN
NCBI GI g2305019
BLAST score 71
E value 5.0e-32

Match length 75 % identity 99

NCBI Description Glycine max 2S albumin pre-propeptide mRNA, complete cds

Seq. No. 34484

Seq. ID LIB3027-003-Q1-B1-C5

Method BLASTN
NCBI GI g206371
BLAST score 103
E value 9.0e-51
Match length 292
% identity 96

NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks

Seq. No. 34485

Seq. ID LIB3027-003-Q1-B1-D3

Method BLASTN
NCBI GI g206371
BLAST score 40
E value 3.0e-13
Match length 52
% identity 94

NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks

Seq. ID

34491

LIB3027-004-Q1-B1-G6



```
34486
Seq. No.
                  LIB3027-004-Q1-B1-A4
Seq. ID
Method
                  BLASTX
                  g4262162
NCBI GI
                  429
BLAST score
                  2.0e-42
E value
                  122
Match length
% identity
                   (AC005275) putative glycosylation enzyme [Arabidopsis
NCBI Description
                  thaliana]
                   34487
Seq. No.
                  LIB3027-004-Q1-B1-A5
Seq. ID
Method
                   BLASTN
                   g736001
NCBI GI
BLAST score
                   230
                   1.0e-126
E value
                   270
Match length
                   97
% identity
NCBI Description G.soja (SH1) Gy5 mRNA for glycinin
                   34488
Seq. No.
                   LIB3027-004-Q1-B1-D11
Seq. ID
                   BLASTN
Method
NCBI GI
                   g18535
                   307
BLAST score
E value
                   1.0e-172
Match length
                   310
                   100
% identity
                  Soybean mRNA for the alpha subunit of beta-conglycinin
NCBI Description
                   34489
Seq. No.
                   LIB3027-004-Q1-B1-D3
Seq. ID
                   BLASTN
Method
                   g56539
NCBI GI
BLAST score
                   60
                   3.0e-25
E value
                   184
Match length
                   90
% identity
                   R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                   >gi 206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
                   34490
Seq. No.
                   LIB3027-004-Q1-B1-D6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2160543
BLAST score
                   121
E value
                   1.0e-61
Match length
                   293
% identity
                   85
                   Pisum sativum ent-kaurene synthase A (LS) mRNA, complete
NCBI Description
```

Method

NCBI GI

BLASTN

g531828



```
BLASTX
Method
                  g4469005
NCBI GI
                  214
BLAST score
                  3.0e-17
E value
                  84
Match length
                  54
% identity
                  (AL035602) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  34492
Seq. No.
                  LIB3027-005-Q1-B1-B5
Seq. ID
                  BLASTN
Method
                  g169972
NCBI GI
                   401
BLAST score
                   0.0e + 00
E value
Match length
                   405
                   100
% identity
NCBI Description Soybean glycinin A-la-B-x subunit mRNA, complete cds
                   34493
Seq. No.
                   LIB3027-005-Q1-B1-D10
Seq. ID
Method
                   BLASTN
                   g56539
NCBI GI
                   99
BLAST score
                   2.0e-48
E value
                   302
Match length
                   94
% identity
                   R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                   >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
                   34494
Seq. No.
                   LIB3027-006-Q1-B1-C11
Seq. ID
                   BLASTN
Method
                   g56539
NCBI GI
                   62
BLAST score
                   2.0e-26
E value
                   241
Match length
 % identity
                   R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                   >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
                   34495
 Seq. No.
                   LIB3027-006-Q1-B1-D10
 Seq. ID
                   BLASTX
 Method
                   q4056415
 NCBI GI
                   208
 BLAST score
                   2.0e-23
 E value
                   70
 Match length
 % identity
                    (AC005322) Similar to the end of DNA repair protein
 NCBI Description
                   gb_X74615 (rad8) gene. [Arabidopsis thaliana]
                    34496
 Seq. No.
                    LIB3027-006-Q1-B1-D12
 Seq. ID
```



```
43
BLAST score
                  2.0e-15
E value
                  87
Match length
% identity
                  87
NCBI Description Cloning vector pSport1, complete cds
                  34497
Seq. No.
                  LIB3027-006-Q1-B1-E10
Seq. ID
                  BLASTN
Method
                  g736001
NCBI GI
                  155
BLAST score
                  7.0e-82
E value
                  243
Match length
                   91
% identity
NCBI Description G.soja (SH1) Gy5 mRNA for glycinin
                   34498
Seq. No.
                   LIB3027-006-Q1-B1-E7
Seq. ID
                   BLASTN
Method
                   q18749
NCBI GI
BLAST score
                   144
                   2.0e-75
E value
                   202
Match length
                   96
% identity
NCBI Description G.max mRNA for seed maturation polypeptide
                   34499
Seq. No.
                   LIB3027-006-Q1-B1-F9
Seq. ID
Method
                   BLASTN
                   g12974
NCBI GI
BLAST score
                   51
                   8.0e-20
E value
                   51
Match length
                   100
% identity
                   Soybean mitochondrial COII gene for cytochrome oxidase
NCBI Description
                   subunit II and tRNA-Met (CAT) gene (upstream)
                   34500
Seq. No.
                   LIB3027-006-Q1-B1-H10
 Seq. ID
                   BLASTN
Method
                   g18535
NCBI GI
                   76
BLAST score
                   7.0e-35
E value
                   88
Match length
                   97
 % identity
                   Soybean mRNA for the alpha subunit of beta-conglycinin
 NCBI Description
                   34501
 Seq. No.
                   LIB3027-006-Q1-B1-H3
 Seq. ID
                   BLASTN
 Method
                   g56539
 NCBI GI
 BLAST score
                   33
                   4.0e-09
 E value
                   152
 Match length
                   86
 % identity
                   R.norvegicus gene encoding prolactin, exon 5
 NCBI Description
```

>gi\_206360\_gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene



## : exon v and flanks

```
34502
Seq. No.
                  LIB3027-006-Q1-B1-H5
Seq. ID
                  BLASTX
Method
                  g138364
NCBI GI
                  384
BLAST score
                  1.0e-57
E value
                  135
Match length
                  83
% identity
NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                  (M62738) coat protein [Bean pod mottle virus]
                  34503
Seq. No.
                  LIB3027-007-Q1-B1-A2
Seq. ID
                  BLASTX
Method
                  g3953471
NCBI GI
                  338
BLAST score
                  5.0e-32
E value
                  91
Match length
                   69
% identity
                  (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
                   34504
Seq. No.
                  LIB3027-007-Q1-B1-H5
Seq. ID
                  BLASTX
Method
                  g633890
NCBI GI
                   276
BLAST score
                   2.0e-24
E value
                   75
Match length
                   64
% identity
                  (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
NCBI Description
                   vulgare]
                   34505
Seq. No.
                   LIB3027-008-Q1-B1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3912997
                   256
BLAST score
                   3.0e-22
E value
                   72
Match length
                   69
% identity
                   FLORAL HOMEOTIC PROTEIN AGL15 >gi 2129535 pir_S71200 AGL15
NCBI Description
                   protein - Arabidopsis thaliana >gi_790635 (U22528) AGL15
                   [Arabidopsis thaliana]
                   34506
 Seq. No.
                   LIB3027-008-Q1-B1-G2
 Seq. ID
Method
                   BLASTN
                   q4324966
 NCBI GI
                   227
 BLAST score
                   1.0e-125
 E value
                   227
 Match length
```

NCBI Description Glycine max ADP-ribosylation factor mRNA, partial cds

100

% identity



```
34507
Seq. No.
                  LIB3027-008-Q1-B1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3413170
BLAST score
                  171
                  3.0e-12
E value
Match length
                  101
% identity
NCBI Description (AJ010227) 40S ribosomal protein S6 [Cicer arietinum]
```

(\*\*\*\*

Seq. No. 34508
Seq. ID LIB3027-010-Q1-B1-A1

Method BLASTN
NCBI GI g1794171
BLAST score 101
E value 1.0e-49
Match length 289
% identity 84

NCBI Description Glycine max lipoxygenase-3 mRNA, complete cds

 Seq. No.
 34509

 Seq. ID
 LIB3027-010-Q1-B1-A6

 Method
 BLASTN

NCBI GI g1389896
BLAST score 32
E value 1.0e-08
Match length 184
% identity 80

NCBI Description Glycine max 68 kDa LEA protein mRNA, complete cds

Seq. No. 34510

Seq. ID LIB3027-010-Q1-B1-E10

Method BLASTX
NCBI GI g3193306
BLAST score 484
E value 6.0e-49
Match length 126
% identity 79

NCBI Description (AF069300) contains similarity to Arabidopsis membrane-associated salt-inducible-like protein

(GB:AL021637) [Arabidopsis thaliana]

Seq. No. 34511

Seq. ID LIB3027-010-Q1-B1-G3

Method BLASTX
NCBI GI g138364
BLAST score 119
E value 4.0e-15
Match length 67
% identity 53

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi\_75639\_pir\_\_GNWXG7 genome polyprotein M -bean pod mottle virus (strain Kentucky G7) >gi\_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 34512

NCBI Description

x hybrida]



```
LIB3027-010-Q1-B1-H5
Seq. ID
                  BLASTX
Method
                  q3913425
NCBI GI
                  635
BLAST score
                  1.0e-66
E value
                  125
Match length
% identity
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                  HELICASE >gi_2275203 (AC002337) RNA helicase isolog
                   [Arabidopsis thaliana]
                  34513
Seq. No.
                  LIB3027-011-Q1-B1-C6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3452136
                  168
BLAST score
                   1.0e-89
E value
                   184
Match length
% identity
                  Glycine max mRNA for glucose-6-phosphate-dehydrogenase,
NCBI Description
                   partial
                   34514
Seq. No.
                   LIB3027-011-Q1-B1-F3
Seq. ID
                   BLASTX
Method
                   g1170746
NCBI GI
                   246
BLAST score
                   2.0e-21
E value
                   78
Match length
                   64
% identity
                   DESICCATION PROTECTANT PROTEIN LEA14 HOMOLOG >gi_472850
NCBI Description
                   (U08108) putative desiccation protectant protein, homolog
                   of Leal4, GenBank Accession Number M88321 [Glycine max]
                   34515
Seq. No.
                   LIB3028-001-Q1-B1-A3
Seq. ID
                   BLASTX
Method
                   q3769472
NCBI GI
                   418
BLAST score
E value
                   4.0e-41
                   109
Match length
                   68
% identity
                   (AF064732) putative phospholipase A2 [Dianthus
NCBI Description
                   caryophyllus]
                   34516
Seq. No.
                   LIB3028-001-Q1-B1-B2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g282964
                   195
BLAST score
E value
                   5.0e-15
                   136
Match length
                   50
 % identity
                   transforming protein (myb) homolog (clone myb.Ph3) - garden
```

petunia >gi\_20563\_emb\_CAA78386\_ (Z13996) protein 1 [Petunia



```
34517
Seq. No.
                  LIB3028-001-Q1-B1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4107099
BLAST score
                  283
E value
                  2.0e-25
                 - 102
Match length
% identity
                  (AB015141) AHP1 [Arabidopsis thaliana]
NCBI Description
                  >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis
                  thaliana]
                  34518
Seq. No.
                  LIB3028-002-Q1-B1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2739374
BLAST score
                  145
E value
                   4.0e-09
                   58
Match length
% identity
NCBI Description (AC002505) hypothetical protein [Arabidopsis thaliana]
                   34519
Seq. No.
                   LIB3028-002-Q1-B1-C11
Seq. ID
                   BLASTX
Method
                   q3128224
NCBI GI
BLAST score
                   523
                   2.0e-53
E value
                   115
Match length
% identity
                   87
                   (AC004077) putative protein serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
                   34520
Seq. No.
                   LIB3028-002-Q1-B1-E2
Seq. ID
                   BLASTN
Method
                   g303900
NCBI GI
                   93
BLAST score
                   7.0e-45
E value
                   309
Match length
% identity
                   41
                   Soybean gene for ubiquitin, complete cds
NCBI Description
                   34521
Seq. No.
                   LIB3028-002-Q1-B1-F8
Seq. ID
                   BLASTX
Method
                   g3540180
NCBI GI
                   320
BLAST score
                   1.0e-29
E value
                   116
Match length
% identity
                   53
                   (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
```

Seq. ID LIB3028-003-Q1-B1-B12

Method BLASTX NCBI GI g3201617



```
BLAST score
                  3.0e-41
E value
                  130
Match length
% identity
NCBI Description (AC004669) hypothetical protein [Arabidopsis thaliana]
                  34523
Seq. No.
                  LIB3028-003-Q1-B1-C3
Seq. ID
                  BLASTX
Method
                  g4455169
NCBI GI
                  159
BLAST score
                  9.0e-11
E value
                  92
Match length
% identity
                  39
                  (AL035521) putative aldehyde dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                  34524
Seq. No.
                  LIB3028-003-Q1-B1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2160189
                   353
BLAST score
                  1.0e-33
E value
Match length
                  126
% identity
                   (AC000132) Similar to A. thaliana receptor-like protein
NCBI Description
                   kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come
                   from this gene. [Arabidopsis thaliana]
                   34525
Seq. No.
                   LIB3028-003-Q1-B1-F2
Seq. ID
                   BLASTX
Method
                   q4467110
NCBI GI
BLAST score
                   599
                   2.0e-62
E value
Match length
                   124
                   89
% identity
                   (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                   34526
Seq. No.
                   LIB3028-003-Q1-B1-G10
Seq. ID
Method
                   BLASTN
                   g2564336
NCBI GI
                   104
BLAST score
E value
                   2.0e-51
                   284
Match length
% identity
                   Brassica campestris mRNA for Tat binding protein 1,
NCBI Description
                   complete cds
                   34527
Seq. No.
                   LIB3028-003-Q1-B1-G11
Seq. ID
Method
                   BLASTN
                   g609224
NCBI GI
BLAST score
                   186
```

1.0e-100

318

E value

Match length



% identity P.sativum mRNA for SAMS-2 >gi\_609558\_gb\_L36681\_PEADENSYNB NCBI Description Pisum sativum S-adenosylmethionine synthase mRNA, complete 34528 Seq. No. LIB3028-003-Q1-B1-G2 Seq. ID Method BLASTX NCBI GI g3043529 147 BLAST score 2.0e-09 E value 38 Match length 66 % identity (AJ002204) polyamine oxidase [Zea mays] NCBI Description Seq. No. 34529 LIB3028-003-Q1-B1-H12 Seq. ID BLASTN Method q2606080 NCBI GI BLAST score 157 E value 4.0e-83 313 Match length % identity 88 NCBI Description Glycine max sucrose synthase (SS) mRNA, complete cds Seq. No. 34530 LIB3028-004-Q1-B1-E11 Seq. ID Method BLASTX NCBI GI g3135264 353 BLAST score 2.0e-33 E value Match length 89 % identity 76 NCBI Description (AC003058) unknown protein [Arabidopsis thaliana] 34531 Seq. No. LIB3028-004-Q1-B1-H12 Seq. ID BLASTN Method NCBI GI g516853 BLAST score 254 1.0e-141 E value Match length 346 27 % identity NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds 34532 Seq. No. LIB3028-005-Q1-B1-B10 Seq. ID Method BLASTX NCBI GI g1168196

BLAST score 210 E value 6.0e-17 Match length 67 % identity 67

14-3-3-LIKE PROTEIN >gi 555974 (U15036) 14-3-3-like protein NCBI Description

[Pisum sativum]

34533 Seq. No.



Seq. ID LIB3028-005-Q1-B1-B8 Method BLASTX NCBI GI q1771162 BLAST score 163 E value 2.0e-13 Match length 65 66 % identity NCBI Description (X98930) SBT2 [Lycopersicon esculentum] >gi 3687307 emb CAA07000 (AJ006379) subtilisin-like protease [Lycopersicon esculentum] Seq. No. 34534 Seq. ID LIB3028-005-Q1-B1-C6 Method BLASTX NCBI GI g4335745 BLAST score 174 E value 2.0e-12 Match length 103 % identity 43 NCBI Description (AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana] Seq. No. 34535 Seq. ID LIB3028-005-Q1-B1-D2 Method BLASTN NCBI GI q3377793 BLAST score 140 6.0e-73 E value Match length 284 % identity 87 NCBI Description Glycine max proteasome IOTA subunit mRNA, complete cds 34536 Seq. No. Seq. ID LIB3028-005-Q1-B1-D5 Method BLASTX g2498706 NCBI GI BLAST score 142 E value 7.0e-09 Match length 73 % identity 41 ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi\_1113103 NCBI Description (U40269) atOrc2p [Arabidopsis thaliana] >gi 3236239 (AC004684) origin recognition complex protein [Arabidopsis thaliana] Seq. No. 34537 Seq. ID LIB3028-005-Q1-B1-D7

Method NCBI GI BLASTX

g1001708

BLAST score E value

314

Match length

7.0e-29

139

% identity

49 NCBI Description (D64004) NifS [Synechocystis sp.]

Seq. No.



```
LIB3028-006-Q1-B1-A10
Seq. ID
                  BLASTX
Method
                  g115797
NCBI GI
                  285
BLAST score
                  1.0e-25
E value
                  94
Match length
                  57
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
NCBI Description
                  (CAB-215) (LHCP) >gi_100026_pir__S16592 chlorophyll
                  a/b-binding protein - garden pea >gi_20658_emb_CAA40365
                  (X57082) chlorophyll a/b-binding protein [Pisum sativum]
                  34539
Seq. No.
                  LIB3028-006-Q1-B1-A5
Seq. ID
Method
                  BLASTN
                  g1944318
NCBI GI
                  284
BLAST score
                  1.0e-158
E value
                  326
Match length
                  99
% identity
NCBI Description Glycine max mRNA for cysteine proteinase inhibitor,
                  complete cds
                  34540
Seq. No.
                  LIB3028-006-Q1-B1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1350720
BLAST score
                  216
                  1.0e-17
E value
                  91
Match length
% identity
                  50
NCBI Description 60S RIBOSOMAL PROTEIN L32
                  34541
Seq. No.
                  LIB3028-006-Q1-B1-E12
Seq. ID
Method
                  BLASTX
                  q1669341
NCBI GI
BLAST score
                  262
                  8.0e-23
E value
Match length
                  118
% identity
                  47
                  (D45066) AOBP (ascorbate oxidase promoter-binding protein)
NCBI Description
                  [Cucurbita maxima]
                  34542
Seq. No.
                  LIB3028-006-Q1-B1-E7
Seq. ID
Method
                  BLASTX
                  g3176098
NCBI GI
BLAST score
                  341
                  3.0e-32
E value
                  107
```

Match length % identity 67

NCBI Description (Y15036) annexin [Medicago truncatula]

Seq. No.

34543

Seq. ID

LIB3028-006-Q1-B1-G7

Method BLASTX



```
q3128218
NCBI GI
BLAST score
                   395
                   2.0e-38
E value
Match length
                   119
% identity
                   66
NCBI Description
                  (AC004077) putative end13 protein [Arabidopsis thaliana]
Seq. No.
                   34544
Seq. ID
                  LIB3028-006-Q1-B1-H1
Method
                  BLASTX
NCBI GI
                  q123650
BLAST score
                   301
E value
                   1.0e-27
Match length
                   109
% identity
                   58
NCBI Description
                  HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245_pir_ S03250 heat
                   shock protein 70 (clone pMON9743) - garden petunia
                  >gi_20557_emb_CAA30018_ (X06932) heat shock protein 70
                   [Petunia x hybrida]
Seq. No.
                  34545
Seq. ID
                  LIB3028-007-Q1-B1-A4
Method
                  BLASTX
NCBI GI
                  q3738299
BLAST score
                   363
E value
                  1.0e-34
Match length
                  101
% identity
                   72
NCBI Description
                  (AC005309) putative glutaredoxin [Arabidopsis thaliana]
                  >gi 4249395 (AC006072) putative glutaredoxin [Arabidopsis
                  thaliana]
Seq. No.
                   34546
Seq. ID
                  LIB3028-007-Q1-B1-A9
Method
                  BLASTN
NCBI GI
                  g2935449
BLAST score
                  73
E value
                  6.0e-33
Match length
                  109
% identity
                  92
NCBI Description Malus domestica histone H2B mRNA, partial cds
Seq. No.
                  34547
Seq. ID
                  LIB3028-007-Q1-B1-B8
Method
                  BLASTX
NCBI GI
                  q4558673
BLAST score
                  244
                  9.0e-21
E value
Match length
                  125
% identity
                  33
NCBI Description
                  (AC007063) hypothetical protein [Arabidopsis thaliana]
```

34548

Seq. ID

LIB3028-007-Q1-B1-C7

Method BLASTN NCBI GI g2760168 BLAST score 44



E value 1.0e-15 Match length 215 % identity 81

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MEE6, complete sequence [Arabidopsis thaliana]

Seq. No. 34549

Seq. ID LIB3028-007-Q1-B1-D10

Method BLASTX
NCBI GI g2894606
BLAST score 208
E value 2.0e-16
Match length 76
% identity 55

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 34550

Seq. ID LIB3028-007-Q1-B1-E7

Method BLASTX
NCBI GI g267079
BLAST score 505
E value 2.0e-51
Match length 131
% identity 75

NCBI Description TUBULIN BETA-6 CHAIN >gi\_320187\_pir\_\_JQ1590 tubulin beta-6

chain - Arabidopsis thalīana >gī\_166904 (M84703) beta-6

tubulin [Arabidopsis thaliana]

Seq. No. 34551

Seq. ID LIB3028-007-Q1-B1-H4

Method BLASTN
NCBI GI g18551
BLAST score 289
E value 1.0e-162
Match length 364
% identity 95

NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

Seq. No. 34552

Seq. ID LIB3028-008-Q1-B1-A10

Method BLASTX
NCBI GI g3608479
BLAST score 240
E value 2.0e-20
Match length 60
% identity 78

NCBI Description (AF088912) ribosomal protein L15 [Petunia x hybrida]

Seq. No. 34553

Seq. ID LIB3028-008-Q1-B1-B2

Method BLASTX
NCBI GI g1488255
BLAST score 172
E value 2.0e-12
Match length 59
% identity 49

(U38416) ferulate-5-hydroxylase [Arabidopsis thaliana] NCBI Description >gi\_2961381\_emb\_CAA18128\_ (AL022141) ferulate-5-hydroxylase (FAH1) [Arabidopsis thaliana] >gi\_3925365 (AF068574) ferulate-5-hydroxylase [Arabidopsis thaliana] 34554 Seq. No. LIB3028-008-Q1-B1-F2 Seq. ID BLASTX Method g2642154 NCBI GI 162 BLAST score 8.0e-14 E value 91 Match length 55 % identity (AC003000) unknown protein [Arabidopsis thaliana] NCBI Description >qi 3790595 (AF079186) RING-H2 finger protein RHC2a [Arabidopsis thaliana] 34555 Seq. No. LIB3028-008-Q1-B1-G7 Seq. ID BLASTN Method g312988 NCBI GI 130 BLAST score 6.0e-67 E value 258 Match length 88 % identity NCBI Description G.max mRNA for beta-tubulin, partial cds

34556 Seq. No. LIB3028-009-Q1-B1-A6 Seq. ID BLASTX Method q549986 NCBI GI 541 BLAST score 2.0e-55 E value

141 Match length % identity 75

(U13149) possible apospory-associated protein [Pennisetum NCBI Description ciliare]

34557 Seq. No.

Seq. ID LIB3028-009-Q1-B1-B1

BLASTN Method g303900 NCBI GI 209 BLAST score 1.0e-114 E value Match length 293 28 % identity

NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No. 34558

Seq. ID LIB3028-009-Q1-B1-C12

Method BLASTX g3522929 NCBI GI 339 BLAST score 6.0e-32 E value Match length 78 % identity 82

NCBI Description (AC002535) putative dTDP-glucose 4-6-dehydratase



[Arabidopsis thaliana] >gi\_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 34559 LIB3028-009-Q1-B1-C6 Seq. ID BLASTX Method q462138 NCBI GI 299 BLAST score 3.0e-27 E value 83 Match length % identity 67

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_169091 (L07500) glyceraldehyde-3-phosphate

dehydrogenase [Pisum sativum] >gi\_1345567\_emb\_CAA51675\_

(X73150) glyceraldehyde 3-phosphate dehydrogenase

(phosphorylating) [Pisum sativum]

Seq. No. 34560

Seq. ID LIB3028-009-Q1-B1-D2 Method BLASTX

NCBI GI g3834322
BLAST score 271
E value 7.0e-24
Match length 96
% identity 56

NCBI Description (AC005679) EST gb\_R30300 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 34561

Seq. ID LIB3028-009-Q1-B1-F7

Method BLASTX
NCBI GI g3695063
BLAST score 341
E value 5.0e-32
Match length 144
% identity 60

NCBI Description (AF064789) rac GTPase activating protein 3 [Lotus

japonicus]

Seq. No. 34562

Seq. ID LIB3028-009-Q1-B1-G12

Method BLASTN
NCBI GI g3059094
BLAST score 125
E value 6.0e-64
Match length 184
% identity 92

NCBI Description Glycine max mRNA for magnesium chelatase subunit

Seq. No. 34563

Seq. ID LIB3028-009-Q1-B1-G6

Method BLASTX
NCBI GI g2739000
BLAST score 449
E value 1.0e-44
Match length 134
% identity 66



```
(AF022459) CYP71D10p [Glycine max]
NCBI Description
                  34564
Seq. No.
                  LIB3028-009-Q1-B1-H10
Seq. ID
                  BLASTX
Method
                  g3335376
NCBI GI
                  203
BLAST score
                  5.0e-16
E value
                  79
Match length
                  44
% identity
                  (AC003028) putative ammonium transporter [Arabidopsis
NCBI Description
                  thaliana]
                  34565
Seq. No.
                  LIB3028-010-Q1-B1-A12
Seq. ID
Method
                  BLASTX
                  g1565225
NCBI GI
                  172
BLAST score
                  2.0e-12
E value
Match length
                  43
% identity
                  34
NCBI Description (X95572) salt-tolerance protein [Arabidopsis thaliana]
                   34566
Seq. No.
Seq. ID
                  LIB3028-010-Q1-B1-D1
Method
                  BLASTN
                   g3869087
NCBI GI
BLAST score
                   48
                   3.0e-18
E value
                   96
Match length
                   88
% identity
                  Nicotiana paniculata mRNA for elongation factor-1 alpha,
NCBI Description
                   complete cds
                   34567
Seq. No.
                   LIB3028-010-Q1-B1-E3
Seq. ID
                   BLASTN
Method
                   g303900
NCBI GI
                   224
BLAST score
                   1.0e-123
E value
                   334
Match length
                   29
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
                   34568
Seq. No.
                   LIB3028-010-Q1-B1-F12
Seq. ID
                   BLASTX
Method
                   g1314277
NCBI GI
                   149
BLAST score
                   1.0e-09
E value
Match length
                   111
 % identity
                   31
NCBI Description (U34919) white homolog [Homo sapiens]
```

Seq. ID LIB3028-011-Q1-B1-E12

Method BLASTN



```
g170087
NCBI GI
BLAST score
                  91
E value
                  7.0e-44
                  171
Match length
                  88
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
                  34570
Seq. No.
                 LIB3028-011-Q1-B1-E8
Seq. ID
Method
                BLASTN
                 q310575
NCBI GI
BLAST score
                 254
                 1.0e-141
E value
Match length
                 413
                  93
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
Seq. No.
                  34571
                 LIB3028-011-Q1-B1-F1
Seq. ID
Method
                 BLASTX
NCBI GI
                 g3176715
BLAST score
                  381
                  8.0e-37
E value
                  117
Match length
                  64
% identity
NCBI Description (AC002392) putative receptor-like protein kinase
                  [Arabidopsis thaliana]
                  34572
Seq. No.
Seq. ID
                  LIB3028-011-Q1-B1-G8
Method
                  BLASTX
NCBI GI
                  g2088643
BLAST score
                  237
E value
                  4.0e-20
Match length
                  64
% identity
                  36
NCBI Description (AF002109) transcription factor SF3 isolog [Arabidopsis
                  thaliana]
Seq. No.
                  34573
Seq. ID
                  LIB3028-011-Q1-B1-H2
                  BLASTN
Method
NCBI GI
                  g1408470
BLAST score
                  38
E value
                  3.0e-12
                  110
Match length
% identity
NCBI Description Arabidopsis thaliana actin depolymerizing factor 1 (AtADF1)
                  mRNA, complete cds
Seq. No.
                  34574
Seq. ID
                  LIB3028-012-Q1-B1-C11
Method
                  BLASTX
NCBI GI
                  g4539333
BLAST score
                  345
```

1.0e-32

110

E value Match length



```
% identity
                  (AL035539) putative amino acid transport protein
NCBI Description
                  [Arabidopsis thaliana]
                  34575
Seq. No.
                  LIB3028-012-Q1-B1-G12
Seq. ID
                  BLASTX
Method
                  g1171642
NCBI GI
                  216
BLAST score
                  2.0e-17
E value
                  90
Match length
                  50
% identity
                  PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK
NCBI Description
                  >gi 481206 pir S38326 protein kinase - Arabidopsis
                  thaliana >gi 166809 (L07248) protein kinase [Arabidopsis
                  thaliana]
                  34576
Seq. No.
                  LIB3028-013-Q1-B1-A11
Seq. ID
                  BLASTX
Method
                  g2129889
NCBI GI
                  269
BLAST score
                  5.0e-31
E value
'Match length
                  95
                  76
% identity
NCBI Description methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
                  34577
Seq. No.
                  LIB3028-013-Q1-B1-C4
Seq. ID
                  BLASTX
Method
                  g2505884
NCBI GI
                  282
BLAST score
                  3.0e-25
E value
                  90
Match length
                  59
% identity
NCBI Description (Y12776) hypothetical protein [Arabidopsis thaliana]
                  34578
Seq. No.
                  LIB3028-013-Q1-B1-E1
Seq. ID
                  BLÁSTX
Method
NCBI GI
                  g951449
                  214
BLAST score
                   6.0e-25
E value
                   96
Match length
                   59
% identity
                  (L46681) aspartic protease precursor [Lycopersicon
NCBI Description
                   esculentum]
                   34579
Seq. No.
                   LIB3028-013-Q1-B1-F1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2463568
BLAST score
                   48
                   3.0e-18
E value
                   173
Match length
```

5210

NCBI Description Glycine max mRNA for squalene synthase, complete cds

81

% identity

E value

Match length

NCBI Description

% identity

4.0e-11 120

thaliana]

42



```
Seq. No.
                  34580
Seq. ID
                  LIB3028-013-Q1-B1-G6
Method
                  BLASTX
NCBI GI
                  q4049632
                  520
BLAST score
E value
                  4.0e-53
Match length
                  129
% identity
                  (AF039406) pyruvate dehydrogenase kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  34581
Seq. ID
                  LIB3028-014-Q1-B1-A9
Method
                  BLASTX
NCBI GI
                  q1781299
BLAST score
                  185
E value
                   9.0e-14
                   55
Match length
                   62
% identity
                  (Y09506) transformer-SR ribonucleoprotein [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   34582
                  LIB3028-014-Q1-B1-B3
Seq. ID
                  BLASTX
Method
                   q3122671
NCBI GI
                   259
BLAST score
E value
                   1.0e-22
Match length
                   85
                   56
% identity
                  HYPOTHETICAL RAE1-LIKE PROTEIN >gi 2129676 pir_S71241
NCBI Description
                   probable export protein - Arabidopsis thaliana >gi 1297188
                   (U53501) Theoretical protein with similarity to Swiss-Prot
                   Accession Number P41838 poly A+ RNA export protein
                   [Arabidopsis thaliana]
Seq. No.
                   34583
Seq. ID
                   LIB3028-014-Q1-B1-B4
Method
                   BLASTX
                   g4544419
NCBI GI
                   249
BLAST score
                   3.0e-21
E value
Match length
                   67
% identity
                   79
                  (AC006955) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34584
Seq. ID
                   LIB3028-014-Q1-B1-C5
Method
                   BLASTX
NCBI GI
                   q4406781
BLAST score
                   161
```

5211

(AC006532) putative Na+/H+ antiporter [Arabidopsis

NCBI Description

```
34585
Seq. No.
Seq. ID
                  LIB3028-014-Q1-B1-D1
Method
                  BLASTN
                  g2570122
NCBI GI
BLAST score
                  33
                  5.0e-09
E value
                  41
Match length
                  95
% identity
NCBI Description S.latifolia mRNA, clone CCLS 30.1-21
                  34586
Seq. No.
                  LIB3028-014-Q1-B1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4572673
                  297
BLAST score
                  5.0e-27
E value
Match length
                  103
                  54
% identity
                  (AC006954) putative sarcosine oxidase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  34587
                  LIB3028-014-Q1-B1-G4
Seq. ID
Method
                  BLASTX
                  g1515454
NCBI GI
BLAST score
                  147
                  1.0e-09
E value
                  69
Match length
                  46
% identity
                  (U64448) lac repressor [Cloning vector pCMVLacI]
NCBI Description
                  34588
Seq. No.
Seq. ID
                  LIB3028-015-Q1-B1-A11
                  BLASTX
Method
NCBI GI
                  g267124
BLAST score
                  184
                  4.0e-23
E value
                  96
Match length
                  61
% identity
                  THIOREDOXIN H-TYPE 1 (TRX-H1) >gi 100387 pir S16590
NCBI Description
                  thioredoxin h1 - common tobacco >gi 20047 emb CAA41415
                   (X58527) thioredoxin [Nicotiana tabacum]
Seq. No.
                  34589
                  LIB3028-015-Q1-B1-C5
Seq. ID
Method
                  BLASTX
                  q1172664
NCBI GI
BLAST score
                   383
                  4.0e-37
E value
                  118
Match length
% identity
                   66
```

5212

PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR

>gi\_419791\_pir\_\_S31165 photosystem I chain III precursor Flaveria trinervia >gi\_298482 bbs\_127083 photosystem I
reaction center subunit III, PSI-RC PsaF [Flaveria

(LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)





trinervia, Peptide, 232 aa] >gi\_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

 Seq. No.
 34590

 Seq. ID
 LIB3028-015-Q1-B1-D2

 Method
 BLASTX

 NCBI GI
 g2746719

 BLAST score
 210

 E value
 7.0e-17

 Match length
 102

 % identity
 48

NCBI Description (AF038386) histone H2B [Capsicum annuum]

Seq. No. 34591 Seq. ID LIB302

Seq. ID LIB3028-015-Q1-B1-E10

Method BLASTN
NCBI GI g2815245
BLAST score 75
E value 5.0e-34
Match length 203
% identity 84

NCBI Description C.arietinum mRNA for class I type 2 metallothionein (clone:

CanMT-2)

Seq. No.

34592

Seq. ID LIB3028-015-Q1-B1-G11

Method BLASTX
NCBI GI g2252824
BLAST score 407
E value 7.0e-40
Match length 104
% identity 73

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.

34593

Seq. ID LIB3028-016-Q1-B1-A11

Method BLASTX
NCBI GI g1076634
BLAST score 186
E value 4.0e-14
Match length 78
% identity 50

NCBI Description protein-serine/threonine kinase NPK15 - common tobacco

>gi 505146 dbj BAA06538 (D31737) protein-serine/threonine

kinase [Nicotiana tabacum]

Seq. No.

34594

34595

Seq. ID

LIB3028-016-Q1-B1-A9

Method BLASTN
NCBI GI g18761
BLAST score 77
E value 3.0e-35
Match length 249
% identity 89

NCBI Description Soybean stem mRNA for 31 kD glycoprotein

Seq. No.



```
LIB3028-016-Q1-B1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3183088
                  164
BLAST score
                  2.0e-11
E value
Match length
                  94
                  38
% identity
                  PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
NCBI Description
                  (LTP) >gi 629658 pir S47084 lipid transfer like protein -
                  cowpea >gi 499034 emb CAA56113 (X79604) lipid transfer
                  like protein [Vigna unguiculata]
                  34596
Seq. No.
Seq. ID
                  LIB3028-016-Q1-B1-D10
Method
                  BLASTX
                  g4510383
NCBI GI
BLAST score
                  256
                  1.0e-22
E value
Match length
                  67
                  79
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34597
Seq. ID
                  LIB3028-017-Q1-B1-C5
Method
                  BLASTX
NCBI GI
                  g2983814
BLAST score
                  151
E value
                  4.0e-10
Match length
                  78
% identity
                  41
                  (AE000739) tryptophan synthase beta subunit [Aquifex
NCBI Description
                  aeolicus]
                  34598
Seq. No.
                  LIB3028-017-Q1-B1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063691
BLAST score
                  267
E value
                  2.0e-23
                  68
Match length
% identity
NCBI Description
                  (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                  34599
Seq. ID
                  LIB3028-018-Q1-B1-A4
Method
                  BLASTX
NCBI GI
                  g2911073
BLAST score
                  177
                  4.0e-13
```

E value Match length 66 % identity

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

34600 Seq. No.

Seq. ID LIB3028-018-Q1-B1-A8

Method BLASTX NCBI GI g1871182



```
BLAST score
                  300
                  1.0e-27
E value
Match length
                  84
% identity
                  67
NCBI Description (U90439) phospholipase D isolog [Arabidopsis thaliana]
                  34601
Seq. No.
                  LIB3028-018-Q1-B1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3021484
BLAST score
                  36
                  7.0e-11
E value
Match length
                  68
% identity
                  88
NCBI Description Lycopersicon esculentum H2B-3 mRNA for histone H2B
                  34602
Seq. No.
                  LIB3028-018-Q1-B1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129879
BLAST score
                  190
E value
                  1.0e-17
Match length
                  108
% identity
NCBI Description chlorophyll a/b-binding protein type II precursor,
                  photosystem I - garden pea >gi 602359 emb CAA57492
                  (X81962) Type II chlorophyll a/b binding protein from
                  photosystem I [Pisum sativum]
Seq. No.
                  34603
Seq. ID
                  LIB3028-018-Q1-B1-C5
Method
                  BLASTN
NCBI GI
                  g2764803
BLAST score
                  122
                  4.0e-62
E value
Match length
                  310
% identity
                  85
NCBI Description G.max mRNA for epoxide hydrolase
Seq. No.
                  34604
Seq. ID
                  LIB3028-018-Q1-B1-D6
Method
                  BLASTX
NCBI GI
                  g2618705
BLAST score
                  257
E value
                  2.0e-26
                  93
Match length
                  43
% identity
NCBI Description (AC002510) putative ABC transporter, 5' partial
                  [Arabidopsis thaliana]
```

LIB3028-018-Q1-B1-E9 Seq. ID

Method BLASTX NCBI GI a4455276 BLAST score 393 E value 3.0e-38 Match length 123



```
% identity
                  (AL035527) peptide transporter-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  34606
Seq. No.
Seq. ID
                  LIB3028-018-Q1-B1-G10
Method
                  BLASTX
NCBI GI
                  q3004564
BLAST score
                  272
                  4.0e-24
E value
Match length
                  106
% identity
                  51
                   (AC003673) putative receptor Ser/Thr protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                  34607
Seq. No.
                  LIB3028-018-Q1-B1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q456567
                  109
BLAST score
                  3.0e-54
E value
                  205
Match length
% identity
                  88
                  Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
NCBI Description
                  cds
Seq. No.
                  34608
                  LIB3028-018-Q1-B1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2618699
BLAST score
                  267
                  2.0e-23
E value
Match length
                  71
% identity
                   63
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34609
                  LIB3028-018-Q1-B1-H5
Seq. ID
Method
                  BLASTN
                   g1053215
NCBI GI
BLAST score
                   165
                   9.0e-88
E value
                   357
Match length
% identity
                   87
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                   nuclear gene encoding chloroplast protein, complete cds
Seq. No.
                   34610
                   LIB3028-018-Q1-B1-H8
Seq. ID
```

Method BLASTX q4455259 NCBI GI 355 BLAST score 8.0e-34 E value Match length 119 59 % identity

(AL035523) putative Ser/Thr protein kinase [Arabidopsis NCBI Description

thaliana]



```
34611
Seq. No.
                  LIB3028-019-Q1-B1-A12
Seq. ID
                  BLASTX
Method
                  g2708331
NCBI GI
                  286
BLAST score
                  1.0e-25
E value
                  94
Match length
                  61
% identity
                   (AF038557) ligand gated channel-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  34612
Seq. No.
                  LIB3028-019-Q1-B1-A7
Seq. ID
                  BLASTN
Method
                   g1256365
NCBI GI
                   41
BLAST score
                   6.0e-14
E value
                   65
Match length
                   91
% identity
NCBI Description Promoter-trapping vector pdeltagusBin19
                   34613
Seq. No.
                   LIB3028-019-Q1-B1-B11
Seq. ID
                   BLASTX
Method
                   g2832640
NCBI GI
                   347
BLAST score
                   6.0e-33
E value
                   105
Match length
                   65
% identity
                  (AL021710) neoxanthin cleavage enzyme - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   34614
Seq. No.
                   LIB3028-019-Q1-B1-B6
Seq. ID
                   BLASTX
Method
                   q309673
NCBI GI
                   213
BLAST score
                   2.0e-17
E value
                   81
Match length
% identity
                   62
NCBI Description (L19651) light harvesting protein [Pisum sativum]
                   34615
Seq. No.
                   LIB3028-019-Q1-B1-B7
Seq. ID
                   BLASTN
Method
                   g1399379
NCBI GI
BLAST score
                   106
E value
                   9.0e-53
                   122
Match length
 % identity
                   97
NCBI Description Glycine max S-adenosyl-L-methionine:delta24-sterol-C-
                   methyltransferase mRNA, complete cds
```

Seq. ID LIB3028-019-Q1-B1-C5

Method BLASTX



```
q542005
NCBI GI
                  181
BLAST score
                  1.0e-13
E value
                  71
Match length
                  56
% identity
                  endoxyloglucan transferase - adzuki bean
NCBI Description
                  >gi_469510_dbj_BAA03925_ (D16458) endo-xyloglucan
                  transferase [Vigna angularis]
                  34617
Seq. No.
Seq. ID
                  LIB3028-019-Q1-B1-C6
Method
                  BLASTN
NCBI GI
                  q18551
                  132
BLAST score
                  3.0e-68
E value
                  236
Match length
% identity
                  89
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                  protein
                  34618
Seq. No.
                  LIB3028-019-Q1-B1-D1
Seq. ID
Method
                  BLASTX
                  g1346701
NCBI GI
                  284
BLAST score
                  2.0e-25
E value
                  110
Match length
% identity
                  48
                  EXOPOLYGALACTURONASE CLONE GBGE184 PRECURSOR (EXOPG)
NCBI Description
                  (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_421831_pir__S34199 exopolygalacturonase (clone GBGe184)
                  - Arabidopsis thaliana >gi 313682 emb CAA51032 (X72291)
                  exopolygalacturonase [Arabidopsis thaliana]
                  >gi_3004440_emb_CAA76127_ (Y16230) polygalacturonase
                  [Arabidopsis thaliana]
                  34619
Seq. No.
Seq. ID
                  LIB3028-019-Q1-B1-E11
                  BLASTX
Method
NCBI GI
                  g4100433
BLAST score
                  234
E value
                  1.0e-19
                  50
Match length
                  82
% identity
NCBI Description (AF000378) beta-glucosidase [Glycine max]
                  34620
Seq. No.
Seq. ID
                  LIB3028-019-Q1-B1-F5
                  BLASTN
Method
NCBI GI
                  q18557
BLAST score
                  84
```

1.0e-39 E value Match length 136 91 % identity

NCBI Description G.max mRNA for ACC synthase

34621

Seq. No.

NCBI GI

E value

BLAST score

176

3.0e-13



```
Seq. ID
                  LIB3028-019-Q1-B1-G11
Method
                  BLASTX
NCBI GI
                  q2055228
BLAST score
                  143
E value
                   6.0e-09
Match length
                  78
% identity
                  41
NCBI Description
                  (AB000129) SRC1 [Glycine max]
                  34622
Seq. No.
Seq. ID
                  LIB3028-019-Q1-B1-H10
Method
                  BLASTX
NCBI GI
                  q3461821
BLAST score
                  184
                   9.0e-14
E value
Match length
                   91
% identity
                   46
NCBI Description
                   (AC004138) putative nucleoside triphosphatase [Arabidopsis
                  thaliana]
                   34623
Seq. No.
Seq. ID
                  LIB3028-020-Q1-B1-A11
Method
                  BLASTX
NCBI GI
                   g3341443
BLAST score
                   315
                   4.0e-29
E value
                  108
Match length
% identity
                   58
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                   34624
Seq. No.
Seq. ID
                   LIB3028-020-Q1-B1-A7
Method
                   BLASTX
NCBI GI
                   g4049354
BLAST score
                   154
E value
                   3.0e-10
Match length
                   62
                   47
% identity
NCBI Description
                   (AL034567) glycine hydroxymethyltransferase (EC
                   2.1.2.1)-like protein [Arabidopsis thaliana]
Seq. No.
                   34625
                   LIB3028-020-Q1-B1-D2
Seq. ID
Method
                   BLASTX
                   g4239692
NCBI GI
BLAST score
                   270
E value
                   9.0e-24
Match length
                   54
% identity
NCBI Description
                  (AJ132745) hypothetical protein [Arabidopsis thaliana]
                   34626
Seq. No.
Seq. ID
                   LIB3028-020-Q1-B1-E3
Method
                   BLASTX
                   g1408296
```



Match length % identity 69 (U61984) phosphoglucomutase A [Dictyostelium discoideum] NCBI Description

34627 Seq. No.

Seq. ID LIB3028-020-Q1-B1-F11

Method BLASTX NCBI GI q1669599 BLAST score 180 3.0e-13 E value Match length 99 % identity 40

NCBI Description (D88746) AR791 [Arabidopsis thaliana]

34628 Seq. No.

LIB3028-020-Q1-B1-G12 Seq. ID

Method BLASTX NCBI GI g4572671 BLAST score 416 3.0e-54 E value 133 Match length % identity 81

NCBI Description (AC006954) putative cyclic nucleotide regulated ion channel

[Arabidopsis thaliana]

34629 Seq. No.

LIB3028-020-Q1-B1-H6 Seq. ID

Method BLASTX NCBI GI q4206122 BLAST score 344 E value 2.0e-32 Match length 123 % identity

(AF097667) protein phosphatase 2C homolog [Mesembryanthemum NCBI Description

crystallinum]

Seq. No. 34630

LIB3028-021-Q1-B1-B1 Seq. ID

Method BLASTX g2244924 NCBI GI BLAST score 164 2.0e-11 E value 53 Match length % identity 55

(Z97339) glutaredoxin [Arabidopsis thaliana] NCBI Description

Seq. No.

34631 Seq. ID LIB3028-021-Q1-B1-B5

Method BLASTX NCBI GI g4160441 BLAST score 123 6.0e-09 E value Match length 106 42 % identity

(AF098674) lateral suppressor protein [Lycopersicon NCBI Description

esculentum]



Seq. No. 34632 Seq. ID LIB3028-021-Q1-B1-B9 Method BLASTX q4377374 NCBI GI BLAST score 251 1.0e-21 E value Match length 122 % identity 39 (AE001684) Adenosylmethionine-8-Amino-7-Oxononanoate NCBI Description Aminotransferase [Chlamydia pneumoniae] Seq. No. 34633 LIB3028-022-Q1-B1-C4 Seq. ID Method BLASTX g4490736 NCBI GI BLAST score 164 E value 7.0e-12 Match length 53 37 % identity (AL035708) putative protein [Arabidopsis thaliana] NCBI Description 34634 Seq. No. LIB3028-022-Q1-B1-D12 Seq. ID Method BLASTX NCBI GI g2244929 BLAST score 293 2.0e-26 E value 128 Match length 50 % identity (Z97339) unnamed protein product [Arabidopsis thaliana] NCBI Description 34635 Seq. No. LIB3028-022-Q1-B1-D4 Seq. ID Method BLASTX NCBI GI q4432814 BLAST score 187 E value 1.0e-14 53 Match length 70 % identity NCBI Description (AC006593) unknown protein [Arabidopsis thaliana] Seq. No. 34636 LIB3028-022-Q1-B1-E9 Seq. ID Method BLASTX NCBI GI g3702327 BLAST score 160 E value 7.0e-11 Match length 62 % identity

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 34637

LIB3028-022-Q1-B1-F1 Seq. ID

BLASTN Method NCBI GI g255578 BLAST score 98 6.0e-48 E value

5221

and the same



Match length 209
% identity 90
NCBI Description small auxin up RNA gene cluster: orf X10A [Glycine max=soybeans, cv. Wayne, Genomic, 666 nt]

Seq. No. 34638
Seq. ID LIB3028-022-Q1-B1-F3

Method BLASTX
NCBI GI g1350720
BLAST score 136
E value 1.0e-08
Match length 44
% identity 61

NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 34639

Seq. ID LIB3028-022-Q1-B1-F6

Method BLASTN
NCBI GI g1431628
BLAST score 118
E value 9.0e-60
Match length 335
% identity 87

NCBI Description V.radiata mRNA for pectinacetylesterase

Seq. No. 34640

Seq. ID LIB3028-022-Q1-B1-G9

Method BLASTX
NCBI GI g2739044
BLAST score 405
E value 1.0e-39
Match length 111
% identity 68

NCBI Description (AF024651) polyphosphoinositide binding protein Ssh1p

[Glycine max]

Seq. No. 34641

Seq. ID LIB3028-022-Q1-B1-H3

Method BLASTX
NCBI GI g3738339
BLAST score 174
E value 5.0e-16
Match length 90
% identity 37

NCBI Description (AC005170) putative kinase [Arabidopsis thaliana]

Seq. No. 34642

Seq. ID LIB3028-023-Q1-B1-C11

Method BLASTX
NCBI GI 94200122
BLAST score 357
E value 5.0e-34
Match length 109
% identity 61

NCBI Description (AJ009555) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34643

5222

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```
LIB3028-023-Q1-B1-C5
Seq. ID
                  BLASTX
Method -
NCBI GI
                  g2104536
                  141
BLAST score
                  1.0e-08
E value
                  56
Match length
                  59
% identity
                  (AF001308) predicted glycosyl transferase [Arabidopsis
NCBI Description
                  thaliana]
                  34644
Seq. No.
                  LIB3028-024-Q1-B1-A6
Seq. ID
                  BLASTN
Method
                   g2182285
NCBI GI
BLAST score
                  57
                   3.0e-23
E value
                  125
Match length
                   86
% identity
                  Sequence of BAC F5I14 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
                   34645
Seq. No.
                   LIB3028-024-Q1-B1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4522012
BLAST score
                   158
                   1.0e-10
E value
Match length
                   93
                   41
% identity
                  (AC007069) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   34646
Seq. No.
                   LIB3028-024-Q1-B1-E11
Seq. ID
Method
                   BLASTX
                   q4006827
NCBI GI
BLAST score
                   313
E value
                   7.0e-29
Match length
                   115
                   55
% identity
                  (AC005970) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
                   34647
Seq. No.
                   LIB3028-024-Q1-B1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3152613
                   280
BLAST score
                   5.0e-25
E value
                   113
Match length
% identity
                  (AC004482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   34648
Seq. No.
                   LIB3028-024-Q1-B1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2828280
```

5223

2

192 7.0e-15

BLAST score

E value



Match length % identity 74 (AL021687) putative protein [Arabidopsis thaliana] NCBI Description >gi 2832633 emb\_CAA16762\_ (AL021711) putative protein [Arabidopsis thaliana] 34649 Seq. No. LIB3028-024-Q1-B1-H8 Seq. ID Method BLASTX NCBI GI q3402684 BLAST score 150 7.0e-10 E value Match length 40 % identity 72 (AC004697) hypothetical protein [Arabidopsis thaliana] NCBI Description 34650 Seq. No. LIB3028-025-Q1-B1-B10 Seq. ID Method BLASTX NCBI GI g1345785 BLAST score 536 1.0e-56 E value Match length 126 % identity CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1) NCBI Description >gi 567935 dbj BAA05640\_ (D26593) chalcone synthase [Camellia sinensis] Seq. No. 34651 LIB3028-025-Q1-B1-F1 Seq. ID Method BLASTX NCBI GI g2982431 BLAST score 203 E value 6.0e-16 125 Match length % identity (AL022224) leucine rich repeat-like protein [Arabidopsis NCBI Description thaliana] Seq. No. 34652 Seq. ID LIB3028-026-Q1-B1-A4 Method BLASTX NCBI GI g3176874 BLAST score 179 4.0e-13 E value Match length 45 69 % identity (AF065639) cucumisin-like serine protease [Arabidopsis NCBI Description thaliana] Seq. No. 34653 LIB3028-026-Q1-B1-F12

Seq. ID LIB3028-029
Method BLASTX
NCBI GI g4468993
PLAST gapes 543

BLAST score 543 E value 8.0e-56 Match length 123



% identity NCBI Description (AL035605) putative protein [Arabidopsis thaliana] Seq. No. 34654 LIB3028-026-Q1-B1-H9 Seq. ID Method BLASTX NCBI GI g3608155 BLAST score 402 E value 3.0e-39 Match length 124 % identity (AC005314) putative RNA helicase [Arabidopsis thaliana] NCBI Description 34655 Seq. No. LIB3028-027-Q1-B2-A5 Seq. ID Method BLASTX NCBI GI g3885334 BLAST score 335 2.0e-31 E value 121 Match length % identity 76 (AC005623) putative argonaute protein [Arabidopsis NCBI Description thaliana] 34656 Seq. No. LIB3028-027-Q1-B2-D9 Seq. ID Method BLASTX NCBI GI q2911797 BLAST score 142 7.0e-09 E value Match length 82 49 % identity NCBI Description (AF008183) 4-coumarate:CoA ligase 2 [Populus balsamifera subsp. trichocarpa X Populus deltoides] Seq. No. 34657 LIB3028-027-Q1-B2-G6 Seq. ID Method BLASTN NCBI GI g1841474 BLAST score 91 9.0e-44E value Match length 171 % identity 89 NCBI Description P.sativum mRNA for Myb-like protein (Myb26) Seq. No. 34658 LIB3028-028-Q1-B1-B12 Seq. ID Method BLASTX NCBI GI q2829910 BLAST score 352 2.0e-33 E value

119 Match length 11 % identity

(AC002291) Unknown protein, contains regulator of NCBI Description chromosome condensation motifs [Arabidopsis thaliana]

Seq. No. 34659

5225



```
LIB3028-028-Q1-B1-B2
Seq. ID
                  BLASTN
Method
                  g3860312
NCBI GI
                  44
BLAST score
                  1.0e-15
E value
Match length
                  70
                  97
% identity
NCBI Description Cicer arietinum mRNA for hypothetical protein, clone Can144
Seq. No.
                  34660
                  LIB3028-028-Q1-B1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1903357
BLAST score
                  366
E value
                  4.0e-35
Match length
                  112
% identity
                  58
                   (AC000104) Strong similarity to Arabidopsis 2A6
NCBI Description
                   (gb X83096). [Arabidopsis thaliana]
Seq. No.
                  34661
Seq. ID
                  LIB3028-028-Q1-B1-B7
Method
                  BLASTX
NCBI GI
                  q1903357
BLAST score
                   223
                   2.0e-18
E value
Match length
                  74
                   59
% identity
                  (AC000104) Strong similarity to Arabidopsis 2A6
NCBI Description
                   (gb X83096). [Arabidopsis thaliana]
Seq. No.
                   34662
Seq. ID
                   LIB3028-028-Q1-B1-F10
                  BLASTN
Method
NCBI GI
                   q56539
                   75
BLAST score
                   4.0e-34
E value
                   234
Match length
% identity
                   93
                  R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                   >gi 206360 gb J00764 RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
                   34663
Seq. No.
Seq. ID
                   LIB3028-028-Q1-B1-G1
Method
                   BLASTX
NCBI GI
                   g4539326
BLAST score
                   439
                   1.0e-43
E value
                   108
Match length
                   77
% identity
                   (AL035679) putative zinc finger protein [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No.

34664

Seq. ID

LIB3028-028-Q1-B1-H6

Method

BLASTX



NCBI GI g123620
BLAST score 196
E value 4.0e-15
Match length 106
% identity 49

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi\_100224\_pir\_\_S14950

heat shock cognate protein 70 - tomato

>gi\_19258\_emb\_CAA37971\_ (X54030) heat shock protein cognate

70 [Lycopersicon esculentum]

Seq. No. 34665

Seq. ID LIB3028-029-Q1-B1-B11

Method BLASTX
NCBI GI g3367522
BLAST score 180
E value 5.0e-20
Match length 125
% identity 40

NCBI Description (AC004392) EST gb\_T04691 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 34666

Seq. ID LIB3028-029-Q1-B1-D10

Method BLASTN
NCBI GI g18551
BLAST score 397
E value 0.0e+00
Match length 397
% identity 100

NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

Seq. No. 34667

Seq. ID LIB3028-029-Q1-B1-D11

Method BLASTX
NCBI GI g128592
BLAST score 309
E value 2.0e-28
Match length 89
% identity 64

NCBI Description POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR

>gi\_82190\_pir\_\_S22495 pollen-specific protein precursor common tobacco >gi 19902 emb CAA43454\_ (X61146) pollen

specific protein [Nicotiana tabacum]

Seq. No. 34668

Seq. ID LIB3028-029-Q1-B1-E5

Method BLASTX
NCBI GI g1730107
BLAST score 241
E value 2.0e-20
Match length 53
% identity 83

NCBI Description LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN

HYDROXYLASE) >gi 421870\_pir\_\_S33144 anthocyanidin

hydroxylase - apple tree >gi\_296844\_emb\_CAA50498\_ (X71360)

anthocyanidin hydroxylase [Malus sp.]



Seq. No. 34669 Seq. ID LIB3028-029-Q1-B1-F4 Method BLASTX NCBI GI g2662077 BLAST score 166 E value 1.0e-11 111 Match length % identity (AB007858) KIAA0398 [Homo sapiens] >gi 3450836 (AF067791) NCBI Description mRNA 5' cap guanine-N-7 methyltransferase [Homo sapiens] >gi 4200033\_dbj\_BAA74464\_ (AB022604) mRNA (quanine-7-)methyltransferase [Homo sapiens] >gi\_4506567\_ref\_NP\_003790.1\_pRNMT\_ UNKNOWN 34670 Seq. No. LIB3028-029-Q1-B1-H9 Seq. ID Method BLASTX · \* g2245394 NCBI GI 268 BLAST score 2.0e-27 E value 95 Match length % identity (U89771) ARF1-binding protein [Arabidopsis thaliana] NCBI Description Seq. No. 34671 LIB3028-030-Q1-B1-A1 Seq. ID Method BLASTN NCBI GI q4220633 BLAST score 51 1.0e-19 E value Match length 264 % identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K7J8, complete sequence [Arabidopsis thaliana] Seq. No. 34672 LIB3028-030-Q1-B1-A9 Seq. ID Method BLASTX g3142303 NCBI GI BLAST score 222 3.0e-18E value Match length 109 % identity 38 (AC002411) Strong similarity to MRP-like ABC transporter NCBI Description gb\_U92650 from A. thaliana and canalicular multi-drug resistance protein gb L49379 from Rattus norvegicus. [Arabidopsis thaliana] Seq. No. 34673 Seq. ID LIB3028-030-Q1-B1-B2 BLASTX Method

NCBI GI g1666171 BLAST score 353 4.0e-34 E value 108 Match length 66 % identity



NCBI Description (Y09105) unknown [Nicotiana plumbaginifolia] 34674 Seq. No. LIB3028-030-Q1-B1-C4 Seq. ID BLASTX Method NCBI GI g3550661 139 BLAST score 2.0e-16 E value Match length 92 % identity 64 (AJ001310) 39 kDa EF-Hand containing protein [Solanum NCBI Description 34675 Seq. No. Seq. ID LIB3028-030-Q1-B1-D7 Method BLASTN NCBI GI g56539 BLAST score 87 3.0e-41E value Match length 285 % identity 94 NCBI Description R.norvegicus gene encoding prolactin, exon 5 >gi 206360\_gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene : exon v and  $\overline{f}$  lanks Seq. No. 34676 Seq. ID LIB3028-030-Q1-B1-E2 Method BLASTX g2347088 NCBI GI 142 BLAST score 6.0e-15 E value Match length 78 % identity 60 (U72765) non-specific lipid transfer protein PvLTP-24 NCBI Description [Phaseolus vulgaris] 34677 Seq. No. Seq. ID LIB3028-030-Q1-B1-H12 BLASTX Method g3785971 NCBI GI BLAST score 232 E value 1.0e-19 96 Match length 56 % identity (AC005560) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi\_4262248\_gb\_AAD14541\_ (AC006200) hypothetical protein [Arabidopsis thaliana] Seq. No. 34678 Seq. ID LIB3028-030-Q1-B1-H8 Method BLASTX NCBI GI g3986172 BLAST score 316

5229

(AB015428) EXGT1 [Pisum sativum]

2.0e-29

95

65

E value Match length

% identity

NCBI Description

190 - 2



```
34679
Seq. No.
                  LIB3028-031-Q1-B1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204268
BLAST score
                  235
                  9.0e-20
E value
Match length
                  118
% identity
                  48
                  (AC005223) 62134 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34680
                  LIB3028-031-Q1-B1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q126307
BLAST score
                  167
E value
                  1.0e-11
Match length
                  132
% identity
NCBI Description
                  TRIACYLGLYCEROL LIPASE PRECURSOR (LIPASE, LINGUAL)
                  >gi 67160 pir_LIRTT triacylglycerol lipase (EC 3.1.1.3)
                  precursor, lingual - rat >gi 56596 emb CAA26179 (X02309)
                  lipase precursor [Rattus norvegicus]
Seq. No.
                  34681
Seq. ID
                  LIB3028-031-Q1-B1-E3
Method
                  BLASTX
NCBI GI
                  q1914683
BLAST score
                  210
                  9.0e-17
E value
Match length
                  67
% identity
                   60
NCBI Description
                  (Y12013) RAD23, isoform I [Daucus carota]
Seq. No.
                  34682
Seq. ID
                  LIB3028-031-Q1-B1-F2
Method
                  BLASTX
NCBI GI
                  g2832616
BLAST score
                   210
                   9.0e-17
E value
Match length
                   46
                  85
% identity
                   (AL021711) heat shock transcription factor - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  34683
Seq. ID
                  LIB3028-032-Q1-B1-B2
Method
                  BLASTX
NCBI GI
                  g1946366
BLAST score
                  145
                   4.0e-09
E value
Match length
                  72
```

Seq. No. 34684

% identity

NCBI Description

Seq. ID LIB3028-032-Q1-B1-D2

49

(U93215) unknown protein [Arabidopsis thaliana]



```
BLASTX
Method
NCBI GI
                  q913445
BLAST score
                   511
                   5.0e-52
E value
                  125
Match length
                   74
% identity
                   (S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase
NCBI Description
                  homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv.
                   red cherry, Peptide, 389 aa] [Lycopersicon esculentum]
                   34685
Seq. No.
                  LIB3028-033-Q1-B1-A5
Seq. ID
Method
                  BLASTN
                   g1236948
NCBI GI
BLAST score
                   66
                   5.0e-29
E value
                   178
Match length
                   86
% identity
NCBI Description Glycine max lipoxygenase L-5 (vlxB) mRNA, complete cds
                   34686
Seq. No.
                   LIB3028-034-Q1-B1-A7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3341443
BLAST score
                   348
                   6.0e-33
E value
Match length
                   99
% identity
                   67
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                   34687
Seq. No.
                   LIB3028-034-Q1-B1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g602292
BLAST score
                   144
E value
                   4.0e-09
Match length
                   81
% identity
                   41
                  (U17987) RCH2 protein [Brassica napus]
NCBI Description
                   34688
Seq. No.
                   LIB3028-034-Q1-B1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2920666
BLAST score
                   258
                   2.0e-22
E value
Match length
                   96
                   54
% identity
                   (AF048978) 2,4-D inducible glutathione S-transferase
NCBI Description
                   [Glycine max]
```

Seq. No. 34689

Seq. ID LIB3028-034-Q1-B1-F11

Method BLASTX
NCBI GI g4049350
BLAST score 141
E value 9.0e-09

```
Match length
% identity
                  33
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
                  34690
Seq. No.
Seq. ID
                  LIB3028-034-Q1-B1-F12
Method
                  BLASTN
NCBI GI
                  q516853
BLAST score
                  181
                  2.0e-97
E value
Match length
                  317
% identity
                   38
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
                  34691
Seq. No.
                  LIB3028-034-Q1-B1-H1
Seq. ID
```

Seq. ID LIB3028-034-Q1-B1Method BLASTX
NCBI GI g3435096
BLAST score 381
E value 9.0e-37
Match length 98
% identity 73

NCBI Description (AF033587) SRZ-80 [Arabidopsis thaliana]

 Seq. No.
 34692

 Seq. ID
 LIB3028-034-Q1-B1-H2

 Method
 BLASTX

Method BLASTX
NCBI GI g1345132
BLAST score 323
E value 4.0e-30
Match length 108
% identity 62

NCBI Description (U47029) ERECTA [Arabidopsis thaliana]

>gi\_1389566\_dbj\_BAA11869 (D83257) receptor protein kinase
[Arabidopsis thaliana] >gi\_3075386 (AC004484) receptor

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 34693

Seq. ID LIB3028-035-Q1-B1-A4

Method BLASTX
NCBI GI g3063448
BLAST score 290
E value 4.0e-26
Match length 126
% identity 47

NCBI Description (AC003981) F22013.10 [Arabidopsis thaliana]

Seq. No. 34694

Seq. ID LIB3028-035-Q1-B1-B2

Method BLASTX
NCBI GI g3776005
BLAST score 222
E value 3.0e-18
Match length 48
% identity 94

NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]



```
Seq. No.
                   34695
                  LIB3028-035-Q1-B1-C4
Seq. ID
Method
                   BLASTX
                   g3746060
NCBI GI
BLAST score
                   377
E value
                   2.0e-36
                   83
Match length
                   78
% identity
                  (AC005311) unknown protein [Arabidopsis thaliana]
NCBI Description
                   34696
Seq. No.
                   LIB3028-035-Q1-B1-F9
Seq. ID
                   BLASTN
Method
                   g1806145
NCBI GI
BLAST score
                   113
                   1.0e-56
E value
                   289
Match length
                   85
% identity
NCBI Description M.sativa mRNA for cdc2 kinase homologue, cdc2MsF
                   34697
Seq. No.
                   LIB3028-035-Q1-B1-H6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3980393
BLAST score
                   359
                   3.0e - 34
E value
Match length
                   98
                   63
% identity
                   (AC004561) putative glutathione S-transferase [Arabidopsis
NCBI Description
                   thaliana]
                   34698
Seq. No.
                   LIB3028-036-Q1-B1-A4
Seq. ID
Method
                   BLASTX
                   q2462758
NCBI GI
BLAST score
                   234
E value
                   1.0e-19
Match length
                   92
% identity
                   54
                   (AC002292) putative RNA-binding protein [Arabidopsis
NCBI Description
                   thalianal
                   34699
Seq. No.
                   LIB3028-036-Q1-B1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3461836
```

BLAST score 422 E value 1.0e-41

Match length 123 % identity

(AC005315) putative protein kinase [Arabidopsis thaliana] NCBI Description >gi\_3927841 (AC005727) putative protein kinase [Arabidopsis

thaliana]

Seq. No.

34700

Seq. ID LIB3028-036-Q1-B1-C9

Method BLASTX

% identity



```
NCBI GI
                  q2342735
BLAST score
                  184
                  8.0e-14
E value
                  81
Match length
                  53
% identity
NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]
                  34701
Seq. No.
                  LIB3028-036-Q1-B1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q18761
BLAST score
                  171
E value
                  2.0e-91
                  255
Match length
                  92
% identity
NCBI Description Soybean stem mRNA for 31 kD glycoprotein
                  34702
Seq. No.
                  LIB3028-036-Q1-B1-E9
Seq. ID
Method
                  BLASTX
                  g886130
NCBI GI
                  167
BLAST score
E value
                  8.0e-12
Match length
                  77
% identity
                  43
NCBI Description (U28148) putative pectinesterase [Medicago sativa]
                  34703
Seq. No.
Seq. ID
                  LIB3028-036-Q1-B1-F3
Method
                  BLASTX
NCBI GI
                  g3746062
BLAST score
                  284
E value
                  2.0e-25
Match length
                  114
% identity
                   48
NCBI Description (AC005311) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   34704
                  LIB3028-036-Q1-B1-G6
Seq. ID
Method
                  BLASTN
                  g170087
NCBI GI
                   233
BLAST score
                   1.0e-128
E value
Match length
                   356
% identity
                   92
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
Seq. No.
                   34705
                  LIB3028-036-Q1-B1-H1
Seq. ID
Method
                  BLASTX
                   q1279640
NCBI GI
                   426
BLAST score
E value
                   4.0e-42
                   93
Match length
                   81
```

NCBI Description (X92204) NAM [Petunia x hybrida]



```
Seq. No.
Seq. ID
                  LIB3028-036-Q1-B1-H11
                  BLASTN
Method
                  q309563
NCBI GI
BLAST score
                  47
                  2.0e-17
E value
Match length
                  79
% identity
                  91
                  Zea mays NADH dehydrogenase subunit 4 (complex I) (nad4)
NCBI Description
                  gene, exon 3
                   34707
Seq. No.
Seq. ID
                  LIB3028-036-Q1-B1-H12
Method
                  BLASTN
NCBI GI
                  g3941288
                   63
BLAST score
                  7.0e-27
E value
                   107
Match length
% identity
                   90
                  Pisum sativum similarity to SCAMP37 (psam2) mRNA, complete
NCBI Description
                   cds
                   34708
Seq. No.
Seq. ID
                  LIB3028-037-Q1-B1-F4
Method
                  BLASTX
NCBI GI
                   g4263704
BLAST score
                   310
E value
                   2.0e-28
Match length
                   88
% identity
                   69
                   (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   34709
                   LIB3028-037-Q1-B1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3386614
BLAST score
                   313
E value
                   7.0e-29
Match length
                   86
% identity
                   (AC004665) putative transcription factor SF3 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   34710
Seq. ID
                   LIB3028-038-Q1-B1-H6
Method
                   BLASTX
NCBI GI
                   g2289003
BLAST score
                   442
E value
                   5.0e-44
Match length
                   126
% identity
                   71
                   (AC002335) membrane transporter D1 isolog [Arabidopsis
NCBI Description
                   thaliana]
```

34711

LIB3028-038-Q1-B1-H9

Seq. No. Seq. ID



Method BLASTN
NCBI GI g2827081
BLAST score 90
E value 4.0e-43
Match length 149
% identity 91

NCBI Description Medicago sativa cytosolic malate dehydrogenase (cmdh) mRNA,

complete cds

Seq. No. 34712

Seq. ID LIB3028-039-Q1-B2-B1

Method BLASTN
NCBI GI g1173641
BLAST score 126
E value 1.0e-64
Match length 229
% identity 90

NCBI Description Glycine max lipoxygenase (lox7) mRNA, complete cds

Seq. No. 34713

Seq. ID LIB3028-039-Q1-B2-B9

Method BLASTN
NCBI GI g170089
BLAST score 268
E value 1.0e-149
Match length 324
% identity 96

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No. 34714

Seq. ID LIB3028-039-Q1-B2-C2

Method BLASTN
NCBI GI g3033373
BLAST score 51
E value 6.0e-20
Match length 95
% identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC F19I3 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3028-039-Q1-B2-C6

34715

Method BLASTX
NCBI GI g2244956
BLAST score 231
E value 4.0e-19
Match length 83
% identity 51

NCBI Description (Z97340) strong similarity to pectinesterase [Arabidopsis

thaliana]

Seq. No. 34716

Seq. ID LIB3028-039-Q1-B2-F1

Method BLASTN
NCBI GI g1778371
BLAST score 134
E value 3.0e-69



Match length 373 % identity 85 NCBI Description Gly cds

ription Glycine max asparagine synthetase 1 (AS1) mRNA, complete

Seq. No. 34717

Seq. ID LIB3028-039-Q1-B2-G9

Method BLASTN
NCBI GI g1841474
BLAST score 35
E value 1.0e-10
Match length 95
% identity 84

NCBI Description P.sativum mRNA for Myb-like protein (Myb26)

Seq. No. 34718

Seq. ID LIB3028-039-Q1-B2-H1

Method BLASTX
NCBI GI g3355483
BLAST score 163
E value 2.0e-11
Match length 58
% identity 48

NCBI Description (AC004218) gibberellin-regulated protein (GASA5)-like

[Arabidopsis thaliana]

Seq. No. 34719

Seq. ID LIB3028-040-Q1-B1-A8

Method BLASTX
NCBI GI g3402694
BLAST score 439
E value 1.0e-43
Match length 131
% identity 66

NCBI Description (AC004697) putative Mlo-hi protein [Arabidopsis thaliana]

Seq. No. 34720

Seq. ID LIB3028-040-Q1-B1-C4

Method BLASTX
NCBI GI g4539314
BLAST score 141
E value 1.0e-08
Match length 53
% identity 58

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 34721

Seq. ID LIB3028-040-Q1-B1-D10

Method BLASTX
NCBI GI g2765093
BLAST score 140
E value 1.0e-08
Match length 100
% identity 38

NCBI Description (Y10983) putative cytochrome P450 [Glycine max]

Seq. No. . 34722



Seq. ID LIB3028-040-Q1-B1-D11 Method BLASTX NCBI GI q1871192 BLAST score 589 E value 3.0e-61Match length 112 % identity NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana] Seq. No. 34723 Seq. ID LIB3028-041-Q1-B1-A12 Method BLASTX NCBI GI a1297189 BLAST score 329 E value 8.0e-31 Match length 107 % identity 62 (U53501) Theoretical protein with similarity to Swiss-Prot NCBI Description Accession Number P19456 plasma membrane ATPase 2 (proton pump) [Arabidopsis thaliana] Seq. No. 34724 LIB3028-041-Q1-B1-A8 Seq. ID Method BLASTN NCBI GI q516853 BLAST score 134 3.0e-69 E value Match length 287 45 % identity NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds Seq. No. 34725 Seq. ID LIB3028-041-Q1-B1-B2 Method BLASTX NCBI GI q541943 BLAST score 273 3.0e-24 E value Match length 55 % identity 85 metallothionein - soybean >gi 228682 prf 1808316A NCBI Description metallothionein-like protein [Glycine max] Seq. No. 34726 Seq. ID LIB3028-041-Q1-B1-E12 Method BLASTX NCBI GI g3281853

BLAST score 141 E value 5.0e-09 Match length 44 % identity 68

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 34727

Seq. ID LIB3028-041-Q1-B1-E8

Method BLASTX NCBI GI g1568637

5238

Seq. ID

Method

NCBI GI



```
BLAST score
                   5.0e-14
E value
Match length
                   109
                   42
% identity
                   (U69554) 6a-hydroxymaackiain methyltransferase [Pisum
NCBI Description
                   sativum]
Seq. No.
                   34728
                   LIB3028-041-Q1-B1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1531758
BLAST score
                   174
E value
                   1.0e-12
                   42
Match length
                   69
% identity
                   (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)
NCBI Description
                   unknown protein [Arabidopsis thaliana]
                   34729
Seq. No.
Seq. ID
                   LIB3028-041-Q1-B1-H9
Method
                   BLASTX
                   q136057
NCBI GI
BLAST score
                   233
E value
                   1.0e-19
Match length
                   81
% identity
                   56
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
                   Coptis japonica >gi 556171 (J04121) triosephosphate
                   isomerase [Coptis japonica]
Seq. No.
                   34730
Seq. ID
                   LIB3028-042-Q1-B1-A10
Method
                   BLASTX
NCBI GI
                   g2654095
BLAST score
                   214
                   3.0e-17
E value
                   87
Match length
% identity
                   51
                   (AF034210) aspartate aminotransferase cytosolic isozyme
NCBI Description
                   AAT2 [Glycine max]
                   34731
Seq. No.
Seq. ID
                   LIB3028-042-Q1-B1-B4
                   BLASTX
Method
NCBI GI
                   g2706515
BLAST score
                   210
                   7.0e-17
E value
Match length
                   86
                   48
% identity
                   (Y12689) isoflavone reductase-like protein [Citrus x
NCBI Description
                   paradisi]
Seq. No.
                   34732
```

5239

LIB3028-042-Q1-B1-C12

BLASTX

g3892056



```
BLAST score
E value
                  8.0e-09
                  54
Match length
                  59
% identity
                  (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34733
                  LIB3028-042-Q1-B1-D2
Seq. ID
Method
                  BLASTX
                  g294666
NCBI GI
BLAST score
                  181
E value
                  2.0e-13
Match length
                  58
% identity
                  60
                  (L13241) beta-ketoacyl-ACP synthase [Ricinus communis]
NCBI Description
                  34734
Seq. No.
Seq. ID
                  LIB3028-042-Q1-B1-F7
Method
                  BLASTX
                  g2880044
NCBI GI
BLAST score
                  142
                  7.0e-09
E value
Match length
                  31
% identity
                  94
                  (AC002340) putative tropinone reductase [Arabidopsis
NCBI Description
                  thaliana]
                  34735
Seq. No.
Seq. ID
                  LIB3028-043-Q1-B1-E3
Method
                  BLASTX
NCBI GI
                  g2760837
BLAST score
                  151
E value
                  5.0e-10
Match length
                  88
% identity
                  (AC003105) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34736
Seq. ID
                  LIB3028-043-Q1-B1-E8
Method
                  BLASTX
                  q2632105
NCBI GI
                  150
BLAST score
                  1.0e-09
E value
Match length
                  37
                  78
% identity
                  (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                  >gi 4539426 emb CAB38959.1 (AL049171) arginyl-tRNA
                  synthetase [Arabidopsis thaliana]
Seq. No.
                  34737
                  LIB3028-043-Q1-B1-G11
Seq. ID
Method
                  BLASTX
                  g2642450
NCBI GI
BLAST score
                  484
                  7.0e-49
E value
```

122

75

Match length

% identity



NCBI Description (AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] >qi 3169188 (AC004401) putative

metal ion transporter (Nramp) [Arabidopsis thaliana]

Seq. No. 34738

Seq. ID LIB3028-043-Q1-B1-G3

Method BLASTX
NCBI GI g2792297
BLAST score 320
E value 9.0e-30
Match length 66
% identity 80

NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No. 34739

Seq. ID LIB3028-043-Q1-B1-H3

Method BLASTX
NCBI GI g2244898
BLAST score 334
E value 2.0e-31
Match length 98
% identity 63

NCBI Description (Z97338) strong similarity to protein phosphatase 2A

regulatory chain, 74K [Arabidopsis thaliana]

Seq. No. 34740

Seq. ID LIB3028-044-Q1-B1-C11

Method BLASTX
NCBI GI g3641252
BLAST score 571
E value 4.0e-59
Match length 117
% identity 90

NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus

domestica]

Seq. No. 34741

Seq. ID LIB3028-044-Q1-B1-F11

Method BLASTX
NCBI GI g4337196
BLAST score 202
E value 7.0e-16
Match length 123
% identity 36

NCBI Description (AC006403) putative serine/threonine receptor kinase

[Arabidopsis thaliana]

Seq. No. 34742

Seq. ID LIB3028-044-Q1-B1-G9

Method BLASTX
NCBI GI g2760319
BLAST score 188
E value 3.0e-14
Match length 107
% identity 50

NCBI Description (AC002130) F1N21.3 [Arabidopsis thaliana]

NCBI GI BLAST score

48



```
Seq. No.
Seq. ID
                  LIB3028-045-Q1-B1-B12
Method
                  BLASTX
NCBI GI
                  g603074
BLAST score
                  228
                  7.0e-19
E value
Match length
                  122
% identity
                  39
NCBI Description (U18197) ATP:citrate lyase [Homo sapiens]
                  34744
Seq. No.
                  LIB3028-045-Q1-B1-B3
Seq. ID
Method
                  BLASTN
                  q2828182
NCBI GI
                  47
BLAST score
                  2.0e-17
E value
                  95
Match length
% identity
                  87
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOJ9, complete sequence [Arabidopsis thaliana]
                  34745
Seq. No.
Seq. ID
                  LIB3028-045-Q1-B1-E1
Method
                  BLASTN
                  q1326160
NCBI GI
                  48
BLAST score
                   4.0e-18
E value
                  94
Match length
% identity
                   95
NCBI Description Phaseolus vulgaris dehydrin mRNA, complete cds
Seq. No.
                   34746
Seq. ID
                  LIB3028-046-Q1-B1-A4
Method
                  BLASTN
NCBI GI
                   g303900
BLAST score
                   310
                   1.0e-174
E value
                  387
Match length
% identity
                   30
                  Soybean gene for ubiquitin, complete cds
NCBI Description
                   34747
Seq. No.
Seq. ID
                   LIB3028-046-Q1-B1-A9
Method
                   BLASTX
                   g464365
NCBI GI
                   205
BLAST score
                   2.0e-16
E value
                   62
Match length
% identity
                  PEROXIDASE P7 >gi_66306_pir__OPNB7 peroxidase (EC 1.11.1.7)
NCBI Description
                   - turnip
                   34748
Seq. No.
Seq. ID
                   LIB3028-046-Q1-B1-B12
                   BLASTN
Method
                   g2687432
```



E value 6.0e-18 Match length 48 100 % identity Plumbago auriculata large subunit 26S ribosomal RNA gene, NCBI Description partial sequence Seq. No. 34749 LIB3028-046-Q1-B1-C9 Seq. ID Method BLASTX q4007792 NCBI GI BLAST score 283 E value 2.0e-25 Match length 96 62 % identity (AL034463) Xenopus 14s cohesin smc1 subunit homolog NCBI Description [Schizosaccharomyces pombe] Seq. No. 34750 LIB3028-046-Q1-B1-D9 Seq. ID Method BLASTX g4056433 NCBI GI BLAST score 142 E value 6.0e-09 Match length 95 % identity 40 (AC005990) Similar to anter-specific proline-rich protein NCBI Description (CEX) gb X60376 from Brassica napus. [Arabidopsis thaliana] 34751 Seq. No. LIB3028-046-Q1-B1-H1 Seq. ID Method BLASTX NCBI GI q4210948 BLAST score 127 E value 2.0e-09 Match length 77 % identity 56 NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis] 34752 Seq. No. Seq. ID LIB3028-046-Q1-B1-H7 Method BLASTX NCBI GI g3885329 BLAST score 333 E value 3.0e-31Match length 83 78 % identity (AC005623) alien-like protein [Arabidopsis thaliana] NCBI Description Seq. No. 34753 Seq. ID LIB3028-047-Q1-B1-H12 Method BLASTX q2244899

Method BLASTX
NCBI GI g2244899
BLAST score 164
E value 1.0e-11
Match length 92
% identity 43

NCBI Description (Z97338) similar to UFD1 protein [Arabidopsis thaliana]



```
Seq. No.
                  34754
                  LIB3028-048-Q1-B1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3643608
BLAST score
                  197
E value
                  3.0e-15
Match length
                  100
% identity
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  34755
Seq. ID
                  LIB3028-048-Q1-B1-D2
Method
                  BLASTX
                  q2651314
NCBI GI
                  148
BLAST score
                  1.0e-11
E value
Match length
                  43
% identity
                  84
                  (ACO02336) putative ribosomal protein S26 [Arabidopsis
NCBI Description
                  thaliana]
                  34756
Seq. No.
Seq. ID
                  LIB3028-048-Q1-B1-D8
                  BLASTN
Method
                  g391604
NCBI GI
BLAST score
                  35
                  3.0e-10
E value
Match length
                  59
                  90
% identity
                  Arabidopsis thaliana ATPK15D mRNA for casein kinase II
NCBI Description
                  catalytic subunit, complete cds
Seq. No.
                  34757
Seq. ID
                  LIB3028-049-Q1-B1-A5
Method
                  BLASTX
NCBI GI
                  g1170619
BLAST score
                  219
E value
                  8.0e-18
Match length
                  52
% identity
                  83
                  KINESIN-LIKE PROTEIN A >gi_479594_pir__S34830
NCBI Description
                  kinesin-related protein katA - Arabidopsis thaliana
                  >gi 303502 dbj BAA01972 (D11371) kinesin-like motor
                  protein heavy chain [Arabidopsis thaliana]
                  >gi 2911084 emb CAA17546 (AL021960) kinesin-related
                  protein katA [Arabidopsis thaliana]
Seq. No.
                  34758
Seq. ID
                  LIB3028-049-Q1-B1-B2
Method
                  BLASTN
NCBI GI
                  q2687725
BLAST score
                  382
E value
                  0.0e+00
```

5244

NCBI Description Glycine max mRNA for putative 2-hydroxydihydrodaidzein

466

98

Match length

% identity

BLAST score

293



## reductase

```
34759
Seq. No.
                  LIB3028-049-Q1-B1-C1
Seq. ID
                  BLASTN
Method
                   g4098318
NCBI GI
BLAST score
                   237
                   1.0e-130
E value
                   501
Match length
                   87
% identity
NCBI Description Triticum aestivum beta-tubulin 1 (tubb1) mRNA, complete cds
Seq. No.
                   34760
                   LIB3028-050-Q1-B1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3935183
BLAST score
                   174
                   5.0e-13
E value
                   75
Match length
                   52
% identity
NCBI Description (AC004557) F17L21.26 [Arabidopsis thaliana]
                   34761
Seq. No.
                   LIB3028-050-Q1-B1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3551247
BLAST score
                   331
                   6.0e-31
E value
                   75
Match length
                   77
% identity
                  (AB012703) 181 [Daucus carota]
NCBI Description
                   34762
Seq. No.
Seq. ID
                   LIB3028-050-Q1-B1-H5
                   BLASTN
Method
NCBI GI
                   q624937
BLAST score
                   40
                   3.0e-13
E value
                   104
Match length
% identity
                   86
NCBI Description A.thaliana RPL16A gene
                   34763
Seq. No.
                   LIB3028-051-Q1-B1-C12
Seq. ID
Method
                   BLASTX
                   g2827992
NCBI GI
                   174
BLAST score
                   9.0e-13
E value
Match length
                   75
                   47
% identity
                  (AF034743) UDP-glucuronosyltransferase [Pisum sativum]
NCBI Description
                   34764
Seq. No.
                   LIB3028-051-Q1-B1-E7
Seq. ID
Method
                   BLASTX
                   g1871184
NCBI GI
```



```
2.0e-26
E value
                  93
Match length
                  59
% identity
                  (U90439) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34765
                  LIB3028-052-Q1-B1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1708025
BLAST score
                  473
                  1.0e-47
E value
Match length
                  99
% identity
                  91
                  GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+]
NCBI Description
                  >gi_840731_emb_CAA56125_ (X79677) glycerol-3-phosphate
                  dehydrogenase (NAD+) [Cuphea lanceolata]
Seq. No.
                  34766
Seq. ID
                  LIB3028-052-Q1-B2-C11
Method
                  BLASTX
NCBI GI
                  g629641
BLAST score
                  239
E value
                  1.0e-20
Match length
                  58
                  79
% identity
                  PsHSC71.0 protein - garden pea >gi 1076530 pir S53500
NCBI Description
                  HSC71.0 protein - garden pea >gi_473217_emb_CAA83548_
                   (Z32537) PsHSC71.0 [Pisum sativum]
Seq. No.
                  34767
                  LIB3028-052-Q1-B2-C9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g303900
                  254
BLAST score
E value
                  1.0e-141
                  377
Match length
% identity
                  33
NCBI Description Soybean gene for ubiquitin, complete cds
                  34768
Seq. No.
                  LIB3028-052-Q1-B2-G4
Seq. ID
Method
                  BLASTX
                  g4049401
NCBI GI
BLAST score
                  139
                  6.0e-09
E value
                  49
Match length
% identity
                  57
                   (AJ131580) glutathione transferase AtGST 10 [Arabidopsis
NCBI Description
                  thaliana]
                  34769
Seq. No.
Seq. ID
                  LIB3028-052-Q1-B2-H9
                  BLASTN
Method
NCBI GI
                  g18551
```

0.0e+00387 Match length

387

BLAST score

E value



```
% identity
NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
                  protein
                  34770
Seq. No.
                  LIB3028-053-Q1-B1-A12
Seq. ID
                  BLASTX
Method
                  q3183088
NCBI GI
BLAST score
                  252
                  7.0e-22
E value
                  93
Match length
                  54
% identity
                  PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
NCBI Description
                   (LTP) >gi_629658_pir__S47084 lipid transfer like protein -
                  cowpea >gi 499034 emb CAA56113 (X79604) lipid transfer
                  like protein [Vigna unguiculata]
                  34771
Seq. No.
                  LIB3028-053-Q1-B1-C1
Seq. ID
Method
                  BLASTX
                  g2827658
NCBI GI
BLAST score
                  198
                  8.0e-16
E value
                  56
Match length
                   66
% identity
                  (AL021637) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34772
                  LIB3028-053-Q1-B1-D12
Seq. ID
                  BLASTN
Method
                  g20728
NCBI GI
BLAST score
                  54
                   9.0e-22
E value
Match length
                   134
                   85
% identity
                  Pea chloroplast GAPA mRNA encoding
NCBI Description
                   glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A
                   (EC 1.2.1.13)
                   34773
Seq. No.
                   LIB3028-053-Q1-B1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4337196
BLAST score
                   254
                   4.0e-22
E value
Match length
                   73
                   64
% identity
                   (AC006403) putative serine/threonine receptor kinase
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 34774

LIB3028-053-Q1-B1-F6 Seq. ID

Method BLASTX NCBI GI q4193382 BLAST score 144 E value 4.0e-09 Match length 65

% identity (AF083336) ribosomal protein S27 [Arabidopsis thaliana] NCBI Description >gi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana] 34775 Seq. No. Seq. ID LIB3028-053-Q1-B1-G12 Method BLASTN NCBI GI g18551 BLAST score 148 1.0e-77 E value Match length 219 92 % identity Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding NCBI Description protein Seq. No. 34776 Seq. ID LIB3028-053-Q1-B1-G4 Method BLASTX NCBI GI g3676469 BLAST score 176 E value 4.0e-13 Match length 60 % identity 53 (AF053884) (R)-(+)-mandelonitrile lyase isoform MDL4 NCBI Description precursor [Prunus serotina] >gi 3676471 (AF053885) (R)-(+)-mandelonitrile lyase isoform MDL4 precursor [Prunus serotina] >qi 4105127 (AF043186) (R)-(+)-mandelonitrile

lyase isoform MDL4 precursor [Prunus serotina] >gi 4105129 (AF043187) (R)-(+)-mandelonitrile lyase isoform MDL4

precursor [Prunus serotina]

Seq. No. 34777

Seq. ID LIB3028-053-Q1-B1-G5

Method BLASTX NCBI GI g3913808 BLAST score 268 E value 1.0e-23 64 Match length 75 % identity

FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME NCBI Description

SYNTHETASE) >gi 2429618 dbj BAA22284 (AB007120)

ferrochelatase [Oryza sativa]

34778 Seq. No.

Seq. ID LIB3028-053-Q1-B1-G7

BLASTN Method NCBI GI q303900 BLAST score 132 E value 3.0e-68 213 Match length 34 % identity

NCBI Description Soybean gene for ubiquitin, complete cds

34779 Seq. No.

Seq. ID LIB3028-054-Q1-B1-A11

Method BLASTN

% identity

69



```
g1173641
NCBI GI
                  94
BLAST score -
                  8.0e-46
E value
Match length
                  152
% identity
                  91
NCBI Description Glycine max lipoxygenase (lox7) mRNA, complete cds
                  34780
Seq. No.
                  LIB3028-054-Q1-B1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3367520
BLAST score
                  286
E value
                  1.0e-25
Match length
                  124
                   40
% identity
                  (AC004392) Similar to protein kinase APK1A,
NCBI Description
                   tyrosine-serine-threonine kinase gb_D12522 from A.
                   thaliana. [Arabidopsis thaliana]
Seq. No.
                   34781
Seq. ID
                  LIB3028-054-Q1-B1-A3
Method
                  BLASTX
NCBI GI
                   g2642606
BLAST score
                   154
                   1.0e-10
E value
                   39
Match length
% identity
                   74
NCBI Description (AF031922) chalcone synthase [Raphanus sativus]
Seq. No.
                   34782
                   LIB3028-054-Q1-B1-B12
Seq. ID
Method
                   BLASTX
                   q629669
NCBI GI
BLAST score
                   365
                   5.0e-35
E value
                   115
Match length
% identity
                   59
NCBI Description hypothetical protein - tomato
                   34783
Seq. No.
                   LIB3028-054-Q1-B1-B4
Seq. ID
                   BLASTX
Method
                   g3176710
NCBI GI
                   205
BLAST score
                   1.0e-19
E value
                   95
Match length
                   56
% identity
                  (AC002392) unknown protein [Arabidopsis thaliana]
NCBI Description
                   34784
Seq. No.
                   LIB3028-054-Q1-B1-C1
Seq. ID
                   BLASTX
Method
                   g4455276
NCBI GI
BLAST score
                   298
                   3.0e-36
E value
                   116
Match length
```

5249



(AL035527) peptide transporter-like protein [Arabidopsis NCBI Description thaliana] 34785 Seq. No. LIB3028-054-Q1-B1-D5 Seq. ID Method BLASTX NCBI GI g2341032 210 BLAST score 3.0e-17 E value Match length 47 83 % identity (AC000104) EST gb ATTS0956 comes from this gene. NCBI Description [Arabidopsis thaliana] 34786 Seq. No. LIB3028-054-Q1-B1-H11 Seq. ID Method BLASTX NCBI GI q3269285 BLAST score 360 2.0e-34 E value Match length 106 63 % identity (AL030978) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 34787 LIB3028-054-Q1-B1-H3 Seq. ID Method BLASTX NCBI GI q1346118 BLAST score 384 3.0e-37 E value 107 Match length 69 % identity GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR NCBI Description >gi\_542101\_pir\_\_S40215 H-protein - Flaveria pringlei
>gi\_2119599\_pir\_\_S60194 H-protein precursor (clone HFP4) Flaveria pringlei >gi\_438001\_emb\_CAA81075\_ (Z25856)
H-protein [Flaveria pringlei] >gi\_3688301\_emb\_CAB16913\_ (Z99764) H-protein [Flaveria pringlei] Seq. No. 34788 LIB3028-054-Q1-B1-H8 Seq. ID Method BLASTX g4309758 NCBI GI BLAST score 148 2.0e-09 E value 37 Match length % identity 78 (AC006217) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 34789

Seq. ID LIB3028-055-Q1-B1-G5

Method BLASTN
NCBI GI g1055367
BLAST score 191
E value 1.0e-103
Match length 311
% identity 91



Glycine max ribulose-1,5-bisphosphate carboxylase small NCBI Description subunit mRNA, complete cds

34790 Seq. No.

LIB3028-056-Q1-B1-D2 Seq. ID

Method BLASTX g3114573 NCBI GI BLAST score 546 4.0e-56 E value 130 Match length 78 % identity

(AF019383) 1-deoxyxylulose-5-phosphate synthase [Mentha x NCBI Description

piperita]

Seq. No. 34791

LIB3028-056-Q1-B1-D9 Seq. ID

Method BLASTN g1370171 NCBI GI 47 BLAST score 2.0e-17 E value Match length 59 95 % identity

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB1X

Seq. No.

34792

LIB3028-056-Q1-B1-F8 Seq. ID

BLASTN Method g56539 NCBI GI BLAST score 40 4.0e-13 E value 100 Match length 85 % identity

R.norvegicus gene encoding prolactin, exon 5 NCBI Description

>gi 206360\_gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

34793 Seq. No.

LIB3028-056-Q1-B1-G10 Seq. ID

Method BLASTX g3860247 NCBI GI BLAST score 371 1.0e-35 E value Match length 72 96 % identity

(AC005824) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

34794

LIB3028-056-Q1-B1-H12 Seq. ID

Method BLASTX g4559330 NCBI GI BLAST score 240 2.0e-20 E value Match length 89 57 % identity

(AC007087) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

34795



```
LIB3029-001-Q1-B1-B4
Seq. ID
                   BLASTX
Method
                   g731651
NCBI GI
                   308
BLAST score
                   3.0e-28
E value
Match length
                   124
% identity
                   46
                   HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN IN
NCBI Description
                   PUT2-SRB2 INTERGENIC REGION >gi 626608_pir__S46746
                   hypothetical protein YHR039c - yeast (Saccharomyces cerevisiae) >gi_488180 (U00062) Yhr039cp [Saccharomyces
                   cerevisiae]
Seq. No.
                   34796
                   LIB3029-001-Q1-B1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244852
BLAST score
                   308
E value
                   3.0e-28
Match length
                   66
                   85
% identity
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   34797
Seq. ID
                   LIB3029-002-Q1-B1-A4
Method
                   BLASTN
NCBI GI
                   q1431744
BLAST score
                   79
E value
                   8.0e-37
Match length
                   151
                   88
% identity
NCBI Description Glycine max sucrose binding protein (sbp) mRNA, complete
                   cds
Seq. No.
                   34798
Seq. ID
                   LIB3029-002-Q1-B1-C3
                   BLASTN
Method
                   q18540
NCBI GI
                   139
BLAST score
                   2.0e-72
E value
                   285
Match length
                   87
% identity
NCBI Description G.max BBI mRNA for proteinase inhibitor
                   34799
Seq. No.
Seq. ID
                   LIB3029-002-Q1-B1-D12
                   BLASTX
Method
                   g1352345
NCBI GI
                   161
BLAST score
                   3.0e-15
E value
                   90
Match length
                   58
% identity
```

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi\_18765\_emb\_CAA40182\_ (X56856) eEF-la [Glycine max]

Seq. No. 34800

Seq. ID LIB3029-002-Q1-B1-E3

BLAST score

E value Match length 105 6.0e-52

105



```
Method
                  BLASTX
                  q4006897
NCBI GI
                   132
BLAST score
                   2.0e-11
E value
Match length
                   122
% identity
                   40
                  (Z99708) globulin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34801
Seq. ID
                   LIB3029-003-Q1-B1-D10
Method
                   BLASTX
NCBI GI
                   q3097321
BLAST score
                   215
                   2.0e-17
E value
                   80
Match length
                   57
% identity
                  (AB013289) Bd 30K [Glycine max]
NCBI Description
                   34802
Seq. No.
Seq. ID
                   LIB3029-003-Q1-B1-E3
Method
                   BLASTX
NCBI GI
                   q4097880
BLAST score
                   126
E value
                   1.0e-13
                   110
Match length
                   45
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                   34803
                   LIB3029-003-Q1-B1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3036802
BLAST score
                   274
                   3.0e-24
E value
Match length
                   112
% identity
                   55
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3805864 emb CAA21484 (AL031986) putative protein
                   [Arabidopsis thaliana]
                   34804
Seq. No.
Seq. ID
                   LIB3029-004-Q1-B1-D8
                   BLASTN
Method
NCBI GI
                   g516102
BLAST score
                   331
E value
                   0.0e + 00
                   412
Match length
                   95
% identity
NCBI Description Soybean phytochrome B (phyB) gene exons 1-5, complete cds
                   34805
Seq. No.
Seq. ID
                   LIB3029-004-Q1-B1-F6
Method
                   BLASTN
NCBI GI
                   g2270991
```



```
% identity
NCBI Description Glycine max metallothionein-II protein mRNA, complete cds
                  34806
Seq. No.
                  LIB3029-004-Q1-B1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3097320
BLAST score
                  276
                  1.0e-154
E value
Match length
                  324
% identity
NCBI Description Glycine max gene for Bd 30K, complete cds
                  34807
Seq. No.
                  LIB3029-004-Q1-B1-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g886099
BLAST score
                  49
E value
                  6.0e-19
                  77
Match length
                  92
% identity
                  Glycine max putative water channel protein (Pip1) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  34808
                  LIB3029-004-Q1-B1-H8
Seq. ID
                  BLASTN
Method
                  q434060
NCBI GI
BLAST score
                  85
                   4.0e-40
E value
Match length
                  153
                  89
% identity
NCBI Description Soybean DNA for basic 7S globulin, complete cds
                   34809
Seq. No.
                  LIB3029-005-Q1-B1-A10
Seq. ID
Method
                  BLASTX
                   g3894194
NCBI GI
BLAST score
                   144
                   1.0e-09
E value
Match length
                   61
% identity
                   46
                   (AC005662) putative strictosidine synthase [Arabidopsis
NCBI Description
                   thaliana]
                   34810
Seq. No.
                   LIB3029-005-Q1-B1-B6
Seq. ID
Method
                   BLASTN
                   g2305019
NCBI GI
BLAST score
                   104
                   2.0e-51
E value
                   271
Match length
```

97 % identity

NCBI Description Glycine max 2S albumin pre-propeptide mRNA, complete cds

34811 Seq. No.

LIB3029-005-Q1-B1-E5 Seq. ID

E value

Match length

7.0e-64 287



```
BLASTX
Method
                  g2801536
NCBI GI
                  328
BLAST score
                  1.0e-30
E value
                  121
Match length
                  54
% identity
NCBI Description (AF039531) lysophospholipase homolog [Oryza sativa]
                  34812
Seq. No.
                  LIB3029-005-Q1-B1-F12
Seq. ID
                  BLASTN
Method
                  g169972
NCBI GI
                  344
BLAST score
                  0.0e + 00
E value
Match length
                  344
                  100
% identity
NCBI Description Soybean glycinin A-la-B-x subunit mRNA, complete cds
                  34813
Seq. No.
                  LIB3029-005-Q1-B1-G11
Seq. ID
Method
                  BLASTX
                  g1871526
NCBI GI
                   359
BLAST score
                   3.0e-34
E value
                  121
Match length
% identity
                   30
                  (X81997) leucine-rich-repeat protein [Helianthus annuus]
NCBI Description
Seq. No.
                   34814
                   LIB3029-006-Q1-B1-A2
Seq. ID
                   BLASTN
Method
                   g210811
NCBI GI
                   89
BLAST score
                   2.0e-42
E value
                   121
Match length
                   94
% identity
NCBI Description Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
                   34815
Seq. No.
                   LIB3029-006-Q1-B1-B3
Seq. ID
                   BLASTN
Method
                   q210811
NCBI GI
BLAST score
                   119
                   3.0e-60
E value
                   317
Match length
                   85
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No.
                   34816
                   LIB3029-006-Q1-B1-D2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2370311
BLAST score
                   125
```

5255



% identity NCBI Description Medicago sativa mRNA for DnaJ-like protein 34817 Seq. No. LIB3029-006-Q1-B1-E11 Seq. ID Method BLASTN NCBI GI g18540 BLAST score 188 1.0e-101 E value 377 Match length 88 % identity

NCBI Description G.max BBI mRNA for proteinase inhibitor

Seq. No. 34818 LIB3029-006-Q1-B1-F6 Seq. ID

BLASTN Method g4220638 NCBI GI 43 BLAST score 5.0e-15 E value

143 Match length 83 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MIF21, complete sequence [Arabidopsis thaliana]

Seq. No. 34819

LIB3029-007-Q1-B1-A9 Seq. ID

Method BLASTX g132944 NCBI GI BLAST score 485 E value 4.0e-49 102 Match length 87 % identity

60S RIBOSOMAL PROTEIN L3 >gi\_81658\_pir\_\_JQ0772 ribosomal NCBI Description

protein L3 (ARP2) - Arabidopsis thaliana >gi\_806279

(M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No. 34820

LIB3029-007-Q1-B1-B12 Seq. ID

Method BLASTX NCBI GI q4539292 BLAST score 331 5.0e-31 E value 92 Match length 70 % identity

NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis

thaliana]

34821 Seq. No.

Seq. ID LIB3029-007-Q1-B1-C11

Method BLASTX NCBI GI q138364 BLAST score 453 7.0e-53 E value Match length 132 % identity 80

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -



bean pod mottle virus (strain Kentucky G7) >gi 210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No. 34822

LIB3029-007-Q1-B1-C2 Seq. ID

BLASTN Method g4519193 NCBI GI 34 BLAST score 1.0e-09 E value

Match length 38 97 % identity

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MDC11, complete sequence

Seq. No. 34823

LIB3029-007-Q1-B1-C3 Seq. ID

BLASTX Method g138364 NCBI GI 265 BLAST score 8.0e-27 E value Match length 99 69 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi\_75639\_pir\_\_GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 34824

LIB3029-007-Q1-B1-E12 Seq. ID

BLASTN Method g18551 NCBI GI 56 BLAST score 7.0e-23 E value 188 Match length 82 % identity

Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding NCBI Description

protein

34825 Seq. No.

LIB3029-007-Q1-B1-H4 Seq. ID

BLASTN Method q1199562 NCBI GI BLAST score 315 1.0e-177 E value 367 Match length 99 % identity

Glycine max 34 kDa maturing seed vacuolar thiol protease NCBI Description

complete cds mRNA,

34826 Seq. No.

LIB3029-008-Q1-B1-C4 Seq. ID

BLASTX Method q4337188 NCBI GI 248 BLAST score 3.0e-21E value Match length 81 54 % identity



```
NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]
                  34827
Seq. No.
                  LIB3029-008-Q1-B1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2388937
BLAST score
                  204
                  3.0e-16
E value
                  72
Match length
                  50
% identity
                  (Z98977) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                  34828
                  LIB3029-008-Q1-B1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3913952
BLAST score
                  350
E value
                  3.0e-33
Match length
                  85
                  73
% identity
                  ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) >gi 2351578
NCBI Description
                  (U82330) adenylate kinase homolog [Prunus armeniaca]
Seq. No.
                  34829
                  LIB3029-008-Q1-B1-H7
Seq. ID
Method
                  BLASTX
                  a3377507
NCBI GI
                  462
BLAST score
E value
                  2.0e-46
                  125
Match length
% identity
                  69
                  (AF056026) auxin transport protein EIR1 [Arabidopsis
NCBI Description
                  thaliana] >gi_3661620 (AF093241) putative auxin efflux
                  carrier AGR [Arabidopsis thaliana] >gi 3746886 (AF087459)
                  polar-auxin-transport efflux component AGRAVITROPIC 1
                   [Arabidopsis thaliana] >gi 4206709 (AF086906) root
                  gravitropism control protein [Arabidopsis thaliana]
                  34830
Seq. No.
```

LIB3029-009-Q1-B1-A7 Seq. ID

Method BLASTN NCBI GI g18535 299 BLAST score E value 1.0e-167 Match length 365 % identity 91

NCBI Description Soybean mRNA for the alpha subunit of beta-conglycinin

34831 Seq. No.

LIB3029-009-Q1-B1-B6 Seq. ID

BLASTX Method q3549626 NCBI GI BLAST score 180 E value 8.0e-14 58 Match length 53 % identity

NCBI Description (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

Seq. ID

Method NCBI GI 34837

BLASTN

g210811

LIB3029-010-Q1-B1-C10



```
Seq. No.
                  34832
                  LIB3029-009-Q1-B1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4097880
                  351
BLAST score
E value
                  2.0e-33
                  99
Match length
                  71
% identity
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                  34833
Seq. ID
                  LIB3029-009-Q1-B1-G3
                  BLASTN
Method
                  q3097320
NCBI GI
                  190
BLAST score
                  1.0e-102
E value
Match length
                  265
% identity
                  95
NCBI Description Glycine max gene for Bd 30K, complete cds
                  34834
Seq. No.
                  LIB3029-009-Q1-B1-H8
Seq. ID
Method
                  BLASTN
                  g210811
NCBI GI
                  110
BLAST score
                   5.0e-55
E value
                  253
Match length
% identity
                   88
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                   34835
Seq. No.
                   LIB3029-010-Q1-B1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2213594
BLAST score
                   221
                   4.0e-18
E value
Match length
                   73
% identity
                   60
NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]
Seq. No.
                   34836
Seq. ID
                   LIB3029-010-Q1-B1-B3
Method
                   BLASTN
                   q2905771
NCBI GI
BLAST score
                   144
                   3.0e-75
E value
Match length
                   156
                   98
% identity
                  Glycine max glyceraldehyde-3 phosphate dehydrogenase
NCBI Description
                   (GAPDH) mRNA, partial cds
```



BLAST score 249
E value 1.0e-138
Match length 392
% identity 91
NCBI Description Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No. 34838
Seq. ID LIB3029-010-Q1-B1-C7

Method BLASTN
NCBI GI g18535
BLAST score 147
E value 5.0e-77
Match length 219
% identity 92

NCBI Description Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No. 34839

Seq. ID LIB3029-010-Q1-B1-D3

Method BLASTN
NCBI GI g169972
BLAST score 349
E value 0.0e+00
Match length 361
% identity 99

NCBI Description Soybean glycinin A-la-B-x subunit mRNA, complete cds

Seq. No. 34840

Seq. ID LIB3029-010-Q1-B1-E7

Method BLASTX
NCBI GI g2495699
BLAST score 168
E value 7.0e-12
Match length 124
% identity 8

NCBI Description HYPOTHETICAL PROTEIN KIAA0032 >gi\_517115\_dbj\_BAA04945\_

(D25215) KIAA0032 [Homo sapiens]

Seq. No. 34841

Seq. ID LIB3029-010-Q1-B1-F12

Method BLASTX
NCBI GI g4263791
BLAST score 161
E value 2.0e-16
Match length 93
% identity 48

NCBI Description (AC006068) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 34842

Seq. ID LIB3029-010-Q1-B1-F6

Method BLASTX
NCBI GI g135859
BLAST score 203
E value 6.0e-16
Match length 59
% identity 69



NCBI Description TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP) >gi\_282919\_pir\_\_S26742 tonoplast intrinsic protein - kidney bean >gi\_21055\_emb\_CAA44669\_ (X62873) tonoplast intrinsic protein [Phaseolus vulgaris] 34843 Seq. No. LIB3029-010-Q1-B1-F8 Seq. ID BLASTX Method g4539010 NCBI GI 122 BLAST score 2.0e-15 E value 124 Match length 42 % identity (AL049481) putative DNA-directed RNA polymerase NCBI Description [Arabidopsis thaliana] 34844 Seq. No. LIB3029-010-Q1-B1-H6 Seq. ID BLASTX Method g2232354 NCBI GI 267 BLAST score 2.0e-23 E value 110 Match length 45 % identity (AF006081) UDPG glucosyltransferase [Solanum berthaultii] NCBI Description 34845 Seq. No. LIB3029-011-Q1-B1-G3 Seq. ID BLASTN Method g3399776 NCBI GI 46 BLAST score 1.0e-16 E value 106 Match length 86 % identity Glycine max symbiotic ammonium transporter (SAT1) mRNA, NCBI Description complete cds 34846 Seq. No. LIB3029-012-Q1-B1-A5 Seq. ID Method BLASTN q256428 NCBI GI 345 BLAST score 0.0e + 00E value 395 Match length 99 % identity KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and NCBI Description Forrest, mRNA, 1259 nt]

LIB3029-012-Q1-B1-C9

Method BLASTN
NCBI GI g18634
BLAST score 80
E value 2.0e-37
Match length 132
% identity 90

NCBI Description Soybean Gyl gene for glycinin subunit G1



```
34848
Seq. No.
                  LIB3029-012-Q1-B1-D1
Seq. ID
Method
                  BLASTX
                  q99992
NCBI GI
                  200
BLAST score
                  1.0e-15
E value
                  83
Match length
                  52
% identity
                  protein disulfide-isomerase (EC 5.3.4.1) precursor
NCBI Description
                  alfalfa (clone B2) >gi_166418 (M82973) putative
                  endomembrane protein; putative [Medicago sativa]
                  34849
Seq. No.
                  LIB3029-012-Q1-B1-D9
Seq. ID
Method
                  BLASTN
                  q210811
NCBI GI
                  133
BLAST score
                  1.0e-68
E value
                  385
Match length
% identity
                  84
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                  34850
Seq. No.
                  LIB3029-012-Q1-B1-E12
Seq. ID
                  BLASTN
Method
                   g295117
NCBI GI
                   236
BLAST score
                   1.0e-130
E value
                   349
Match length
                   97
% identity
NCBI Description Soybean lipoxygenase-1 mRNA
                   34851
Seq. No.
                   LIB3029-012-Q1-B1-F7
Seq. ID
                   BLASTX
Method
                   q4455232
NCBI GI
                   478
BLAST score
E value
                   3.0e-48
                   131
Match length
                   66
% identity
                  (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                   34852
Seq. No.
                   LIB3029-012-Q1-B1-G1
Seq. ID
                   BLASTN
Method
                   q21834
NCBI GI
BLAST score
                   44
                   2.0e-15
E value
Match length
                   84
                   88
% identity
                   Wheat mRNA for cytosolic phosphoglycerate kinase (EC
NCBI Description
```

2.7.2.3)

LIB3029-012-Q1-B1-G2

34853

Seq. No.

Seq. ID



```
BLASTX
Method
NCBI GI
                  q1931651
                  394
BLAST score
                  2.0e-38
E value
                  125
Match length
                  62
% identity
                  (U95973) membrane-associated salt-inducible protein isolog
NCBI Description
                   [Arabidopsis thaliana]
                  34854
Seq. No.
                  LIB3029-012-Q1-B1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g229707
BLAST score
                  551
                  8.0e-57
E value
                  109
Match length
                  91
% identity
NCBI Description Bean pod mottle virus
                  34855
Seq. No.
                  LIB3030-001-Q1-B1-D11
Seq. ID
Method
                  BLASTX
                  g2262105
NCBI GI
BLAST score
                  199
E value
                  8.0e-16
Match length
                  81
% identity
                   41
                  (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
                   34856
Seq. No.
                  LIB3030-001-Q1-B1-G6
Seq. ID
                  BLASTX
Method
                   g2160189
NCBI GI
BLAST score
                   296
                   8.0e-27
E value
Match length
                   127
% identity
                   49
                   (AC000132) Similar to A. thaliana receptor-like protein
NCBI Description
                   kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475, gb_ATTS4362 come
                   from this gene. [Arabidopsis thaliana]
                   34857
Seq. No.
                   LIB3030-001-Q1-B1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3378650
BLAST score
                   159
                   3.0e-17
E value
Match length
                   83
% identity
                  (X97606) abscisic acid activated [Medicago sativa]
NCBI Description
Seq. No.
                   34858
                   LIB3030-002-Q1-B1-A3
```

Seq. ID

Method BLASTX NCBI GI g3461829 179 BLAST score 3.0e-13 E value



```
Match length
% identity
                   49
                  (AC004138) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  34859
Seq. No.
                  LIB3030-002-Q1-B1-B5
Seq. ID
Method
                  BLASTX
                  g3947733
NCBI GI
BLAST score
                  251
                  1.0e-21
E value
                  98
Match length
                   54
% identity
NCBI Description
                  (AJ009719) NL25 [Solanum tuberosum]
                   34860
Seq. No.
                  LIB3030-002-Q1-B1-C8
Seq. ID
                  BLASTN
Method
                   q914912
NCBI GI
BLAST score
                   45
                   2.0e-16
E value
                   214
Match length
                   85
% identity
NCBI Description Brassica napus elongation factor EF-1A mRNA, partial cds
Seq. No.
                   34861
                   LIB3030-002-Q1-B1-C9
Seq. ID
                   BLASTX
Method
                   g529516
NCBI GI
                   589
BLAST score
                   3.0e-61
E value
                   123
Match length
                   79
% identity
                  (L29099) beta-fructosidase [Solanum tuberosum]
NCBI Description
Seq. No.
                   34862
                   LIB3030-002-Q1-B1-D1
Seq. ID
Method
                   BLASTN
                   g1066856
NCBI GI
                   73
BLAST score
E value
                   2.0e-33
                   117
Match length
                   91
% identity
                   Glycine max acetyl coenzyme A carboxylase (ACCase-B) gene,
NCBI Description
                   5' end of cds
                   34863
Seq. No.
Seq. ID
                   LIB3030-002-Q1-B1-D7
Method
                   BLASTN
NCBI GI
                   g4263753
```

Method BLASTN
NCBI GI g4263753
BLAST score 37
E value 2.0e-11

Match length 112 % identity 88

NCBI Description Arabidopsis thaliana chromosome V map near 60.5 cM,

complete sequence [Arabidopsis thaliana]

Seq. No. 34864

Method

NCBI GI

BLASTN

g18551



```
LIB3030-003-01-B1-B5
Seq. ID
Method
                  BLASTX
                  g2388580
NCBI GI
BLAST score
                  284
                  1.0e-25
E value
                  91
Match length
                  62
% identity
                  (AC000098) Similar to Sequence 10 from patent 5477002
NCBI Description
                   (gb_1253956). [Arabidopsis thaliana]
                  34865
Seq. No.
                  LIB3030-003-Q1-B1-D3
Seq. ID
                  BLASTX
Method
                  g1707007
NCBI GI
                  223
BLAST score
                  3.0e-18
E value
                  127
Match length
% identity
                  (U78721) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  34866
Seq. No.
                  LIB3030-003-Q1-B1-D9
Seq. ID
                  BLASTX
Method
                   g2108252
NCBI GI
BLAST score
                   320
                   1.0e-29
E value
Match length
                   127
                   40
% identity
                   (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
NCBI Description
                   >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
                   [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1
                   (ALO49483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
                   34867
Seq. No.
                   LIB3030-003-Q1-B1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3721856
                   145
BLAST score
E value
                   4.0e-09
Match length
                   30
                   77
% identity
                  (AB014057) beta-Amyrin Synthase [Panax ginseng]
NCBI Description
                   34868
Seq. No.
Seq. ID
                   LIB3030-004-Q1-B1-B11
                   BLASTX
Method
                   q4559351
NCBI GI
                   141
BLAST score
E value
                   1.0e-08
                   40
Match length
% identity
                  (AC006585) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   34869
Seq. No.
                   LIB3030-004-Q1-B1-D1
Seq. ID
```



```
BLAST score
                  0.0e+00
E value
Match length
                  350
                   99
% identity
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                  protein
                  34870
Seq. No.
                  LIB3030-004-Q1-B1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4335739
BLAST score
                   328
E value
                   1.0e-30
Match length
                   94
                   61
% identity
                  (AC006248) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   34871
Seq. No.
                   LIB3030-004-Q1-B1-F8
Seq. ID
Method
                   BLASTX
                   g2982243
NCBI GI
                   265
BLAST score
E value
                   4.0e-23
Match length
                   80
% identity
                   61
                  (AF051204) hypothetical protein [Picea mariana]
NCBI Description
                   34872
Seq. No.
                   LIB3030-004-Q1-B1-H4
Seq. ID
                   BLASTX
Method
                   q3702966
NCBI GI
BLAST score
                   404
E value
                   1.0e-39
Match length
                   112
% identity
                   (AF079486) rac GTP binding protein Arac8 [Arabidopsis
NCBI Description
                   thaliana]
                   34873
Seq. No.
                   LIB3030-005-Q1-B1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3819710
BLAST score
                   352
E value
                   2.0e-33
Match length
                   84
                   73
% identity
                   (AJ224161) delta-8 sphingolipid desaturase [Arabidopsis
NCBI Description
                   thaliana]
                   34874
Seq. No.
                   LIB3030-005-Q1-B1-B10
Seq. ID
                   BLASTX
Method
                   g3080353
NCBI GI
                   224
BLAST score
```

**\***=

2.0e-18

112

43

E value

Match length

% identity

Seq. ID

34880

LIB3030-005-Q1-B1-E12



```
NCBI Description (AL022580) cytochrome P450 [Arabidopsis thaliana]
                  34875
Seq. No.
                  LIB3030-005-Q1-B1-C1
Seq. ID
                  BLASTX
Method
                  q3252854
NCBI GI
                  205
BLAST score
                  1.0e-16
E value
                  57
Match length
                  75
% identity
                  (AF020424) glutamate decarboxylase isozyme 2 [Nicotiana
NCBI Description
                  tabacum]
                  34876
Seq. No.
                  LIB3030-005-Q1-B1-C7
Seq. ID
                  BLASTX
Method
                   g3702368
NCBI GI
                   214
BLAST score
                   3.0e-17
E value
                   69
Match length
                   59
% identity
                   (AJ001855) alpha subunit of F-actin capping protein
NCBI Description
                   [Arabidopsis thaliana]
                   34877
Seq. No.
                   LIB3030-005-Q1-B1-D5
Seq. ID
                   BLASTN
Method
                   g975703
NCBI GI
BLAST score
                   40
                   4.0e-13
E value
                   119
Match length
                   50
% identity
NCBI Description P.sativum GR gene
                   34878
Seq. No.
                   LIB3030-005-Q1-B1-D6
Seq. ID
                   BLASTX
Method
                   g2073450
NCBI GI
                   428
BLAST score
                   3.0e-42
E value
                   93
Match length
                   85
% identity
                   (Y12859) Krm protein [Lotus japonicus]
NCBI Description
                   34879
Seq. No.
                   LIB3030-005-Q1-B1-D8
Seq. ID
                   BLASTX
Method
                   q4204695
NCBI GI
BLAST score
                   179
                   4.0e-13
E value
Match length
                   93
                   41
 % identity
                   (AF117062) putative inositol polyphosphate 5-phosphatase
NCBI Description
                   At5P1 [Arabidopsis thaliana]
```



```
Method
                  BLASTX
NCBI GI
                  g1703036
BLAST score
                  181
E value
                  2.0e-13
Match length
                  78
                  46
% identity
                 5'-AMP-ACTIVATED PROTEIN KINASE, BETA-1 SUBUNIT (AMPK
NCBI Description
                  BETA-1 CHAIN) (40 KD SUBUNIT) >gi 1335858 (U42411)
                  5'-AMP-activated protein kinase, beta subunit [Rattus
                  norvegicus]
                  34881
Seq. No.
                  LIB3030-005-Q1-B1-H6
Seq. ID
Method
                  BLASTX
                  g2190259
NCBI GI
                  423
BLAST score
                  8.0e-42
E value
                  102.
Match length
               78
% identity
NCBI Description (D86385) A-type cyclin [Catharanthus roseus]
                  34882
Seq. No.
Seq. ID
                  LIB3030-006-Q1-B1-B1
Method
                  BLASTX
NCBI GI
                  g2290532
BLAST score
                  402
                  3.0e-39
E value
Match length
                  121
% identity
NCBI Description (U94748) AN11 [Petunia x hybrida]
Seq. No.
                  34883
                  LIB3030-006-Q1-B1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2244985
BLAST score
                  295
                  1.0e-26
E value
                  96
Match length
% identity
                  68
                 (Z97340) similarity to peroxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34884
                  LIB3030-006-Q1-B1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4371280
BLAST score
                  414
                  1.0e-40
E value
                  126
Match length
% identity
                  67
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]
```

Seq. ID LIB3030-006-Q1-B1-E3

Method BLASTX
NCBI GI g3242447
BLAST score 218
E value 7.0e-18



```
Match length
                   69
% identity
NCBI Description (AB003131) endonuclease [Zinnia elegans]
                   34886
Seq. No.
                   LIB3030-007-Q1-B1-A11
Seq. ID
                   BLASTX
Method
                   g4220474
NCBI GI
                   294
BLAST score
                   1.0e-26
E value
                   102
Match length
                   54
 % identity
NCBI Description (AC006069) putative myosin heavy chain [Arabidopsis
                   thaliana]
                   34887
 Seq. No.
                   LIB3030-007-Q1-B1-A12
 Seq. ID
                   BLASTX
 Method
                   q4335857
NCBI GI
                   344
BLAST score
                   2.0e-32
E value
                   126
Match length
                   50
 % identity
 NCBI Description (AF049347) berberine bridge enzyme [Berberis stolonifera]
                   34888
 Seq. No.
                   LIB3030-007-Q1-B1-C7
 Seq. ID
                   BLASTX
 Method
                   g2827637
 NCBI GI
                   211
 BLAST score
                    6.0e-17
 E value
                   111
 Match length
                    40
 % identity
 NCBI Description (AL021636) putative protein [Arabidopsis thaliana]
                    34889
 Seq. No.
                    LIB3030-007-Q1-B1-D5
 Seq. ID
 Method
                    BLASTX
                    q2465923
 NCBI GI
                    272
 BLAST score
 E value
                    5.0e-24
                    122
 Match length
                    26
 % identity
                    (AF024648) receptor-like serine/threonine kinase
 NCBI Description
                    [Arabidopsis thaliana]
                    34890
 Seq. No.
                    LIB3030-007-Q1-B1-E3
 Seq. ID
 Method
                    BLASTN
                    g18683
 NCBI GI
 BLAST score
                    75
                    5.0e-34
 E value
                    207
 Match length
```

% identity

74

NCBI Description G.max N-20t gene

```
LIB3030-007-Q1-B1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3193316
BLAST score
                  242
E value
                  2.0e-20
Match length
                  125
% identity
                  49
                  (AF069299) contains similarity to nucleotide sugar
NCBI Description
                  epimerases [Arabidopsis thaliana]
                  34892
Seq. No.
                  LIB3030-007-Q1-B1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1041706
BLAST score
                  542
                  1.0e-55
E value
                  120
Match length
                  79
% identity
NCBI Description
                  (U30480) expansin At-EXP6 [Arabidopsis thaliana]
                  34893
Seq. No.
                  LIB3030-008-Q1-B1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462744
BLAST score
                  176
                  8.0e-13
É value
Match length
                  125
% identity
                  31
NCBI Description
                  (AC002292) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  34894
Seq. ID
                  LIB3030-008-Q1-B1-C9
Method
                  BLASTX
NCBI GI
                  q4415937
BLAST score
                  140
                  1.0e-08
E value
                  108
Match length
                  30
% identity
                  (AC006418) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34895
                  LIB3030-008-Q1-B1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244851
BLAST score
                  203
E value
                  5.0e-16
Match length
                  115
% identity
                  40
                  (Z97337) amine oxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34896
Seq. ID
                  LIB3030-009-Q1-B1-A1
Method
```

Method BLASTN
NCBI GI g3059094
BLAST score 166
E value 2.0e-88
Match length 328



% identity 88
NCBI Description Glycine max mRNA for magnesium chelatase subunit

Seq. No. 34897

Seq. ID LIB3030-009-Q1-B1-A2

Method BLASTX
NCBI GI 94455192
BLAST score 185
E value 7.0e-14
Match length 109
% identity 38

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 34898

Seq. ID LIB3030-009-Q1-B1-B12

Method BLASTX
NCBI GI g115797
BLAST score 431
E value 1.0e-42
Match length 99
% identity 82

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-215) (LHCP) >gi\_100026\_pir\_\_S16592 chlorophyll a/b-binding protein - garden pea >gi\_20658\_emb\_CAA40365\_ (X57082) chlorophyll a/b-binding protein [Pisum sativum]

Seq. No. 34899

Seq. ID LIB3030-009-Q1-B1-B4

Method BLASTX
NCBI GI g544129
BLAST score 160
E value 2.0e-11
Match length 53
% identity 62

NCBI Description VIGNAIN PRECURSOR (BEAN ENDOPEPTIDASE) (CYSTEINE PROTEINASE

EP-C1) >gi 20994 emb\_CAA44816\_ (X63102) endopeptidase

[Phaseolus vulgaris]

Seq. No. 34900

Seq. ID LIB3030-009-Q1-B1-B5

Method BLASTX
NCBI GI g1168940
BLAST score 224
E value 2.0e-18
Match length 83
% identity 59

NCBI Description CHORISMATE MUTASE PRECURSOR (CM-1) >gi 629509 pir S38958

chorismate mutase precursor - Arabidopsis thaliana >gi\_429153\_emb\_CAA81286\_ (Z26519) chorismate mutase

precursor [Arabidopsis thaliana]

Seq. No. 34901

Seq. ID LIB3030-009-Q1-B1-B6

MethodBLASTNNCBI GIg310575BLAST score286E value1.0e-160



Match length % identity 94

NCBI Description Glycine max nodulin-26 mRNA, complete cds

Seq. No.

34902

Seq. ID Method

LIB3030-009-Q1-B1-C12

NCBI GI

BLASTX g2627181

BLAST score E value

476 6.0e-48

Match length % identity

117 74

NCBI Description

(D89619) cycloartenol synthase [Pisum sativum]

Seq. No.

34903

Seq. ID

LIB3030-009-Q1-B1-D12

Method NCBI GI BLASTX q3850588 527

BLAST score E value Match length

8.0e-54 141

49

% identity NCBI Description

(AC005278) Contains similarity to gb\_AB011110 KIAA0538

protein from Homo sapiens brain and to phospholipid-binding domain C2 PF\_00168. ESTs gb\_AA585988 and gb\_T04384 come

from this gene. [Arabidopsis thaliana]

Seq. No.

34904

BLASTX

Seq. ID

LIB3030-009-Q1-B1-D3

Method NCBI GI BLAST score E value

g4049518 195 3.0e-19

Match length % identity

139 40

NCBI Description

(AL031852) conserved hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. Seq. ID

34905

Method

LIB3030-009-Q1-B1-D8

NCBI GI BLAST score BLASTX q4510339 583

E value Match length

2.0e-60

% identity

147 40

NCBI Description

(AC006921) putative ABC transporter protein [Arabidopsis

thaliana]

Seq. No.

34906

74

Seq. ID

% identity

LIB3030-009-Q1-B1-F10

Method BLASTX NCBI GI g2852449 BLAST score 470 E value 3.0e-47 Match length 119



NCBI Description (D88207) protein kinase [Arabidopsis thaliana] >gi\_2947061 (AC002521) putative protein kinase [Arabidopsis thaliana]

Seq. No. 34907

Seq. ID LIB3030-009-Q1-B1-F3

Method BLASTX
NCBI GI g280401
BLAST score 508
E value 1.0e-51
Match length 130
% identity 73

NCBI Description H+-transporting ATPase (EC 3.6.1.35) - curled-leaved

tobacco >gi\_170206 (M27888) H+-translocating ATPase

[Nicotiana plumbaginifolia]

Seq. No. 34908

Seq. ID LIB3030-009-Q1-B1-H4

Method BLASTX
NCBI GI g2578440
BLAST score 142
E value 4.0e-09
Match length 73
% identity 37

NCBI Description (X67425) pectinesterase [Pisum sativum]

Seq. No. 34909

Seq. ID LIB3030-009-Q1-B1-H8

Method BLASTX
NCBI GI 94105782
BLAST score 156
E value 2.0e-10
Match length 41
% identity 80

NCBI Description (AF049922) PGP169-12 [Petunia x hybrida]

Seq. No. 34910

Seq. ID LIB3030-010-Q1-B1-A9

Method BLASTX
NCBI GI g2833329
BLAST score 443
E value 3.0e-44
Match length 99
% identity 36

NCBI Description ADP, ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE

NUCLEOTIDE TRANSLOCATOR) (ANT) >gi\_1438860 (L11618) ADP/ATP carrier protein [Anopheles gambiae] >gi 1438862 (L11617)

ADP/ATP carrier protein [Anopheles gambiae]

Seq. No. 34911

Seq. ID LIB3030-010-Q1-B1-C9

Method BLASTX
NCBI GI g131199
BLAST score 158
E value 1.0e-10
Match length 110
% identity 40

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR



(LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi\_81470\_pir\_\_S00453 photosystem I protein psaH precursor - spinach >gi\_21287\_emb\_CAA34749\_ (X16858) psaH [Spinacia oleracea]

```
34912
Seq. No.
                  LIB3030-010-Q1-B1-D12
Seq. ID
                  BLASTX
Method
                  q4539303
NCBI GI
                  184
BLAST score
                  1.0e-13
E value
                   94
Match length
                   37
% identity
                  (AL049480) putative protein [Arabidopsis thaliana]
NCBI Description
                   34913
Seq. No.
                   LIB3030-010-Q1-B1-G5
Seq. ID
                   BLASTX
Method
                   g2281090
NCBI GI
                   142
BLAST score
                   4.0e-13
E value
                   90
Match length
                   42
% identity
                  (AC002333) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   34914
Seq. No.
                   LIB3030-010-Q1-B1-H3
Seq. ID
```

BLASTX Method g1888357 NCBI GI 234 BLAST score 9.0e-20 E value 76 Match length 63 % identity

(X98130) alpha-mannosidase [Arabidopsis thaliana] NCBI Description >gi 1890154 emb\_CAA72432\_ (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

34915 Seq. No.

LIB3030-011-Q1-B1-A11 Seq. ID

BLASTX Method g4337175 NCBI GI 170 BLAST score 3.0e-12 E value 50 Match length 64 % identity

(AC006416) ESTs gb\_T20589, gb\_T04648, gb AA597906, NCBI Description

gb\_T04111, gb\_R84180, gb\_R65428, gb\_T44439, gb\_T76570, gb\_R90004, gb\_T45020, gb\_T42457, gb\_T20921, gb\_AA042762 and gb AA720210 come from this gene. [Arabidopsis thaliana]

34916

Seq. No. LIB3030-011-Q1-B1-C11 Seq. ID

BLASTN Method g347454 NCBI GI 33 BLAST score 5.0e-09 E value 101 Match length



% identity Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3' NCBI Description end 34917 Seq. No. Seq. ID LIB3030-011-Q1-B1-E11 BLASTX Method NCBI GI g4056506 BLAST score 565 2.0e-58 E value Match length 136 74 % identity (AC005896) nodulin-like protein [Arabidopsis thaliana] NCBI Description Seq. No. 34918 Seq. ID LIB3030-011-Q1-B1-H3

Method BLASTN NCBI GI q170455 BLAST score 52 9.0e-21 E value Match length 148 84 % identity

Tomato heat shock cognate protein 80 gene, 3' end NCBI Description

Seq. No. 34919 LIB3030-012-Q1-B1-C10 Seq. ID Method BLASTX NCBI GI q128592 BLAST score 149 6.0e-10 E value Match length 54 57 % identity

POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR NCBI Description

>gi\_82190\_pir\_\_S22495 pollen-specific protein precursor common tobacco >gi 19902 emb CAA43454 (X61146) pollen

specific protein [Nicotiana tabacum]

Seq. No. 34920

Seq. ID LIB3030-012-Q1-B1-C6

Method BLASTX NCBI GI g2511693 BLAST score 166 4.0e-12 E value 58 Match length % identity 55

(Z99954) cysteine proteinase precursor [Phaseolus vulgaris] NCBI Description

34921 Seq. No.

Seq. ID LIB3030-012-Q1-B1-D9

Method BLASTN NCBI GI q1055367 BLAST score 191 E value 1.0e-103 Match length 319 90 % identity

Glycine max ribulose-1,5-bisphosphate carboxylase small NCBI Description

subunit mRNA, complete cds



```
Seq. No.
                  34922
Seq. ID
                  LIB3030-012-Q1-B1-E8
Method
                  BLASTX
                  g2832646
NCBI GI
BLAST score
                  178
E value
                  5.0e-13
                  78
Match length
% identity
                  (AL021710) MuDR transposable element - like protein
NCBI Description
                  [Arabidopsis thaliana]
                  34923
Seq. No.
Seq. ID
                  LIB3030-012-Q1-B1-F10
Method
                  BLASTX
NCBI GI
                  q1705463
BLAST score
                  372
                  8.0e-36
E value
Match length
                  117
% identity
                  66
                  BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi_2129547_pir__S71201
NCBI Description
                  biotin sythase - Arabidopsis thaliana >gi_1045316 (U24147)
                  biotin sythase [Arabidopsis thaliana] >gi_1403662 (U31806)
                  BIO2 protein [Arabidopsis thaliana] >gi_1769457 (L34413)
                  biotin synthase [Arabidopsis thaliana] >gi_2288983
                   (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana]
                  >gi 1589016 prf 2209438A biotin synthase [Arabidopsis
                  thalianal
                  34924
Seq. No.
Seq. ID
                  LIB3030-012-Q1-B1-H10
Method
                  BLASTX
NCBI GI
                  g4006915
BLAST score
                  250
E value
                  2.0e-21
Match length
                  109
% identity
                  (299708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34925
Seq. ID
                  LIB3030-012-Q1-B1-H3
Method
                  BLASTX
NCBI GI
                  q3600039
BLAST score
                  487
E value
                  4.0e-49
                  143
Match length
% identity
                  61
NCBI Description
                  (AF080119) similar to Schizosaccharomyces pombe isp4
                  protein (GB:D14061) [Arabidopsis thaliana]
Seq. No.
                  34926
                  LIB3039-001-Q1-E1-E2
```

Seq. ID

Method BLASTN NCBI GI g168650 BLAST score 226 E value 1.0e-124 Match length 351



% identity 93
NCBI Description Zea mays ubiquitin fusion protein (UBF9) gene, complete cds
Seq. No. 34927
Seq. ID LIB3039-001-Q1-E1-F7

Method BLASTX
NCBI GI g1405561
BLAST score 276
E value 2.0e-24
Match length 56
% identity 98

NCBI Description (X98540) FSGTP1 [Fagus sylvatica]

Seq. No. 34928

Seq. ID LIB3039-001-Q1-E1-F8

Method BLASTX
NCBI GI g3341443
BLAST score 293
E value 1.0e-29
Match length 116
% identity 61

NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 34929

Seq. ID LIB3039-001-Q1-E1-H8

Method BLASTN
NCBI GI g170091
BLAST score 64
E value 9.0e-28
Match length 180
% identity 84

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 34930

Seq. ID LIB3039-002-Q1-E1-A10

Method BLASTX
NCBI GI g3341443
BLAST score 315
E value 4.0e-29
Match length 114
% identity 56

NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 34931

Seq. ID LIB3039-002-Q1-E1-A11

Method BLASTN
NCBI GI g169974
BLAST score 122
E value 4.0e-62
Match length 350
% identity 84

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 34932

Seq. ID LIB3039-002-Q1-E1-A9

Method BLASTN

Match length

% identity



```
NCBI GI
                  q169974
BLAST score
                  138
                  8.0e-72
E value
Match length
                  178
% identity
                  94
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                  34933
                  LIB3039-002-Q1-E1-D11
Seq. ID
Method
                  BLASTX
                  g3341443
NCBI GI
                  175
BLAST score
                  1.0e-12
E value
Match length
                  74
                  50
% identity
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
Seq. No.
                  34934
                  LIB3039-002-Q1-E1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g126151
BLAST score
                  167
E value
                   5.0e-12
Match length
                   61
% identity
                   56
                  LECTIN PRECURSOR (AGGLUTININ) (SBA) >gi 282898 pir S27365
NCBI Description
                  lectin precursor - soybean >gi 170006 (K00821) lectin
                  prepeptide [Glycine max]
Seq. No.
                  34935
Seq. ID
                  LIB3039-002-Q1-E1-E6
                  BLASTX
Method
NCBI GI
                  q3341443
BLAST score
                  339
E value
                   8.0e-32
Match length
                  127
% identity
                   54
NCBI Description
                 (AJ223074) acid phosphatase [Glycine max]
                   34936
Seq. No.
                  LIB3039-002-Q1-E1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3341443
BLAST score
                   250
E value
                   3.0e-29
Match length
                  126
% identity
                   55
NCBI Description (AJ223074) acid phosphatase [Glycine max]
Seq. No.
                   34937
Seq. ID
                  LIB3039-002-Q1-E1-H6
Method
                  BLASTX
                  q2795803
NCBI GI
BLAST score
                  187
E value
                   5.0e-14
```



NCBI Description (AC003674) putative beta-1,3-endoglucanase [Arabidopsis

thaliana] >gi\_3355491 (AC004218) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No. 34938

Seq. ID LIB3039-002-Q1-E1-H7

Method BLASTN
NCBI GI g296408
BLAST score 127
E value 3.0e-65
Match length 215
% identity 90

NCBI Description G.max ADR12 mRNA

Seq. No. 34939

Seq. ID LIB3039-002-Q1-E1-H8

Method BLASTX
NCBI GI g2244839
BLAST score 368
E value 2.0e-35
Match length 117
% identity 62

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34940

Seq. ID LIB3039-003-Q1-E1-A2

Method BLASTN
NCBI GI g3452136
BLAST score 187
E value 1.0e-101
Match length 239
% identity 95

NCBI Description Glycine max mRNA for glucose-6-phosphate-dehydrogenase,

partial

Seq. No. 34941

Seq. ID LIB3039-003-Q1-E1-B12

Method BLASTN
NCBI GI g169974
BLAST score 106
E value 1.0e-52
Match length 268
% identity 91

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 34942

Seq. ID LIB3039-003-Q1-E1-B2

Method BLASTX
NCBI GI g2058280
BLAST score 253
E value 3.0e-23
Match length 88
% identity 65

NCBI Description (X97381) atran3 [Arabidopsis thaliana]

Seq. No. 34943

Seq. ID LIB3039-003-Q1-E1-C12



```
Method
                   BLASTN
NCBI GI
                   q170089
BLAST score
                   246
E value
                   1.0e-136
Match length
                   330
% identity
                   94
                  G.max vegetative storage protien mRNA (VSP27), complete cds
NCBI Description
Seq. No.
                   34944
                  LIB3039-003-Q1-E1-D12
Seq. ID
Method
                  BLASTN
NCBI GI
                   g169974
BLAST score
                   117
                   3.0e-59
E value
                  213
Match length
                   89
% identity
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   34945
                  LIB3039-003-Q1-E1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                   q18764
BLAST score
                   35
E value
                   1.0e-10
Match length
                   71
% identity
                   87
                  G.max tefS1 gene for elongation factor EF-la
NCBI Description
Seq. No.
                   34946
Seq. ID
                   LIB3039-003-Q1-E1-E6
Method
                   BLASTN
NCBI GI
                   g18761
BLAST score
                   40
                   4.0e-13
E value
Match length
                   116
% identity
                   85
NCBI Description
                  Soybean stem mRNA for 31 kD glycoprotein
                   34947
Seq. No.
Seq. ID
                   LIB3039-004-Q1-E1-A12
Method
                   BLASTX
NCBI GI
                   g2961372
BLAST score
                   169
E value
                   5.0e-17
Match length
                   76
                   66
% identity
NCBI Description
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
                   thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal
```

protein L2 [Arabidopsis thaliana]

Seq. No. 34948

Seq. ID LIB3039-004-Q1-E1-B2

Method BLASTX
NCBI GI g3341443
BLAST score 228
E value 4.0e-19
Match length 96



% identity (AJ223074) acid phosphatase [Glycine max] NCBI Description 34949 Seq. No. Seq. ID LIB3039-004-Q1-E1-B5 Method BLASTX NCBI GI q2052379 BLAST score 142 E value 5.0e-09 Match length 69 % identity 45 (U66343) calreticulin [Arabidopsis thaliana] NCBI Description 34950 Seq. No. LIB3039-004-Q1-E1-C3 Seq. ID Method BLASTX g232031 NCBI GI BLAST score 191 E value 1.0e-14 Match length 97 % identity 46 ELONGATION FACTOR 1 BETA' >gi\_322851\_pir\_\_\$29224 NCBI Description translation elongation factor eEF-1 beta chain - rice >gi\_218161\_dbj\_BAA02253\_ (D12821) elongation factor 1 beta' [Oryza sativa] 34951 Seq. No. Seq. ID LIB3039-004-Q1-E1-E3 BLASTX Method NCBI GI g3687251 BLAST score 420 3.0e-41 E value Match length 118 69 % identity (AC005169) unknown protein [Arabidopsis thaliana] NCBI Description 34952 Seq. No. Seq. ID LIB3039-005-Q1-E1-A6 Method BLASTX NCBI GI g3341443 BLAST score 305 7.0e-28 E value Match length 121 % identity 51 NCBI Description (AJ223074) acid phosphatase [Glycine max] Seq. No. 34953 Seq. ID LIB3039-005-Q1-E1-A9 Method BLASTN NCBI GI g169974 BLAST score 173 E value 1.0e-92 Match length 253

Seq. No. 34954

NCBI Description

% identity

92

Glycine max vspA gene, complete cds

Seq. ID

Method



```
LIB3039-005-Q1-E1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1495767
BLAST score
                   37
E value
                   1.0e-11
Match length
                  77
% identity
                   87
                  P.sativum mRNA for 110 kD chloroplast inner envelope
NCBI Description
                  protein IEP110
Seq. No.
                   34955
                  LIB3039-005-Q1-E1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                   g18551
BLAST score
                   392
                   0.0e + 00
E value
Match length
                   396
                   100
% identity
NCBI Description
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
                  protein
Seq. No.
                   34956
Seq. ID
                  LIB3039-005-Q1-E1-C12
Method
                  BLASTX
NCBI GI
                   g2500354
BLAST score
                   159
                   3.0e-11
E value
Match length
                   52
% identity
                   62
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
Seq. No.
                   34957
                  LIB3039-005-Q1-E1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3236238
BLAST score
                   449
E value
                   1.0e-44
Match length
                   97
% identity
                   82
NCBI Description
                   (AC004684) putative ARF1 GTPase activating protein
                   [Arabidopsis thaliana] >gi 4519792 dbj BAA75744.1
                   (AB017876) Aspl [Arabidopsis thaliana]
                   34958
Seq. No.
Seq. ID
                  LIB3039-005-Q1-E1-C6
                  BLASTN
Method
NCBI GI
                   g18644
BLAST score
                   240
E value
                   1.0e-132
Match length
                  312
% identity
                   94
NCBI Description
                  Soybean mRNA for HMG-1 like protein
Seq. No.
                   34959
```

LIB3039-005-Q1-E1-F8

BLASTN

```
g170091
NCBI GI
BLAST score
                  322
                  0.0e+00
E value
Match length
                  374
% identity
                  97
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
                  34960
Seq. No.
                  LIB3039-005-Q1-E1-G9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g414831
BLAST score
                  131
                  2.0e-67
E value
Match length
                  239
                  97
% identity
NCBI Description Glycine max (Rablp) mRNA, complete cds
                  34961
Seq. No.
Seq. ID
                  LIB3039-005-Q1-E1-H9
Method
                  BLASTN
NCBI GI
                  q169974
BLAST score
                  260
E value
                  1.0e-144
Match length
                  384
% identity
                  92
NCBI Description Glycine max vspA gene, complete cds
                  34962
Seq. No.
Seq. ID
                  LIB3039-006-Q1-E1-A9
Method
                  BLASTN
                  g1173641
NCBI GI
                  70
BLAST score
                  2.0e-31
E value
                  106
Match length
% identity
                  92
NCBI Description
                  Glycine max lipoxygenase (lox7) mRNA, complete cds
Seq. No.
                  34963
Seq. ID
                  LIB3039-006-Q1-E1-B3
Method
                  BLASTN
NCBI GI
                  g170053
BLAST score
                  41
                  5.0e-14
E value
Match length
                  65
                  92
% identity
NCBI Description Soybean ribosomal protein S11 mRNA, 3' end
Seq. No.
                  34964
                  LIB3039-006-Q1-E1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1350720
```

BLAST score 198 E value 9.0e-19 75 Match length % identity 63

NCBI Description 60S RIBOSOMAL PROTEIN L32



```
34965
Seg. No.
Seq. ID
                  LIB3039-006-Q1-E1-D3
Method
                  BLASTN
NCBI GI
                  q510875
BLAST score
                   40
                   3.0e-13
E value
Match length
                   99
                   86
% identity
NCBI Description P.vulgaris PvME1 gene
                   34966
Seq. No.
                  LIB3039-006-Q1-E1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1076510
BLAST score
                   169
                   2.0e-12
E value
Match length
                   48
                   71
% identity
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean
NCBI Description
                   >gi_829119_emb_CAA52414_ (X74403) cyclophilin [Phaseolus
                   vulgaris]
                   34967
Seq. No.
Seq. ID
                   LIB3039-006-Q1-E1-E5
                   BLASTN
Method
NCBI GI
                   q170091
BLAST score
                   156
E value
                   1.0e-82
Match length
                   236
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
Seq. No.
                   34968
                   LIB3039-006-Q1-E1-H2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1370199
BLAST score
                   49
E value
                   1.0e-18
Match length
                   77
% identity
                   91
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAC1
                   34969
Seq. No.
Seq. ID
                   LIB3039-007-Q1-E1-B8
Method
                   BLASTX
NCBI GI
                   g3135264
BLAST score
                   241
```

E value 2.0e-20 Match length 75 % identity

NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 34970

Seq. ID LIB3039-007-Q1-E1-C1

Method BLASTN

```
NCBI GI
                  g170091
BLAST score
                  287
E value
                  1.0e-160
Match length
                  295
% identity
                  99
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
Seq. No.
                  34971
                  LIB3039-007-Q1-E1-C2
Seq. ID
Method
                  BLASTX
                  g82080
NCBI GI
BLAST score
                  239
                  3.0e-20
E value
                  89
Match length
                  57
% identity
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi 226872 prf _1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                  34972
Seq. No.
Seq. ID
                  LIB3039-007-Q1-E1-C7
Method
                  BLASTX
NCBI GI
                  q4510379
BLAST score
                  252
                  9.0e-22
E value
                  80
Match length
% identity
                  57
                  (AC007017) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34973
Seq. ID
                  LIB3039-007-Q1-E1-E2
Method
                  BLASTX
NCBI GI
                  q3341443
BLAST score
                  191
E value
                  1.0e-14
Match length
                   92
                   47
% identity
NCBI Description
                  (AJ223074) acid phosphatase [Glycine max]
Seq. No.
                  34974
Seq. ID
                  LIB3039-007-Q1-E1-H12
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                  178
E value
                  1.0e-95
                  313
Match length
                  90
% identity
NCBI Description
                  Glycine max vspA gene, complete cds
                  34975
Seq. No.
```

Seq. ID LIB3039-007-Q1-E1-H2

Method BLASTX NCBI GI q1053059 BLAST score 165 E value 1.0e-11 Match length 63



```
% identity
                   (U38423) histone H3 [Triticum aestivum]
NCBI Description
Seq. No.
                   34976
Seq. ID
                   LIB3039-007-Q1-E1-H6
Method
                   BLASTN
                   g170091
NCBI GI
BLAST score
                   321
                   0.0e+00
E value
Match length
                   389
                   96
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
                   34977
Seq. No.
                   LIB3039-007-Q1-E1-H8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g169974
BLAST score
                   91
                   8.0e-44
E value
Match length
                   203
% identity
                   86
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   34978
Seq. ID
                   LIB3039-008-Q1-E1-B5
Method
                   BLASTX
NCBI GI
                   g3402687
BLAST score
                   181
                   2.0e-13
E value
                   53
Match length
% identity
                   62
NCBI Description
                  (AC004697) unknown protein [Arabidopsis thaliana]
                   34979
Seq. No.
Seq. ID
                   LIB3039-008-Q1-E1-D5
Method
                   BLASTX
NCBI GI
                   g576775
BLAST score
                   236
                   5.0e-20
E value
Match length
                   80
                   68
% identity
NCBI Description
                   (U16992) ubiquitin-carboxy extension protein fusion
                   [Filobasidiella neoformans]
Seq. No.
                   34980
                   LIB3039-008-Q1-E1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4454026
```

Method BLASTX
NCBI GI g4454026
BLAST score 116
E value 1.0e-11
Match length 74
% identity 55

NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No. 34981

Seq. ID LIB3039-008-Q1-E1-E7



Method BLASTN
NCBI GI g169974
BLAST score 145
E value 6.0e-76
Match length 281
% identity 88

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 34982

Seq. ID LIB3039-008-Q1-E1-G3

Method BLASTN
NCBI GI g303900
BLAST score 233
E value 1.0e-128
Match length 389
% identity 35

NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No.

34983

Seq. ID LIB3039-008-Q1-E1-G7

Method BLASTN
NCBI GI g2598656
BLAST score 151
E value 2.0e-79
Match length 278
% identity 89

NCBI Description Vicia faba mRNA for elongation factor 1-alpha (EF1-a)

Seq. No.

34984

Seq. ID LIB3039-008-Q1-E1-H3

Method BLASTN
NCBI GI g170091
BLAST score 291
E value 1.0e-163
Match length 367
% identity 95

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 34985

Seq. ID LIB3039-009-Q1-E1-A8

Method BLASTN
NCBI GI g169974
BLAST score 99
E value 1.0e-48
Match length 147
% identity 92

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 34986

Seq. ID LIB3039-009-Q1-E1-B2

Method BLASTX
NCBI GI g3894158
BLAST score 269
E value 1.0e-23
Match length 115
% identity 46



NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No. 34987

Seq. ID LIB3039-009-Q1-E1-D9

Method BLASTN NCBI GI q18551 BLAST score 322 E value 0.0e+00Match length 382 % identity 96

NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

34988

Seq. No.

LIB3039-009-Q1-E1-E11 Seq. ID

Method BLASTN NCBI GI g169974 BLAST score 262 1.0e-145 E value Match length 382 92 % identity

NCBI Description Glycine max vspA gene, complete cds

Seq. No.

34989 Seq. ID LIB3039-009-Q1-E1-F12

Method BLASTX

NCBI GI q134145 BLAST score 156 E value 2.0e-10 Match length 101 % identity 25

STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE NCBI Description

PROTEIN A) >gi 99886 pir S08511 28K protein - soybean

>gi 169898 (M37530) 28 kDa protein [Glycine max] >gi\_169975

(M76981) vegetative storage protein [Glycine max]

>qi 226867 prf 1609232B 28kD qlycoprotein [Glycine max] >gi 444325 prf 1906374A vegetative storage protein

[Glycine max]

Seq. No. 34990

LIB3039-009-Q1-E1-F6 Seq. ID

BLASTX Method NCBI GI g3341443 BLAST score 261 E value 7.0e-23 Match length 81 % identity 59

NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 34991

Seq. ID LIB3039-009-Q1-E1-G4

Method BLASTN NCBI GI g435678 BLAST score 37 E value 1.0e-11 Match length 53



% identity 92 NCBI Description L.esculentum Mill (cv. Rutgers) mRNA for ribosomal protein S25

 Seq. No.
 34992

 Seq. ID
 LIB3039-009-Q1-E1-H3

 Method
 BLASTX

 NCBI GI
 g548774

 BLAST score
 166

BLAST score 166
E value 9.0e-12
Match length 60
% identity 62

NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi\_542158\_pir\_\_S38360 ribosomal

protein L7a - rice >gi\_303855\_dbj\_BAA02156\_ (D12631)

ribosomal protein L7A [Oryza sativa]

Seq. No. 34993

Seq. ID LIB3039-010-Q1-E1-A10 Method BLASTN

NCBI GI g1262439
BLAST score 341
E value 0.0e+00
Match length 357
% identity 99

NCBI Description Glycine max lipoxygenase (vlxC) mRNA, complete cds

Seq. No. 34994

Seq. ID LIB3039-010-Q1-E1-A12

Method BLASTX
NCBI GI 9421867
BLAST score 277
E value 8.0e-25
Match length 89
% identity 67

NCBI Description ubiquitin / ribosomal protein CEP52 - turnip >gi\_347064 (L21898) ubiquitin/ribosomal protein [Brassica rapa]

>gi\_395079\_emb\_CAA80863\_(Z24738) ubiquitin/ribosomal

protein [Brassica rapa]

Seq. No. 34995

Seq. ID LIB3039-010-Q1-E1-B9

Method BLASTX
NCBI GI g120666
BLAST score 200
E value 4.0e-25
Match length 99
% identity 60

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66012\_pir\_\_DESKG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - garden snapdragon

Seq. No. 34996

Seq. ID LIB3039-010-Q1-E1-C10

Method BLASTN
NCBI GI g170091
BLAST score 202
E value 1.0e-110



Match length 302 % identity 92

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 34997

Seq. ID LIB3039-010-Q1-E1-D11

Method BLASTX
NCBI GI g3341443
BLAST score 190
E value 2.0e-14
Match length 113
% identity 44

NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 34998

Seq. ID LIB3039-010-Q1-E1-E8

Method BLASTX
NCBI GI 9730241
BLAST score 191
E value 1.0e-14
Match length 84
% identity 46

NCBI Description DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN

GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) >gi\_473947\_dbj\_BAA06126\_ (D29643) similar to Canis oligosaccharyltransferase 48 kDa subunit (M98392). [Homo

sapiens]

Seq. No. 34999

Seq. ID LIB3039-010-Q1-E1-F1

Method BLASTX
NCBI GI g1710530
BLAST score 376
E value 3.0e-36
Match length 108
% identity 62

NCBI Description 60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir\_\_S71256

ribosomal protein L27a - Arabidopsis thaliana

>gi\_1107487\_emb\_CAA63025\_ (X91959) 60S ribosomal protein

L27a [Arabidopsis thaliana]

Seq. No. 35000

Seq. ID LIB3039-010-Q1-E1-F12

Method BLASTX
NCBI GI g480390
BLAST score 234
E value 1.0e-19
Match length 83
% identity 55

NCBI Description lectin BMA - Bowringia mildbraedii

Seq. No. 35001

Seq. ID LIB3039-010-Q1-E1-F5

Method BLASTN NCBI GI g169974



```
BLAST score
E value
                  1.0e-177
Match length
                  379
                  96
% identity
                  Glycine max vspA gene, complete cds
NCBI Description
                  35002
Seq. No.
Seq. ID
                  LIB3039-010-Q1-E1-F7
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                  143
E value
                  3.0e-09
Match length
                  69
                  45
% identity
NCBI Description
                  (AJ223074) acid phosphatase [Glycine max]
Seq. No.
                  35003
                  LIB3039-010-Q1-E1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g541943
BLAST score
                  179
E value
                  3.0e-15
Match length
                  56
% identity
                  79
                  metallothionein - soybean >gi_228682_prf__1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
Seq. No.
                  35004
                  LIB3039-010-Q1-E1-G7
Seq. ID
Method
                  BLASTX
                  g2431771
NCBI GI
BLAST score
                  156
E value
                  1.0e-10
Match length
                  51
% identity
                  61
NCBI Description
                  (U62753) acidic ribosomal protein P2b [Zea mays]
Seq. No.
                  35005
                  LIB3039-010-Q1-E1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                  235
                  1.0e-129
E value
                  303
Match length
```

% identity 94

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35006

Seq. ID LIB3039-010-Q1-E1-H5

Method BLASTN NCBI GI q169974 BLAST score 145 E value 8.0e-76 277 Match length 91 % identity

NCBI Description Glycine max vspA gene, complete cds



 Seq. No.
 35007

 Seq. ID
 LIB3039-011-Q1-E1-A12

 Method
 BLASTX

 NCBI GI
 g2129721

 BLAST score
 178

 E value
 8.0e-18

104

56

NCBI Description ribosomal protein S15 - Arabidopsis thaliana

>gi 1107485\_emb\_CAA63028 (X91962) 40S ribosomal protein

S15 [Arabidopsis thaliana]

Seq. No. 35008

Match length

% identity

Seq. ID LIB3039-011-Q1-E1-A9

Method BLASTX
NCBI GI g3876716
BLAST score 255
E value 4.0e-22
Match length 80
% identity 51

NCBI Description (Z46242) similar to Zinc finger, C3HC4 type (RING finger)

[Caenorhabditis elegans]

Seq. No. 35009

Seq. ID LIB3039-011-Q1-E1-B3

Method BLASTN
NCBI GI g169974
BLAST score 173
E value 1.0e-92
Match length 348
% identity 88

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35010

Seq. ID LIB3039-011-Q1-E1-C3

Method BLASTX
NCBI GI g3914431
BLAST score 141
E value 5.0e-16
Match length 77
% identity 58

NCBI Description PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)

(MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)

>gi\_2285802\_dbj\_BAA21651\_ (D78173) 26S proteasome alpha

subunit [Spinacia oleracea]

Seq. No. 35011

Seq. ID LIB3039-011-Q1-E1-D3

Method BLASTX
NCBI GI g3914136
BLAST score 258
E value 2.0e-22
Match length 100
% identity 52

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NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)

>gi\_2632171\_emb\_CAA05771\_ (AJ002958) lipid transfer protein

[Cicer arietinum]



```
Seq. No.
                   35012
Seq. ID
                  LIB3039-011-Q1-E1-E6
Method
                  BLASTX
NCBI GI
                   g2961372
BLAST score
                   140
                   9.0e-09
E value
                   97
Match length
% identity
                   34
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
NCBI Description
                   thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal
                  protein L2 [Arabidopsis thaliana]
Seq. No.
                   35013
                   LIB3039-011-Q1-E1-E9
Seq. ID
Method
                  BLASTN
NCBI GI
                   g170091
BLAST score
                   289
E value
                   1.0e-162
Match length
                   369
                   95
% identity
NCBI Description
                  Glycine max vegetative storage protein (vspB) gene,
                   complete cds
                   35014
Seq. No.
Seq. ID
                   LIB3039-011-Q1-E1-F7
Method
                  BLASTN
NCBI GI
                   g170091
BLAST score
                   245
E value
                   1.0e-135
Match length
                   357
                   92
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
                   35015
Seq. No.
                   LIB3039-012-Q1-E1-A11
Seq. ID
Method
                   BLASTN
                   g169974
NCBI GI
BLAST score
                   54
                   6.0e-22
E value
Match length
                   158
                   84
% identity
NCBI Description
                  Glycine max vspA gene, complete cds
                   35016
Seq. No.
Seq. ID
                   LIB3039-012-Q1-E1-C3
Method
                   BLASTX
NCBI GI
                   q1076510
BLAST score
                   186
E value
                   3.0e-14
```

Match length 58

% identity NCBI Description

peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean >gi\_829119\_emb\_CAA52414\_ (X74403) cyclophilin [Phaseolus

vulgaris]

BLAST score

E value Match length 105 4.0e-52



```
Seq. No.
                   35017
Seq. ID
                   LIB3039-012-Q1-E1-C8
Method
                   BLASTN
NCBI GI
                   g169974
BLAST score
                   159
E value
                   2.0e-84
Match length
                   259
% identity
                   90
NCBI Description
                  Glycine max vspA gene, complete cds
                   35018
Seq. No.
                   LIB3039-012-Q1-E1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3341443
BLAST score
                   224
                   3.0e-20
E value
Match length
                   94
                   59
% identity
NCBI Description
                   (AJ223074) acid phosphatase [Glycine max]
                   35019
Seq. No.
Seq. ID
                   LIB3039-012-Q1-E1-D5
Method
                   BLASTX
NCBI GI
                   q4006867
BLAST score
                   178
                   3.0e-13
E value
Match length
                   67
% identity
                   55
                  (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   35020
                   LIB3039-012-Q1-E1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2961300
BLAST score
                   210
E value
                   6.0e-17
Match length
                   84
                   52
% identity
NCBI Description
                   (AJ225027) ribosomal protein L24 [Cicer arietinum]
                   35021
Seq. No.
Seq. ID
                   LIB3039-012-Q1-E1-E12
Method
                   BLASTX
NCBI GI
                   q3341443
BLAST score
                   216
E value
                   2.0e-17
Match length
                   88
% identity
                   49
                   (AJ223074) acid phosphatase [Glycine max]
NCBI Description
Seq. No.
                   35022
Seq. ID
                   LIB3039-012-Q1-E1-E2
Method
                   BLASTN
NCBI GI
                   g456713
```



% identity 46 NCBI Description Glycine max gene for ubiquitin, complete cds

Seq. No. 35023

Seq. ID LIB3039-012-Q1-E1-E9

Method BLASTN
NCBI GI g170091
BLAST score 193
E value 1.0e-104
Match length 356
% identity 97

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 35024

Seq. ID LIB3039-012-Q1-E1-F11

Method BLASTN
NCBI GI g410285
BLAST score 100
E value 6.0e-49
Match length 211
% identity 87

NCBI Description Pisum sativum rho (ras-related) GTP-binding protein mRNA,

complete cds

Seq. No. 35025

Seq. ID LIB3039-012-Q1-E1-F7

Method BLASTN
NCBI GI g1336081
BLAST score 73
E value 7.0e-33
Match length 325
% identity 82

NCBI Description Glycine max var. Century ascorbate peroxidase 2 (APx2)

mRNA, complete cds

Seq. No. 35026

Seq. ID LIB3039-012-Q1-E1-H2

Method BLASTN
NCBI GI g169974
BLAST score 231
E value 1.0e-127
Match length 355
% identity 91

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35027

Seq. ID LIB3039-013-Q1-E1-A4

Method BLASTX
NCBI GI g4538965
BLAST score 180
E value 3.0e-13
Match length 87
% identity 45

NCBI Description (AL049488) hypothetical protein [Arabidopsis thaliana]

Seq. No. 35028

NCBI GI

BLAST score

g169974



```
LIB3039-013-Q1-E1-B9
Seq. ID
Method
                  BLASTN
                  g170087
NCBI GI
BLAST score
                  32
                  1.0e-08
E value
Match length
                  60
                  88
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
                  35029
Seq. No.
Seq. ID
                  LIB3039-013-Q1-E1-D12
Method
                  BLASTX
NCBI GI
                  g136057
BLAST score
                  277
E value
                  2.0e-37
Match length
                  85
% identity
                  92
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
                  Coptis japonica >gi 556171 (J04121) triosephosphate
                  isomerase [Coptis japonica]
Seq. No.
                  35030
Seq. ID
                  LIB3039-013-Q1-E1-D4
                  BLASTX
Method
NCBI GI
                  q2961300
BLAST score
                  142
                  7.0e-09
E value
                  59
Match length
% identity
                  51
NCBI Description (AJ225027) ribosomal protein L24 [Cicer arietinum]
Seq. No.
                  35031
Seq. ID
                  LIB3039-014-Q1-E1-B5
Method
                  BLASTX
                  g3341443
NCBI GI
BLAST score
                  302
                  1.0e-27
E value
Match length
                  116
                  53
% identity
NCBI Description (AJ223074) acid phosphatase [Glycine max]
                  35032
Seq. No.
Seq. ID
                  LIB3039-014-Q1-E1-B8
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                  199
E value
                  1.0e-108
Match length
                  319
% identity
                  91
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                  35033
Seq. ID
                  LIB3039-014-Q1-E1-D3
Method
                  BLASTN
```

```
E value
                   4.0e~83
Match length
                  208
% identity
                  94
NCBI Description
                  Glycine max vspA gene, complete cds
Seq. No.
                  35034
                  LIB3039-014-Q1-E1-F8
Seq. ID
Method
                  BLASTX
                  g4127352
NCBI GI
BLAST score
                  321
                  9.0e-30
E value
Match length
                  122
% identity
                   48
NCBI Description
                  (AJ010451) glutathione transferase [Alopecurus myosuroides]
                  35035
Seq. No.
                  LIB3039-014-Q1-E1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3292849
BLAST score
                  317
                  3.0e-29
E value
Match length
                  85
% identity
                  72
NCBI Description
                   (AJ007582) arginine methyltransferase [Arabidopsis
                  thaliana]
Seq. No. Seq. ID
                   35036
                  LIB3039-015-Q1-E1-A4
Method
                  BLASTX
                  g2558962
NCBI GI
BLAST score
                  169
E value
                   4.0e-12
Match length
                  75
                   49
% identity
NCBI Description
                  (AF025667) histone H2B1 [Gossypium hirsutum]
                   35037
Seq. No.
Seq. ID
                  LIB3039-015-Q1-E1-B9
Method
                  BLASTX
NCBI GI
                   g488573
BLAST score
                   242
                   1.0e-20
E value
Match length
                   81
                   63
% identity
NCBI Description
                  (U09463) histone H3.2 [Medicago sativa]
                   35038
Seq. No.
                  LIB3039-015-Q1-E1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                   q134145
BLAST score
                   144
E value
                   2.0e-09
Match length
                   44
% identity
                   64
                  STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE
NCBI Description
```

PROTEIN A) >gi\_99886\_pir\_\_S08511 28K protein - soybean >gi\_169898 (M37530) 28 kDa protein [Glycine max] >gi\_169975



(M76981) vegetative storage protein [Glycine max] >gi 226867 prf 1609232B 28kD glycoprotein [Glycine max] >qi 444325 prf 1906374A vegetative storage protein [Glycine max]

Seq. No. 35039 LIB3039-015-Q1-E1-F7 Seq. ID Method BLASTN g169974 NCBI GI BLAST score 212 1.0e-116 E value 316 Match length 92 % identity NCBI Description Glycine max vspA gene, complete cds

35040

Seq. No. LIB3039-015-Q1-E1-G7 Seq. ID Method BLASTN NCBI GI g169974 BLAST score 146 2.0e-76 E value Match length 290 % identity 88

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35041 LIB3039-015-Q1-E1-H2 Seq. ID BLASTX

Method g3283026 NCBI GI BLAST score 180 E value 3.0e-13 Match length 113 % identity 34

NCBI Description (AF051562) putative transposase [Arabidopsis thaliana]

Seq. No. 35042

LIB3039-015-Q1-E1-H9 Seq. ID

Method BLASTN NCBI GI g18551 BLAST score 375 0.0e + 00E value Match length 383 99 % identity

NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

35043 Seq. No.

Seq. ID LIB3039-016-Q1-E1-A3

Method BLASTN NCBI GI q18644 BLAST score 272 E value 1.0e-151 Match length 316 97 % identity

Soybean mRNA for HMG-1 like protein NCBI Description

Seq. No. 35044

Method

NCBI GI

BLASTX

g3482925



```
Seq. ID
                  LIB3039-016-Q1-E1-C10
Method
                  BLASTN
NCBI GI
                  q169974
BLAST score
                  189
E value
                  1.0e-102
Match length
                  380
% identity
                  88
NCBI Description
                  Glycine max vspA gene, complete cds
                  35045
Seq. No.
                  LIB3039-016-Q1-E1-E7
Seq. ID
                  BLASTX
Method
                  g3152583
NCBI GI
BLAST score
                  197
                  3.0e-15
E value
Match length
                  119
                   41
% identity
NCBI Description
                   (AC002986) Contains similarity to inhibitor of apoptosis
                  protein gb U45881 from D. melanogaster. [Arabidopsis
                   thaliana]
Seq. No.
                   35046
Seq. ID
                  LIB3039-017-Q1-E1-A10
Method
                  BLASTX
NCBI GI
                  q541950
BLAST score
                  136
                  1.0e-08
E value
                   51
Match length
                   55
% identity
                  SPCP1 protein - soybean >gi 310576 (L12257) nodulin-26
NCBI Description
                   [Glycine max]
                   35047
Seq. No.
Seq. ID
                  LIB3039-017-Q1-E1-D3
Method
                   BLASTX
NCBI GI
                   g2281449
BLAST score
                  183
                   1.0e-13
E value
Match length
                  55
                   78
% identity
                  (U90214) leucine zipper transcription factor TGA2.1
NCBI Description
                   [Nicotiana tabacum]
                   35048
Seq. No.
                   LIB3039-017-Q1-E1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                   q169974
BLAST score
                   222
E value
                   1.0e-122
Match length
                   321
                   93
% identity
NCBI Description Glycine max vspA gene, complete cds
                   35049
Seq. No.
Seq. ID
                  LIB3039-017-Q1-E1-E12
```



170

68

54

4.0e-12

E value

Match length -

% identity

```
BLAST score
E value
                  2.0e-13
Match length
                   69
                  54
% identity
NCBI Description
                   (AC003970) Highly similar to cinnamyl alcohol
                  dehydrogenase, gi 1143445 [Arabidopsis thaliana]
Seq. No.
                  35050
                  LIB3039-017-Q1-E1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170091
BLAST score
                  329
E value
                  0.0e+00
Match length
                  361
                  98
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
Seq. No.
                  35051
Seq. ID
                  LIB3039-017-Q1-E1-H9
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                  235
E value
                  1.0e-19
                  98
Match length
                  52
% identity
NCBI Description (AJ223074) acid phosphatase [Glycine max]
                  35052
Seq. No.
Seq. ID
                  LIB3039-018-Q1-E1-A4
Method
                  BLASTN
NCBI GI
                  q558922
BLAST score
                  67
E value
                  3.0e-29
Match length
                  179
                  92
% identity
                  Lupinus albus farnesyl pyrophosphate synthase (fps1) mRNA,
NCBI Description
                  complete cds
                   35053
Seq. No.
Seq. ID
                  LIB3039-018-Q1-E1-B10
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                  324
E value
                   4.0e-30
Match length
                  113
% identity
                  58
NCBI Description (AJ223074) acid phosphatase [Glycine max]
Seq. No.
                  35054
Seq. ID
                  LIB3039-018-Q1-E1-C9
Method
                  BLASTX
NCBI GI
                  g4262140
BLAST score
```

(ACO05275) putative C-type U1 snRNP [Arabidopsis thaliana] NCBI Description 35055 Seq. No. LIB3039-018-Q1-E1-D11 Seq. ID BLASTN Method g169974 NCBI GI 75 BLAST score 5.0e-34E value 315 Match length 81 % identity Glycine max vspA gene, complete cds NCBI Description 35056 Seq. No. LIB3039-018-Q1-E1-G8 Seq. ID BLASTXMethod g122070 NCBI GI BLAST score 166 4.0e-12 E value 51 Match length 67 % identity HISTONE H3 >gi\_82483\_pir\_\_A25564 histone H3 - rice NCBI Description >gi\_169793 (M15664) histone 3 [Oryza sativa] >gi\_940018  $(U2\overline{5}664)$  histone H3 [Oryza sativa] 35057 Seq. No. LIB3039-018-Q1-E1-H1 Seq. ID BLASTX Method NCBI GI g3292831 BLAST score 206 2.0e-16 E value 97 Match length 39 % identity (AL031018) putative serine/threonine kinase [Arabidopsis NCBI Description thaliana] 35058 Seq. No. LIB3039-019-Q1-E1-B2 Seq. ID BLASTN Method NCBI GI g456567 82

Method BLASTN
NCBI GI 9456567
BLAST score 82
E value 3.0e-38
Match length 146
% identity 89

NCBI Description Pisum sativum ubiquitin conjugating enzyme (UBC4), complete

cds

Seq. No. 35059

Seq. ID LIB3039-019-Q1-E1-C7

Method BLASTN
NCBI GI g310575
BLAST score 80
E value 4.0e-37
Match length 144
% identity 89

NCBI Description Glycine max nodulin-26 mRNA, complete cds

Seq. No. 35060



```
LIB3039-019-Q1-E1-G4
Seq. ID
Method
                  BLASTN
                  g169974
NCBI GI
                  286
BLAST score
                  1.0e-160
E value
                   378
Match length
% identity
NCBI Description Glycine max vspA gene, complete cds
                   35061
Seq. No.
                  LIB3039-019-Q1-E1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3341443
                   164
BLAST score
                   1.0e-11
E value
                   115
Match length
% identity
                   41
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                   35062
Seq. No.
                   LIB3039-019-Q1-E1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2982432
BLAST score
                   169
                   5.0e-12
E value
                   40
Match length
                   78
% identity
                  (AL022224) putative protein [Arabidopsis thaliana]
NCBI Description
                   35063
Seq. No.
                   LIB3039-020-Q1-E1-B7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4193387
                   125
BLAST score
                   7.0e-64
E value
                   317
Match length
% identity
                   85
                  Hevea brasiliensis translationally controlled tumor protein
NCBI Description
                   (TCTP) mRNA, complete cds
                   35064
Seq. No.
                   LIB3039-020-Q1-E1-C10
Seq. ID
                   BLASTN
Method
                   g2565428
NCBI GI
                   45
BLAST score
                   4.0e-16
E value
                   101
Match length
                   86
% identity
                   Onobrychis viciifolia glycine-rich protein mRNA, complete
NCBI Description
                   cds
                   35065
Seq. No.
                   LIB3039-020-Q1-E1-C5
Seq. ID
                   BLASTN
Method
                   q169899
NCBI GI
```

181

2.0e-97

BLAST score

E value



```
Match length
                  93
% identity
                  G.max 31 kDa protein mRNA, 3' end
NCBI Description
                  35066
Seq. No.
                  LIB3039-020-Q1-E1-E12
Seq. ID
                  BLASTN
Method
NCBI GI
                  q296408
BLAST score
                  57
                  2.0e-23
E value
                  264
Match length
% identity
                  84
NCBI Description G.max ADR12 mRNA
                  35067
Seq. No.
Seq. ID
                  LIB3039-020-Q1-E1-G12
Method
                  BLASTN
                  g170091
NCBI GI
BLAST score
                  310
                  1.0e-174
E value
Match length
                  390
% identity
                  95
NCBI Description
                  Glycine max vegetative storage protein (vspB) gene,
                  complete cds
Seq. No.
                  35068
Seq. ID
                  LIB3039-020-Q1-E1-H6
Method
                  BLASTX
                  g541943
NCBI GI
                  270
BLAST score
                  6.0e-24
E value
Match length
                  55
% identity
                  84
                  metallothionein - soybean >gi_228682_prf__1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
                  35069
Seq. No.
Seq. ID
                  LIB3039-021-Q1-E1-C8
Method
                  BLASTN
                  g169974
NCBI GI
BLAST score
                  195
                  1.0e-105
E value
Match length
                  319
                  90
% identity
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                  35070
Seq. ID
```

LIB3039-021-Q1-E1-F3

BLASTX Method NCBI GI g2443836 BLAST score 167 6.0e-12 E value Match length 64 59 % identity

(AF020793) tonoplast intrinsic protein homolog MSMCP1 NCBI Description

[Medicago sativa]



```
Seq. No.
                  LIB3039-021-Q1-E1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2257524
                  271
BLAST score
                  2.0e-25
E value
                  133
Match length
                  51
% identity
                  (AB004537) HYPOTHETICAL 47.4KD PROTEIN IN SHP1-SEC17
NCBI Description
                  INTERGENIC REGION [Schizosaccharomyces pombe]
                  35072
Seq. No.
Seq. ID
                  LIB3039-021-Q1-E1-G1
                  BLASTN
Method
NCBI GI
                  g2463568
                  227
BLAST score
                  1.0e-124
E value
                  363
Match length
                  91
% identity
NCBI Description Glycine max mRNA for squalene synthase, complete cds
Seq. No.
                  35073
Seq. ID
                  LIB3039-022-Q1-E1-B1
Method
                  BLASTN
NCBI GI
                  q169974
                  240
BLAST score
                  1.0e-132
E value
                  378
Match length
                  92
% identity
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                  35074
Seq. ID
                  LIB3039-022-Q1-E1-B10
                  BLASTN
Method
NCBI GI
                  q169974
BLAST score
                  98
E value
                  3.0e-48
Match length
                  150
                  91
% identity
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                  35075
Seq. ID
                  LIB3039-022-Q1-E1-C12
Method
                  BLASTN
                  q170087
NCBI GI
BLAST score
                  139
E value
                  2.0e-72
                  235
Match length
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
Seq. No.
                   35076
```

Seq. ID LIB3039-022-Q1-E1-D9

Method BLASTX
NCBI GI g134145
BLAST score 171
E value 2.0e-12



```
Match length
                   47
% identity
                   STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE
NCBI Description
                   PROTEIN A) >gi 99886_pir__S08511 28K protein - soybean
                   >gi 169898 (M37530) 28 kDa protein [Glycine max] >gi_169975
                   (M76981) vegetative storage protein [Glycine max]
                   >gi_226867_prf__1609232B 28kD glycoprotein [Glycine max]
>gi_444325_prf__1906374A vegetative storage protein
                   [Glycine max]
                   35077
Seq. No.
Seq. ID
                   LIB3039-022-Q1-E1-E9
Method
                   BLASTN
NCBI GI
                   g169964
BLAST score
                   94
                   2.0e-45
E value
                   234
Match length
% identity
                   90
NCBI Description Soybean glutathione reductase (GR) mRNA, complete cds
                   35078
Seq. No.
                   LIB3039-022-Q1-E1-F11
Seq. ID
Method
                   BLASTN
NCBI GI
                   q169974
BLAST score
                   282
                   1.0e-157
E value
                   353
Match length
                   95
% identity
NCBI Description Glycine max vspA gene, complete cds
                   35079
Seq. No.
                   LIB3039-023-Q1-E1-B10
Seq. ID
Method
                   BLASTX
                   g3341443
NCBI GI
BLAST score
                   188
                   3.0e-14
E value
                   89
Match length
% identity
                    46
                   (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                    35080
Seq. No.
                   LIB3039-023-Q1-E1-B4
Seq. ID
                   BLASTX
Method
                    g1053057
NCBI GI
                    182
BLAST score
                    1.0e-13
E value
                    78
Match length
                    55
% identity
                   (U38422) histone H3 [Triticum aestivum]
NCBI Description
                    35081
Seq. No.
                    LIB3039-023-Q1-E1-C4
Seq. ID
```

BLASTX Method

NCBI GI g3341443 BLAST score 157 9.0e-11 E value 74 Match length

NCBI GI

E value

BLAST score



```
% identity
NCBI Description (AJ223074) acid phosphatase [Glycine max]
                   35082
Seq. No.
Seq. ID
                   LIB3039-023-Q1-E1-D7
Method
                   BLASTX
                   g2695711
NCBI GI
                   281
BLAST score
                   4.0e-25
E value
Match length
                   86
% identity
                   58
NCBI Description (AJ001370) cytochome b5 [Olea europaea]
Seq. No.
                   35083
                   LIB3039-023-Q1-E1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1762939
BLAST score
                   164
E value
                   1.0e-11
Match length
                   58
                   55
% identity
                   (U66266) ORF; able to induce HR-like lesions [Nicotiana
NCBI Description
                   tabacum]
                   35084
Seq. No.
                   LIB3039-023-Q1-E1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q122087
BLAST score
                   143
                   6.0e-09
E value
Match length
                   61
% identity
                   57
                   HISTONE H3 >gi 81849_pir__S04520 histone H3 (clone pH3c-1)
NCBI Description
                   - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136)
                    [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone
                   H3 (AA 1-136) [Medicago satīva] >gi_21797_emb_CAA25451
                    (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459)
                   histone H3.1 [Medicago sativa] >gi 2565419 (AF026803)
                   histone H3 [Onobrychis viciifolia]
                   35085
Seq. No.
                   LIB3039-023-Q1-E1-F1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g169974
                   90
BLAST score
                   4.0e-43
E value
Match length
                   170
                   88
% identity
NCBI Description Glycine max vspA gene, complete cds
                   35086
Seq. No.
Seq. ID
                   LIB3039-023-Q1-E1-F3
Method
                   BLASTX
```

g3341443

289 4.0e-26





Match length 63 % identity (AJ223074) acid phosphatase [Glycine max] NCBI Description 35087 Seq. No. LIB3039-023-Q1-E1-G1 Seq. ID BLASTX Method g2460203 NCBI GI 220 BLAST score 6.0e-18 E value Match length 85 % identity 52 (AF021244) coronatine-induced protein 1 [Arabidopsis NCBI Description thaliana] 35088 Seq. No. LIB3039-023-Q1-E1-G10 Seq. ID Method BLASTX g1272410 NCBI GI 179 BLAST score 3.0e-13 E value 82 Match length 46 % identity (U52045) immunophilin precursor [Vicia faba] NCBI Description ي "لمو" ـ 35089 Seq. No. LIB3039-023-Q1-E1-G7 Seq. ID BLASTX Method g2129726 NCBI GI 233 BLAST score 1.0e-19 E value 72 Match length 72 % identity RNA polymerase II third largest chain RPB35.5A -NCBI Description Arabidopsis thaliana >gi 514318 (L34770) RNA polymerase II third largest subunit [Arabidopsis thaliana] >gi\_4544370\_gb\_AAD22281.1\_AC006920\_5 (AC006920) RNA polymerase II, third largest subunit [Arabidopsis thaliana] 35090 Seq. No. LIB3039-023-Q1-E1-H7 Seq. ID BLASTX Method g3341443 NCBI GI 311 BLAST score 1.0e-28 E value 115 Match length 55 % identity (AJ223074) acid phosphatase [Glycine max] NCBI Description 35091 Seq. No. LIB3039-024-Q1-E1-A2 Seq. ID BLASTN Method

5307

g297877

8.0e-20

51

167

83

NCBI GI

E value

BLAST score

Match length

% identity



NCBI Description A.thaliana UBC10 mRNA for ubiquitin conjugating enzyme homolog >gi\_349212\_gb\_L00640\_ATHUBCC Arabidopsis thaliana ubiquitin conjugating enzyme mRNA, complete cds

 Seq. No.
 35092

 Seq. ID
 LIB3039-024-Q1-E1-B2

 Method
 BLASTN

 NCBI GI
 g1173641

 BLAST score
 77

 E value
 1.0e-35

E value 1.0e-3
Match length 101
% identity 94

NCBI Description Glycine max lipoxygenase (lox7) mRNA, complete cds

 Seq. No.
 35093

 Seq. ID
 LIB3039-024-Q1-E1-B3

 Method
 BLASTN

 NCBI GI
 g456713

 BLAST score
 119

BLAST score 119
E value 2.0e-60
Match length 275
% identity 51

NCBI Description Glycine max gene for ubiquitin, complete cds

Seq. No. 35094 Seq. ID LIB3039-024-Q1-E1-D1

Method BLASTN
NCBI GI g169974
BLAST score 275
E value 1.0e-153
Match length 387
% identity 93

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35095 Seq. ID LIB3039-024-Q1-E1-D5

Method BLASTX
NCBI GI g1762939
BLAST score 193
E value 8.0e-15
Match length 85
% identity 48

NCBI Description (U66266) ORF; able to induce HR-like lesions [Nicotiana

tabacum]

Seq. No. 35096

Seq. ID LIB3039-024-Q1-E1-E6

Method BLASTN
NCBI GI g170091
BLAST score 161
E value 1.0e-85
Match length 201
% identity 95

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 35097

E value

Match length

4.0e-87



```
LIB3039-024-Q1-E1-F11
Seq. ID
                  BLASTN
Method
                  g169974
NCBI GI
                  67
BLAST score
                  2.0e-29
E value
                  155
Match length
                  92
% identity
NCBI Description Glycine max vspA gene, complete cds
                  35098
Seq. No.
                  LIB3039-024-Q1-E1-H10
Seq. ID
Method
                  BLASTN
                  q169974
NCBI GI
                  269
BLAST score
                  1.0e-150
E value
                  353
Match length
                  94
% identity
NCBI Description Glycine max vspA gene, complete cds
                  35099
Seq. No.
Seq. ID
                  LIB3039-024-Q1-E1-H4
Method
                  BLASTN
                  g170091
NCBI GI
                  108
BLAST score
                  5.0e-54
E value
                  168
Match length
                  92
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
                  35100
Seq. No.
Seq. ID
                  LIB3039-025-Q1-E1-A12
Method
                  BLASTN
                  g169974
NCBI GI
                  166
BLAST score
                  2.0e-88
E value
                  230
Match length
                  93
% identity
NCBI Description Glycine max vspA gene, complete cds
                   35101
Seq. No.
                  LIB3039-026-Q1-E1-A3
Seq. ID
                  BLASTX
Method
                  g3341443
NCBI GI
BLAST score
                  171
                   3.0e-12
E value
                   82
Match length
                   52
% identity
NCBI Description (AJ223074) acid phosphatase [Glycine max]
                   35102
Seq. No.
Seq. ID
                   LIB3039-026-Q1-E1-A4
Method
                   BLASTN
                   g169974
NCBI GI
BLAST score
                   164
```



```
% identity
NCBI Description Glycine max vspA gene, complete cds
                  35103
Seq. No.
                  LIB3039-026-Q1-E1-A6
Seq. ID
                  BLASTN
Method
                  g1336081
NCBI GI
                  65
BLAST score
                  4.0e-28
E value
                  209
Match length
                  83
% identity
                  Glycine max var. Century ascorbate peroxidase 2 (APx2)
NCBI Description
                  mRNA, complete cds
                  35104
Seq. No.
                  LIB3039-026-Q1-E1-B4
Seq. ID
Method
                  BLASTX
                  g3341443
NCBI GI
                   309
BLAST score
                  2.0e-28
E value
                  101
Match length
                   58
% identity
NCBI Description (AJ223074) acid phosphatase [Glycine max]
                   35105
Seq. No.
                   LIB3039-026-Q1-E1-C2
Seq. ID
                   BLASTN
Method
                   g169974
NCBI GI
                   131
BLAST score
                   1.0e-67
E value
                   215
Match length
                   90
% identity
NCBI Description Glycine max vspA gene, complete cds
                   35106
Seq. No.
                   LIB3039-026-Q1-E1-E10
Seq. ID
                   BLASTN
Method
                   g169974
NCBI GI
                   258
BLAST score
                   1.0e-143
E value
                   366
Match length
                   93
 % identity
NCBI Description Glycine max vspA gene, complete cds
                   35107
 Seq. No.
                   LIB3039-026-Q1-E1-E6
 Seq. ID
                   BLASTX
 Method
                   q1806146
 NCBI GI
                   192
 BLAST score
                   8.0e-15
 E value
                   86
 Match length
                   53
 % identity
 NCBI Description (X97317) cdc2MsF [Medicago sativa]
```

5310

35108

BLASTN

LIB3039-026-Q1-E1-F1

Seq. No. Seq. ID

Method



```
g170089
NCBI GI
                  297
BLAST score
                  1.0e-166
E value
Match length
                  349
                  96
% identity
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
                  35109
Seq. No.
                  LIB3039-026-Q1-E1-G1
Seq. ID
                  BLASTX
Method
                  g2511574
NCBI GI
                  279
BLAST score
                  3.0e-32
E value
                  110
Match length
% identity
                  70
                  (Y13176) multicatalytic endopeptidase [Arabidopsis
NCBI Description
                  thaliana] >gi 3421075 (AF043520) 20S proteasome subunit
                  PAB1 [Arabidopsis thaliana]
Seq. No.
                  35110
                  LIB3039-026-Q1-E1-G11
Seq. ID
Method
                  BLASTX
                  g548852
NCBI GI
BLAST score
                  286
                  1.0e-25
E value
Match length
                  82
                  66
% identity
                  40S RIBOSOMAL PROTEIN S21 >gi_481227_pir__S38357 ribosomal
NCBI Description
                  protein S21 - rice >gi 303839 dbj BAA02158 (D12633) 40S
                  subunit ribosomal protein [Oryza sativa]
Seq. No.
                  35111
                  LIB3039-026-Q1-E1-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                  275
                  1.0e-153
E value
Match length
                  395
% identity
                  93
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                  35112
                  LIB3039-026-Q1-E1-G6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g169974
BLAST score
                  255
E value
                  1.0e-141
Match length
                  351
                  93
% identity
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                  35113
                  LIB3039-026-Q1-E1-G7
```

Seq. ID

Method BLASTN q169974 NCBI GI BLAST score 281 E value 1.0e-157



Match length 373 % identity 94

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35114

Seq. ID LIB3039-026-Q1-E1-H10

Method BLASTX
NCBI GI g1654140
BLAST score 159
E value 3.0e-11
Match length 41
% identity 78

NCBI Description (U37840) lipoxygenase [Lycopersicon esculentum]

Seq. No. 35115

Seq. ID LIB3039-026-Q1-E1-H12

Method BLASTN
NCBI GI g169974
BLAST score 43
E value 2.0e-15
Match length 103
% identity 85

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35116

Seq. ID LIB3039-027-Q1-E1-A4

Method BLASTN
NCBI GI g310575
BLAST score 170
E value 8.0e-91
Match length 294
% identity 92

NCBI Description Glycine max nodulin-26 mRNA, complete cds

Seq. No. 35117

Seq. ID LIB3039-027-Q1-E1-A9

Method BLASTX
NCBI GI g3068714
BLAST score 172
E value 3.0e-12
Match length 113
% identity 36

NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 35118

Seq. ID LIB3039-027-Q1-E1-B12

Method BLASTN
NCBI GI g3318610
BLAST score 142
E value 6.0e-74
Match length 272
% identity 94

NCBI Description Glycine max mRNA for mitochondrial phosphate transporter,

complete cds

Seq. No. 35119

Seq. ID LIB3039-027-Q1-E1-C1



```
BLASTN
Method
                  g310575
NCBI GI
                  140
BLAST score
                  7.0e-73
E value
                  323
Match length
                  88
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                  35120
Seq. No.
                  LIB3039-027-Q1-E1-F12
Seq. ID
                  BLASTN
Method
                  g11576
NCBI GI
                  243
BLAST score
                  1.0e-134
E value
                  331
Match length
                   94
% identity
                  Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,
NCBI Description
                  NADH dehydrogenase and ORF
                   35121
Seq. No.
                  LIB3039-027-Q1-E1-F9
Seq. ID
                  BLASTN
Method
                   g170053
NCBI GI
BLAST score
                   183
                   1.0e-98
E value
                   183
Match length
                   100
% identity
NCBI Description Soybean ribosomal protein S11 mRNA, 3' end
                   35122
Seq. No.
                   LIB3039-027-Q1-E1-G6
Seq. ID
                   BLASTX
Method
                   g2244910
NCBI GI
                   209
BLAST score
                   1.0e-16
E value
                   69
Match length
                   51
% identity
NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]
                   35123
 Seq. No.
                   LIB3039-028-Q1-E1-B5
 Seq. ID
                   BLASTN
Method
 NCBI GI
                   q1196896
 BLAST score
                   59
                   1.0e-24
 E value
                   75
 Match length
 % identity
NCBI Description Glycine max acidic ribosomal protein PO mRNA, complete cds
                   35124
 Seq. No.
                   LIB3039-028-Q1-E1-E3
 Seq. ID
                   BLASTN
 Method
```

Method BLASTN
NCBI GI g18644
BLAST score 54
E value 1.0e-21
Match length 206
% identity 82



```
NCBI Description Soybean mRNA for HMG-1 like protein
                    35125
 Seq. No.
                    LIB3039-028-Q1-E1-E7
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g4263712
                    203
 BLAST score
                    5.0e-16
 E value
 Match length
                    56
                    71
 % identity
                    (AC006223) putative ribosomal protein S12 [Arabidopsis
 NCBI Description
                    thaliana]
                    35126
 Seq. No.
                    LIB3039-028-Q1-E1-G1
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g2262177
                    176
 BLAST score
                    1.0e-19
 E value
                    72
 Match length
                    71
  % identity
                    (AC002329) hypothetical protein similar to T18A10.3
 NCBI Description
                    [Arabidopsis thaliana]
                    35127
 Seq. No.
                    LIB3039-028-Q1-E1-G11
Seq. ID
                    BLASTN
 Method
                    g169974
 NCBI GI
                    140
 BLAST score
                    6.0e-73
 E value
                    308
 Match length
  % identity
                    86
  NCBI Description Glycine max vspA gene, complete cds
                    35128
  Seq. No.
                    LIB3039-029-Q1-E1-B6
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                    g1076485
  BLAST score
                    188
                    2.0e-17
  E value
                     66
  Match length
  % identity
                     68
  NCBI Description
                    SAM-synthetase - chickpea (fragment)
                    >gi_732576_emb_CAA59508_ (X85252) SAM-synthetase [Cicer
                    arietinum]
                     35129
  Seq. No.
  Seq. ID
                    LIB3039-029-Q1-E1-B9
  Method
                    BLASTN
                     g396818
  NCBI GI
  BLAST score
                    176
                     3.0e-94
  E value
  Match length
                     300
  % identity
                     90
```

5314

NCBI Description P.sativum pspor1 mRNA encoding porin

35130

Seq. No.



```
LIB3039-029-Q1-E1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3355468
BLAST score
                  154
E value
                  1.0e-10
Match length
                  55
% identity
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  35131
                  LIB3039-029-Q1-E1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q729442
BLAST score
                  226
E value
                  1.0e-26
Match length
                  105
% identity
                   40
                  PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR
NCBI Description
                  >gi 166380 (M80235) glucose-regulated endoplasmic reticular
                  protein precursor [Medicago sativa]
                  35132
Seq. No.
Seq. ID
                  LIB3039-029-Q1-E1-F3
                  BLASTX
Method
NCBI GI
                   g3341443
BLAST score
                   309
                   2.0e-28
E value
Match length
                   101
% identity
                   59
NCBI Description (AJ223074) acid phosphatase [Glycine max]
Seq. No.
                   35133
                   LIB3039-029-Q1-E1-F5
Seq. ID
Method
                   BLASTN
                   g169974
NCBI GI
BLAST score
                   138
                   1.0e-71
E value
                   366
Match length
                   85
% identity
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   35134
                   LIB3039-030-Q1-E1-A3
Seq. ID
                   BLASTX
Method
                   g3021485
NCBI GI
                   117
BLAST score
                   4.0e-14
E value
                   89
Match length
                   55
% identity
NCBI Description (AJ224932) histone H2B-3 [Lycopersicon esculentum]
Seq. No.
                   35135
                   LIB3039-030-Q1-E1-A6
Seq. ID
```

5315

BLASTN

44

g170053

Method

NCBI GI BLAST score

E value

Match length % identity

387

NCBI Description Glycine max vspA gene, complete cds



```
1.0e-15
E value
                  160
Match length
                  82
% identity
                  Soybean ribosomal protein S11 mRNA, 3' end
NCBI Description
Seq. No.
                  35136
                  LIB3039-030-Q1-E1-A8
Seq. ID
                  BLASTX
Method
                  q3341443
NCBI GI
                  304
BLAST score
E value
                  8.0e-28
                  95
Match length
                   62
% identity
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                   35137
Seq. No.
                  LIB3039-030-Q1-E1-B11
Seq. ID
Method
                  BLASTN
                   g170091
NCBI GI
                   315
BLAST score
                   1.0e-177
E value
Match length
                   363
                   97
% identity
NCBI Description Glycine max vegetative storage protein (vspB) gene,
                   complete cds
                   35138
Seq. No.
Seq. ID
                   LIB3039-030-Q1-E1-C4
                   BLASTN
Method
NCBI GI
                   q166379
BLAST score
                   98
                   8.0e-48
E value
Match length
                   286
                   86
% identity
                  Alfalfa glucose-regulated endoplasmic reticular protein
NCBI Description
                   mRNA, complete cds
                   35139
Seq. No.
Seq. ID
                   LIB3039-030-Q1-E1-D2
                   BLASTN
Method
                   g169974
NCBI GI
BLAST score
                   153
E value
                   1.0e-80
                   337
Match length
% identity
                   87
NCBI Description Glycine max vspA gene, complete cds
                   35140
Seq. No.
                   LIB3039-030-Q1-E1-D8
Seq. ID
                   BLASTN
Method
                   g169974
NCBI GI
BLAST score
                   192
                   1.0e-104
```



```
Seq. No.
Seq. ID
                  LIB3039-030-Q1-E1-F11
                  BLASTX
Method
                  q282964
NCBI GI
BLAST score
                  350
E value
                   3.0e-33
                   69
Match length
                   87
% identity
                  transforming protein (myb) homolog (clone myb.Ph3) - garden
NCBI Description
                  petunia >gi_20563_emb_CAA78386_ (Z13996) protein 1 [Petunia
                  x hybrida]
                   35142
Seq. No.
Seq. ID
                   LIB3039-030-Q1-E1-F12
                   BLASTN
Method
NCBI GI
                   g170091
BLAST score
                   284
                   1.0e-159
E value
                   372
Match length
                   94
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
                   35143
Seq. No.
Seq. ID
                   LIB3039-030-Q1-E1-F7
                   BLASTN
Method
NCBI GI
                   g18551
                   206
BLAST score
                   1.0e-112
E value
Match length
                   334
% identity
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                   protein
                   35144
Seq. No.
Seq. ID
                   LIB3039-031-Q1-E1-B3
Method
                   BLASTN
                   g169974
NCBI GI
BLAST score
                   287
                   1.0e-160
E value
Match length
                   379
% identity
                   94
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   35145
                   LIB3039-031-Q1-E1-C6
Seq. ID
                   BLASTN
Method
                   g303900
NCBI GI
                   277
BLAST score
```

1.0e-154 E value 355 Match length 32 % identity

NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No.

35146

LIB3039-031-Q1-E1-C8 Seq. ID

Method BLASTN

Match length

% identity

285

91



```
g169974
NCBI GI
BLAST score
                  62
E value
                  1.0e-26
                  126
Match length
% identity
                  87
NCBI Description Glycine max vspA gene, complete cds
                  35147
Seq. No.
Seq. ID
                  LIB3039-031-Q1-E1-C9
Method
                  BLASTX
NCBI GI
                  q3341443
BLAST score
                  320
                  1.0e-29
E value
                  88
Match length
% identity
NCBI Description (AJ223074) acid phosphatase [Glycine max]
Seq. No.
                  35148
                  LIB3039-031-Q1-E1-G7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q170089
BLAST score
                  177
                  5.0e-95
E value
                  321
Match length
                  89
% identity
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
                  35149
Seq. No.
Seq. ID
                  LIB3039-031-Q1-E1-H3
Method
                  BLASTX
NCBI GI
                  g322750
BLAST score
                  273
                  3.0e-24
E value
Match length
                  85
% identity
                  73
                  ubiquitin / ribosomal protein CEP52 - wood tobacco
NCBI Description
                  >gi 170217 (M74100) ubiquitin fusion protein [Nicotiana
                  sylvestris]
                  35150
Seq. No.
                  LIB3039-032-Q1-E1-A10
Seq. ID
                  BLASTN
Method
                  q296408
NCBI GI
BLAST score
                  74
                  2.0e-33
E value
Match length
                  178
% identity
                  86
NCBI Description G.max ADR12 mRNA
                   35151
Seq. No.
Seq. ID
                  LIB3039-032-Q1-E1-A12
Method
                  BLASTN
                  q170091
NCBI GI
                  177
BLAST score
                   5.0e-95
E value
```

E value

Match length

% identity

3.0e-24

NCBI Description (AJ223074) acid phosphatase [Glycine max]



```
Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
                  35152
Seq. No.
Seq. ID
                  LIB3039-032-Q1-E1-A2
Method
                  BLASTX
NCBI GI
                  g1053057
                  164
BLAST score
                  2.0e-11
E value
                  78
Match length
                  51
% identity
                  (U38422) histone H3 [Triticum aestivum]
NCBI Description
                  35153
Seq. No.
Seq. ID
                  LIB3039-032-Q1-E1-A9
                  BLASTN
Method
NCBI GI
                  g2225884
                  120
BLAST score
                   6.0e-61
E value
                  336
Match length
                  84
% identity
                  Solanum tuberosum mRNA for eukaryotic initiation factor
NCBI Description
                  5A5, complete cds
                   35154
Seq. No.
Seq. ID
                  LIB3039-032-Q1-E1-B5
Method
                  BLASTX
                   g1172817
NCBI GI
                   198
BLAST score
                   2.0e-15
E value
                   99
Match length
% identity
                   45
                   60S RIBOSOMAL PROTEIN L11B (L16B) >gi_550547_emb_CAA57396_
NCBI Description
                   (X81800) ribosomal protein L16 [Arabidopsis thaliana]
                   >gi_4539392_emb_CAB37458.1_ (AL035526) ribosomal protein
                   L11, cytosolic [Arabidopsis thaliana]
Seq. No.
                   35155
                   LIB3039-032-Q1-E1-D3
Seq. ID
                   BLASTN
Method
NCBI GI
                   q1053044
BLAST score
                   47
E value
                   1.0e-17
Match length
                   133
                   92
% identity
NCBI Description Glycine max histone H3 gene, partial cds, clone S1
                   35156
Seq. No.
                   LIB3039-032-Q1-E1-E2
Seq. ID
                   BLASTX
Method
                   g3341443
NCBI GI
BLAST score
                   274
```



```
35157
Seq. No.
                  LIB3039-032-Q1-E1-E9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q170091
BLAST score
                  292
E value
                  1.0e-163
                  360
Match length
                  95
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
                  35158
Seq. No.
Seq. ID
                  LIB3039-032-Q1-E1-F7
                  BLASTN
Method
                  q169974
NCBI GI
BLAST score
                  206
E value
                   1.0e-112
Match length
                   358
% identity
                   89
                  Glycine max vspA gene, complete cds
NCBI Description
                   35159
Seq. No.
                  LIB3039-032-Q1-E1-G10
Seq. ID
                  BLASTX
Method
                   q2388943
NCBI GI
                   183
BLAST score
E value
                   1.0e-13
                   50
Match length
% identity
                   (Z98978) SPAC27E2.03c, putative gtp-binding protein,
NCBI Description
                   len:392a a, similar eg. to YBR025C, YBN5_YEAST, P38219,
                   hypothetica 1 44.2 kd protein, (394aa), fasta scores,
                   opt:1664, E():0, (63.7% identity in 391 aa overlap), also
                   sim
                   35160
Seq. No.
Seq. ID
                   LIB3039-032-Q1-E1-H12
                   BLASTN
Method
                   q170091
NCBI GI
                   231
BLAST score
E value
                   1.0e-127
                   359
Match length
% identity
                   91
                   Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
                   35161
Seq. No.
```

LIB3039-033-Q1-E1-A2 Seq. ID

BLASTN Method g170091 NCBI GI 287 BLAST score E value 1.0e-160 363 Match length 95 % identity

Glycine max vegetative storage protein (vspB) gene, NCBI Description

complete cds



```
35162
Seq. No.
                  LIB3039-033-Q1-E1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169899
BLAST score
                  69
                  2.0e-30
E value
Match length
                  125
% identity
                  89
NCBI Description G.max 31 kDa protein mRNA, 3' end
Seq. No.
                  35163
                  LIB3039-033-Q1-E1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4185511
BLAST score
                  353
E value
                  1.0e-33
Match length
                  85
                  79
% identity
                  (AF102822) actin depolymerizing factor 4 [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                   35164
                  LIB3039-033-Q1-E1-D5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                   43
                   2.0e-15
E value
Match length
                   151
% identity
                   83
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   35165
                   LIB3039-033-Q1-E1-E9
Seq. ID
Method
                   BLASTN
                   g2920665
NCBI GI
                   198
BLAST score
E value
                   1.0e-107
Match length
                   226
% identity
                   97
                  Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                   (GSTa) mRNA, complete cds
Seq. No.
                   35166
                   LIB3039-033-Q1-E1-F11
Seq. ID
                   BLASTN
Method
                   g170091
NCBI GI
BLAST score
                   310
                   1.0e-174
E value
```

341 Match length 98 % identity

Glycine max vegetative storage protein (vspB) gene, NCBI Description

complete cds

35167 Seq. No.

LIB3039-034-Q1-E1-E12 Seq. ID

Method BLASTX NCBI GI g1076742



```
BLAST score
                  5.0e-15
E value
Match length
                  44
% identity
                  80
                  cyclin - rice >gi_558621_emb_CAA57555_ (X82035) cyclin
NCBI Description
                  [Oryza sativa]
                  35168
Seq. No.
                  LIB3039-034-Q1-E1-E5
Seq. ID
Method
                  BLASTN
                  g2529657
NCBI GI
BLAST score
                  33
                  5.0e-09
E value
Match length
                  33
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T30B22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  35169
Seq. No.
                  LIB3039-034-Q1-E1-G7
Seq. ID
Method
                  BLASTN
                   g170091
NCBI GI
BLAST score
                   92
                   2.0e-44
E value
                   220
Match length
                   85
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
                   35170
Seq. No.
                   LIB3039-034-Q1-E1-H5
Seq. ID
Method
                   BLASTN
                   q1208679
NCBI GI
                   59
BLAST score
                   1.0e-24
E value
                   79
Match length
                   94
% identity
                  Glycine arenaria histone H3 gene, partial cds, clone
NCBI Description
                   H3-DARE
                   35171
Seq. No.
                   LIB3039-035-Q1-E1-A7
Seq. ID
                   BLASTN
Method
                   q169974
NCBI GI
                   159
BLAST score
                   2.0e-84
E value
                   239
Match length
% identity
                   92
NCBI Description Glycine max vspA gene, complete cds
                   35172
Seq. No.
                   LIB3039-035-Q1-E1-B4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3341443
                   251
BLAST score
```

5322

1.0e-21

86

E value Match length



```
% identity
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
Seq. No.
                  35173
                  LIB3039-035-Q1-E1-B6
Seq. ID
                  BLASTN
Method
                  q169974
NCBI GI
BLAST score
                  138
                  1.0e-71
E value
Match length
                  310
% identity
                  87
NCBI Description Glycine max vspA gene, complete cds
                  35174
Seq. No.
Seq. ID
                  LIB3039-035-Q1-E1-F8
Method
                  BLASTX
                  q3560529
NCBI GI
BLAST score
                  198
E value
                  2.0e-15
Match length
                  71
% identity
                  61
                  (AF039598) light harvesting chlorophyll A/B binding protein
NCBI Description
                  [Prunus persica]
Seq. No.
                  35175
Seq. ID
                  LIB3039-035-Q1-E1-G7
Method
                  BLASTX
NCBI GI
                  g2500376
BLAST score
                  313
                  7.0e-29
E value
                  100
Match length
% identity
                  63
NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi 4262177 gb_AAD14494_
                   (AC005508) 23552 [Arabidopsis thaliana]
Seq. No.
                  35176
Seq. ID
                  LIB3039-036-Q1-E1-B1
Method
                  BLASTN
                  g2225884
NCBI GI
                  106
BLAST score
E value
                  2.0e-52
Match length
                  242
% identity
                   86
NCBI Description Solanum tuberosum mRNA for eukaryotic initiation factor
                  5A5, complete cds
                   35177
Seq. No.
                  LIB3039-036-Q1-E1-C10
Seq. ID
                   BLASTN
Method
                   g169974
NCBI GI
BLAST score
                   210
E value
                   1.0e-114
                   382
Match length
                   90
% identity
```

Seq. No. 35178

NCBI Description Glycine max vspA gene, complete cds



```
LIB3039-036-Q1-E1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3402683
BLAST score
                  404
                  2.0e-39
E value
Match length
                  117
% identity
                  68
                  (AC004697) patatin-like protein [Arabidopsis thaliana]
NCBI Description
                  35179
Seq. No.
                  LIB3039-036-Q1-E1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1173027
BLAST score
                  234
                  8.0e-24
E value
                  99
Match length
                  61
% identity
                  60S RIBOSOMAL PROTEIN L31 >qi 915313 (U23784) ribosomal
NCBI Description
                  protein L31 [Nicotiana glutinosa]
                  35180
Seq. No.
                  LIB3039-036-Q1-E1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g586076
BLAST score
                  310
                  2.0e-28
E value
Match length
                  89
% identity
                  65
                  TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta
NCBI Description
                  chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
                  tubulin 1 [Lupinus albus]
                  35181
Seq. No.
                  LIB3039-037-Q1-E1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                  264
E value
                  1.0e-147
                  348
Match length
                  94
% identity
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                  35182
                  LIB3039-037-Q1-E1-C9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1944318
BLAST score
                  78
                  7.0e-36
E value
Match length
                  294
% identity
                  82
NCBI Description
                  Glycine max mRNA for cysteine proteinase inhibitor,
                  complete cds
```

Seq. No. 35183

Seq. ID LIB3039-037-Q1-E1-D6

Method BLASTX NCBI GI g1350680



158 BLAST score 3.0e-11 E value Match length 47 % identity 68

NCBI Description 60S RIBOSOMAL PROTEIN L1

35184 Seq. No.

LIB3039-037-Q1-E1-D9 Seq. ID

Method BLASTN NCBI GI g499067 BLAST score 38 4.0e-12 E value 90 Match length % identity 86

NCBI Description G.max gmr2 gene

Seq. No.

35185 LIB3039-037-Q1-E1-E12 Seq. ID

Method BLASTN NCBI GI q169974 BLAST score 283 E value 1.0e-158 Match length 363 % identity 94

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35186

Seq. ID LIB3039-037-Q1-E1-F9

Method BLASTN g169974 NCBI GI 267 BLAST score 1.0e-148 E value 359 Match length 94 % identity

NCBI Description Glycine max vspA gene, complete cds

35187 Seq. No.

LIB3039-037-Q1-E1-G11 Seq. ID

Method BLASTX g1350944 NCBI GI 194 BLAST score 6.0e-15 E value 77 Match length

55 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S17

35188 Seq. No.

LIB3039-037-Q1-E1-G9 Seq. ID

BLASTN Method NCBI GI g169974 BLAST score 102 2.0e-50 E value 170 Match length % identity

NCBI Description Glycine max vspA gene, complete cds

35189 Seq. No.

NCBI GI

E value

BLAST score

124

2.0e-63



```
LIB3039-038-Q1-E1-B6
Seq. ID
                  BLASTN
Method
                  g170091
NCBI GI
                  173
BLAST score
                  8.0e-93
E value
Match length
                  213
                  95
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
                  35190
Seq. No.
Seq. ID
                  LIB3039-038-Q1-E1-C4
                  BLASTN
Method
NCBI GI
                  q1944318
BLAST score
                  41
                  5.0e-14
E value
Match length
                  154
                  87
% identity
NCBI Description Glycine max mRNA for cysteine proteinase inhibitor,
                  complete cds
                  35191
Seq. No.
                  LIB3039-038-Q1-E1-C5
Seq. ID
                  BLASTX
Method
                  g2244866
NCBI GI
                  138
BLAST score
                  1.0e-08
E value
                  49
Match length
                   49
% identity
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
                   35192
Seq. No.
                   LIB3039-038-Q1-E1-E10
Seq. ID
                   BLASTN
Method
NCBI GI
                   q169974
BLAST score
                   113
E value
                   6.0e-57
Match length
                   161
                   93
% identity
NCBI Description Glycine max vspA gene, complete cds
                   35193
Seq. No.
                   LIB3039-038-Q1-E1-G5
Seq. ID
                   BLASTN
Method
                   g169974
NCBI GI
                   204
BLAST score
                   1.0e-111
E value
Match length
                   280
                   93
 % identity
NCBI Description Glycine max vspA gene, complete cds
                   35194
 Seq. No.
                   LIB3039-038-Q1-E1-H8
 Seq. ID
                   BLASTN
 Method
                   q493019
```



```
Match length 180 % identity 92 NCBI Description Gly
```

Glycine max delta-aminolevulinic acid dehydratase (Alad)

mRNA, complete cds

Seq. No. 35195

Seq. ID LIB3039-039-Q1-E1-A10

Method BLASTX
NCBI GI g2959781
BLAST score 548
E value 2.0e-56
Match length 112
% identity 89

NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No. 35196

Seq. ID LIB3039-039-Q1-E1-A12

Method BLASTN
NCBI GI g1173641
BLAST score 66
E value 9.0e-29
Match length 129
% identity 93

NCBI Description Glycine max lipoxygenase (lox7) mRNA, complete cds

Seq. No. 35197

Seq. ID LIB3039-039-Q1-E1-B1

Method BLASTX
NCBI GI g3063396
BLAST score 186
E value 2.0e-14
Match length 60
% identity 63

NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 35198

Seq. ID LIB3039-039-Q1-E1-C7

Method BLASTN
NCBI GI g169974
BLAST score 279
E value 1.0e-156
Match length 375
% identity 94

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35199

Seq. ID LIB3039-039-Q1-E1-G10

Method BLASTX
NCBI GI g3341443
BLAST score 212
E value 4.0e-17
Match length 80
% identity 54

NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 35200

Seq. ID LIB3039-039-Q1-E1-H1

Match length

% identity

241

93



```
BLASTX
Method
                  g1351014
NCBI GI
BLAST score
                  292
E value
                  2.0e-26
Match length
                  83
% identity
                  70
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010)
                  ribosomal protein S8 [Oryza sativa]
Seq. No.
                  35201
                  LIB3039-039-Q1-E1-H3
Seq. ID
Method
                  BLASTN
                  g169974
NCBI GI
BLAST score
                  219
                  1.0e-120
E value
Match length
                  350
% identity
                  91
NCBI Description Glycine max vspA gene, complete cds
                  35202
Seq. No.
Seq. ID
                  LIB3039-040-Q1-E1-A3
Method
                  BLASTN
                  g170042
NCBI GI
BLAST score
                  71
                  1.0e-31
E value
Match length
                  82
% identity
                  96
NCBI Description Glycine max cv Prize protein kinase mRNA
                  35203
Seq. No.
                  LIB3039-040-Q1-E1-B2
Seq. ID
Method
                  BLASTX
                  q4335763
NCBI GI
                  160
BLAST score
                  6.0e-11
E value
Match length
                   63
% identity
                   49
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
                   35204
Seq. No.
                  LIB3039-040-Q1-E1-C1
Seq. ID
                  BLASTN
Method
                  g169974
NCBI GI
                  83
BLAST score
                   6.0e-39
E value
                   307
Match length
                   82
% identity
NCBI Description Glycine max vspA gene, complete cds
                   35205
Seq. No.
                   LIB3039-040-Q1-E1-C10
Seq. ID
Method
                   BLASTN
                   g170042
NCBI GI
BLAST score
                   142
                   4.0e-74
E value
```



NCBI Description Glycine max cv Prize protein kinase mRNA Seq. No. 35206

Seq. ID LIB3039-040-Q1-E1-C5

Method BLASTX
NCBI GI g1169533
BLAST score 367
E value 2.0e-35
Match length 90
% identity 84

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)

>gi\_515827\_emb\_CAA56645\_ (X80474) enolase [Neocallimastix

frontalis]

Seq. No. 35207

Seq. ID LIB3039-040-Q1-E1-G3

Method BLASTX
NCBI GI g3341443
BLAST score 327
E value 1.0e-30
Match length 93
% identity 69

NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 35208

Seq. ID LIB3039-040-Q1-E1-G8

Method BLASTN
NCBI GI g18764
BLAST score 35
E value 2.0e-10
Match length 107
% identity 83

NCBI Description G.max tefS1 gene for elongation factor EF-1a

Seq. No. 35209

Seq. ID LIB3039-040-Q1-E1-H5

Method BLASTN
NCBI GI g169897
BLAST score 68
E value 5.0e-30
Match length 180
% identity 84

NCBI Description G.max 28 kDa protein, complete cds

Seq. No. 35210

Seq. ID LIB3039-041-Q1-E1-A10

Method BLASTN
NCBI GI 9829118
BLAST score 44
E value 8.0e-16
Match length 124
% identity 84

NCBI Description P.vulgaris gene for cyclophilin

Seq. No. 35211

Seq. ID LIB3039-041-Q1-E1-A3

5329



```
BLASTX
Method
                  g1174621
NCBI GI
BLAST score
                  164
E value
                  8.0e-12
Match length
                  66
% identity
                  50
                  T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)
NCBI Description
                  (CCT-THETA) >qi 1083259 pir JC4073 TCP-1 containing
                  cytosolic chaperonin (CCT) theta chain - mouse
                  >gi 695625 emb CAA85521 (Z37164) CCTtheta, theta subunit
                  of the chaperonin containing TCP-1 (CCT) [Mus musculus]
Seq. No.
                  35212
Seq. ID
                  LIB3039-041-Q1-E1-B1
Method
                  BLASTX
NCBI GI
                  q2335099
BLAST score
                  150
E value
                  3.0e-10
Match length
                  59
                  56
% identity
NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]
Seq. No.
                  35213
Seq. ID
                  LIB3039-041-Q1-E1-D5
Method
                  BLASTN
NCBI GI
                  q170091
BLAST score
                  145
E value
                  4.0e-76
Match length
                  209
% identity
                  92
NCBI Description Glycine max vegetative storage protein (vspB) gene,
                  complete cds
                  35214
Seq. No.
                  LIB3039-041-Q1-E1-E1
Seq. ID
Method
                  BLASTN
                  g169897
NCBI GI
BLAST score
                  196
                  1.0e-106
E value
Match length
                  268
% identity
                  93
NCBI Description G.max 28 kDa protein, complete cds
                  35215
Seq. No.
                  LIB3039-041-Q1-E1-E10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g169974
BLAST score
                  81
```

7.0e-38 E value Match length 228 % identity 85

NCBI Description Glycine max vspA gene, complete cds

35216 Seq. No.

LIB3039-041-Q1-E1-E12 Seq. ID

Method BLASTN NCBI GI g166913



48

% identity

```
BLAST score
                  1.0e-11
E value
                  57
Match length
                  91
% identity
                  Arabidopsis thaliana alpha-2 tubulin (TUA2) gene, exon and
NCBI Description
                  35217
Seq. No.
                  LIB3039-041-Q1-E1-F2
Seq. ID
                  BLASTN
Method
NCBI GI
                  q169974
                  242
BLAST score
                  1.0e-134
E value
                  302
Match length
                  95
% identity
NCBI Description Glycine max vspA gene, complete cds
                  35218
Seq. No.
Seq. ID
                  LIB3039-041-Q1-E1-G11
                  BLASTN
Method
NCBI GI
                  g170087
BLAST score
                  166
                  2.0e-88
E value
                  265
Match length
                  92
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
Seq. No.
                  35219
                  LIB3039-041-Q1-E1-G5
Seq. ID
Method
                  BLASTN
                  q169974
NCBI GI
BLAST score
                  87
E value
                  2.0e-41
Match length
                  183
                  87
% identity
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   35220
                   LIB3039-042-Q1-E1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3687251
BLAST score
                   231
E value
                   1.0e-19
Match length
                   68
% identity
                   65
                  (AC005169) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   35221
                  LIB3039-042-Q1-E1-A5
Seq. ID
                   BLASTN
Method
                   g456713
NCBI GI
BLAST score
                   103
                   7.0e-51
E value
                   235
Match length
```

NCBI Description Glycine max gene for ubiquitin, complete cds



```
35222
Seq. No.
                  LIB3039-042-Q1-E1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                  163
E value
                  1.0e-86
                  271
Match length
                  90
% identity
                  Glycine max vspA gene, complete cds
NCBI Description
Seq. No.
                  35223
Seq. ID
                  LIB3039-042-Q1-E1-E11
Method
                  BLASTN
NCBI GI
                  q829118
BLAST score
                  92
E value
                  3.0e-44
Match length
                  203
% identity
                  90
NCBI Description P.vulgaris gene for cyclophilin
                  35224
Seq. No.
Seq. ID
                  LIB3039-042-Q1-E1-H4
                  BLASTN
Method
NCBI GI
                  q303900
BLAST score
                  300
                  1.0e-168
E value
Match length
                  368
                  31
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
                  35225
Seq. No.
Seq. ID
                  LIB3039-043-Q1-E1-A8
Method
                  BLASTN
                  q169974
NCBI GI
BLAST score
                   41
                   6.0e-14
E value
Match length
                   61
                   92
% identity
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   35226
                  LIB3039-043-Q1-E1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173187
                   170
BLAST score
                   4.0e-12
E value
Match length
                   83
% identity
                   49
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
NCBI Description
                   ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                   strawberry >gi_643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
```

Seq. No. 35227

Seq. ID LIB3039-043-Q1-E1-C6

Method BLASTN NCBI GI g170089



BLAST score 6.0e-45 E value Match length 221 % identity 86

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No. 35228

LIB3039-043-Q1-E1-D1 Seq. ID

Method BLASTN NCBI GI g169974 BLAST score 58 E value 4.0e-24 Match length 214 % identity 82

Glycine max vspA gene, complete cds NCBI Description

Seq. No.

35229

Seq. ID LIB3039-043-Q1-E1-D3

Method BLASTX NCBI GI g2129742 BLAST score 195 E value 4.0e-15 Match length 55 % identity

stress-induced protein OZI1 precursor - Arabidopsis NCBI Description

thaliana >gi 790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi 2252869 (AF013294) No

definition line found [Arabidopsis thaliana]

Seq. No. 35230

LIB3039-043-Q1-E1-E1 Seq. ID

Method BLASTN g169897 NCBI GI BLAST score 198 E value 1.0e-107 262 Match length % identity 94

NCBI Description G.max 28 kDa protein, complete cds

Seq. No. 35231

LIB3039-043-Q1-E1-E4 Seq. ID

Method BLASTX NCBI GI g81979 209 BLAST score 9.0e-17 E value 85 Match length 51 % identity

chymotrypsin inhibitor (Kunitz) WCI-2 precursor - winged NCBI Description

bean >gi\_248875\_bbs\_96759 (S96733) Kunitz chymotrypsin inhibitor 2, WCI-2 [Psophocarpus tetragonolobus=winged beans, DC., Peptide, 207 aa] [Psophocarpus tetragonolobus]

>gi\_497834\_dbj\_BAA06512\_ (D31703) putative Kunitz chymotrypsin inhibitor [Psophocarpus tetragonolobus]

Seq. No. 35232



```
LIB3039-043-Q1-E1-E5
Seq. ID
                  BLASTN
Method
                  g3341442
NCBI GI
                  46
BLAST score
                  8.0e-17
E value
Match length
                  129
% identity
                  89
NCBI Description Glycine max mRNA for root nodule acid phosphatase
                  35233
Seq. No.
Seq. ID
                  LIB3039-043-Q1-E1-F9
                  BLASTN
Method
                  g303900
NCBI GI
                  167
BLAST score
                   6.0e-89
E value
                  307
Match length
                   30
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
                   35234
Seq. No.
Seq. ID
                  LIB3039-043-Q1-E1-G1
                  BLASTN
Method
                   q169974
NCBI GI
                   213
BLAST score
                   1.0e-116
E value
                   225
Match length
                   99
% identity
NCBI Description Glycine max vspA gene, complete cds
                   35235
Seq. No.
                   LIB3039-043-Q1-E1-G2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2347088
BLAST score
                   227
                   6.0e-19
E value
                   77
Match length
% identity
                  (U72765) non-specific lipid transfer protein PvLTP-24
NCBI Description
                   [Phaseolus vulgaris]
                   35236
Seq. No.
                   LIB3039-043-Q1-E1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3341443
BLAST score
                   147
                   1.0e-09
E value
Match length
                   51
                   53
% identity
NCBI Description (AJ223074) acid phosphatase [Glycine max]
                   35237
Seq. No.
                   LIB3039-043-Q1-E1-G4
Seq. ID
Method
                   BLASTX
                   g3341443
NCBI GI
                   303
BLAST score
```

1.0e-27

84

E value

Match length

```
% identity
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
Seq. No.
                  35238
Seq. ID
                  LIB3039-043-Q1-E1-G5
Method
                  BLASTX
NCBI GI
                  q3341443
BLAST score
                  246
                  4.0e-21
E value
                  76
Match length
% identity
NCBI Description (AJ223074) acid phosphatase [Glycine max]
                  35239
Seq. No.
Seq. ID
                  LIB3039-043-Q1-E1-H3
Method
                  BLASTN
NCBI GI
                  q169974
BLAST score
                  223
E value
                  1.0e-122
Match length
                  349
                  92
% identity
NCBI Description Glycine max vspA gene, complete cds
                  35240
Seq. No.
Seq. ID
                  LIB3039-044-Q1-E1-C6
Method
                  BLASTN
NCBI GI
                  q169974
BLAST score
                  199
                  1.0e-108
E value
```

Match length 363 % identity 89

35241

NCBI Description Glycine max vspA gene, complete cds

LIB3039-044-Q1-E1-E11 Seq. ID BLASTN Method NCBI GI g303900 BLAST score 33 4.0e-09 E value Match length 53 % identity 91

Seq. No.

NCBI Description Soybean gene for ubiquitin, complete cds

35242 Seq. No.

LIB3039-044-Q1-E1-E7 Seq. ID

BLASTN Method g3982595 NCBI GI BLAST score 362 0.0e+00E value 385 Match length 99 % identity

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

35243 Seq. No.

LIB3039-045-Q1-E1-A12 Seq. ID

Method BLASTX g464621 NCBI GI

5335



BLAST score 251
E value 1.0e-21
Match length 88
% identity 59
NCBI Description 60S RIBO
ribosomo
>gi\_195:
[Mesemb:

60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi\_280374\_pir\_\_S28586 ribosomal protein ML16 - common ice plant

>gi 19539\_emb\_CAA49175\_ (X69378) ribosomal protein YL16

[Mesembryanthemum crystallinum]

Seq. No. 35244

Seq. ID LIB3039-045-Q1-E1-A2

Method BLASTX
NCBI GI 94455334
BLAST score 185
E value 7.0e-14
Match length 75
% identity 48

NCBI Description (AL035525) myosin-like protein [Arabidopsis thaliana]

Seq. No. 35245

Seq. ID LIB3039-045-Q1-E1-A3

Method BLASTX
NCBI GI g312179
BLAST score 194
E value 6.0e-15
Match length 70
% identity 59

NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase

(phosphorylating) [Zea mays] >gi\_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]

>gi 1185554 (U45858) glyceraldehyde-3-phosphate

dehydrogenase [Zea mays]

Seq. No. 35246

Seq. ID LIB3039-045-Q1-E1-A8

Method BLASTN
NCBI GI g169974
BLAST score 41
E value 6.0e-14
Match length 61
% identity 92

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35247

Seq. ID LIB3039-045-Q1-E1-C3

Method BLASTN
NCBI GI g169974
BLAST score 149
E value 3.0e-78
Match length 224
% identity 92

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35248

Seq. ID LIB3039-045-Q1-E1-E2

Method BLASTN NCBI GI g169974



```
BLAST score
                  104
                  2.0e-51
E value
                  152
Match length
                  93
% identity
                  Glycine max vspA gene, complete cds
NCBI Description
                  35249
Seq. No.
                  LIB3039-045-Q1-E1-F5
Seq. ID
Method
                  BLASTX
                  g1076510
NCBI GI
BLAST score
                  310
                  1.0e-28
E value
                  88
Match length
                  69
% identity
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean
NCBI Description
                  >gi_829119_emb_CAA52414_ (X74403) cyclophilin [Phaseolus
                  vulgaris]
                  35250
Seq. No.
                  LIB3039-045-Q1-E1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4007792
                  172
BLAST score
                  3.0e-12
E value
Match length
                  44
% identity
                  (AL034463) Xenopus 14s cohesin smcl subunit homolog
NCBI Description
                   [Schizosaccharomyces pombe]
Seq. No.
                  35251
                  LIB3039-046-Q1-E1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3947719
BLAST score
                  189
E value
                  2.0e-14
Match length
                   64
% identity
                   66
                   (AJ012653) ribosomal protein S28 [Prunus persica]
NCBI Description
                   >gi 3947721 emb CAA10102 (AJ012654) ribosomal protein S28
                   [Prunus persica] >gi_3947723_emb_CAA10103_ (AJ012655)
                   ribosomal protein S28 [Prunus persica]
Seq. No.
                   35252
                  LIB3039-046-Q1-E1-A10
Seq. ID
                  BLASTX
Method
                   g1350969
NCBI GI
                   151
BLAST score
                   7.0e-10
E value
                   80
Match length
                   42
% identity
                  40S RIBOSOMAL PROTEIN S26 (S31) >gi_971284_dbj_BAA07208_
NCBI Description
                   (D38011) ribosomal protein S31 [Oryza sativa]
```

Seq. No. 35253

Seq. ID LIB3039-046-Q1-E1-C12

Method BLASTN NCBI GI g169974



```
BLAST score
                  2.0e-39
E value
Match length
                  116
% identity
                  93
NCBI Description Glycine max vspA gene, complete cds
                  35254
Seq. No.
                  LIB3039-046-Q1-E1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g169900
BLAST score
                  183
                  8.0e-14
E value
Match length
                  82
                   50
% identity
NCBI Description
                  (M37529) 31 kDa protein [Glycine max]
Seq. No.
                   35255
                  LIB3039-046-Q1-E1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4544386
BLAST score
                   236
E value
                   7.0e-20
Match length
                   91
                   58
% identity
                  (AC007047) putative cell division control protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   35256
Seq. ID
                   LIB3039-046-Q1-E1-G3
Method
                   BLASTN
                   q170091
NCBI GI
BLAST score
                   329
                   0.0e + 00
E value
                   385
Match length
                   96
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
Seq. No.
                   35257
                   LIB3039-047-Q1-E1-A2
Seq. ID
                   BLASTN
Method
                   g169974
NCBI GI
                   240
BLAST score
                   1.0e-132
E value
                   392
Match length
% identity
                   91
NCBI Description Glycine max vspA gene, complete cds
                   35258
Seq. No.
                   LIB3039-047-Q1-E1-B1
Seq. ID
Method
                   BLASTN
                   a170089
NCBI GI
                   221
BLAST score
                   1.0e-121
E value
                   268
Match length
                   96
% identity
```

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds



```
35259
Seq. No.
                  LIB3039-047-Q1-E1-B2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q170091
BLAST score
                  307
                  1.0e-172
E value
                  395
Match length
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
                  35260
Seq. No.
Seq. ID
                  LIB3039-047-Q1-E1-C1
                  BLASTN
Method
NCBI GI
                  g170087
BLAST score
                  180
E value
                   1.0e-96
                   214
Match length
                   98
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
                   35261
Seq. No.
                   LIB3039-047-Q1-E1-C5
Seq. ID
                   BLASTN
Method
                   g169974
NCBI GI
BLAST score
                   197
                   1.0e-107
E value
                   345
Match length
% identity
                   90
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   35262
                   LIB3039-047-Q1-E1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4371280
BLAST score
                   507
                   1.0e-51
E value
                   126
Match length
% identity
                   80
                  (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   35263
                   LIB3039-047-Q1-E1-F1
Seq. ID
                   BLASTX
Method
                   g3341443
NCBI GI
                   328
BLAST score
                   2.0e-30
E value
                   109
Match length
                   62
% identity
NCBI Description (AJ223074) acid phosphatase [Glycine max]
Seq. No.
                   35264
                   LIB3039-047-Q1-E1-F2
Seq. ID
```

BLASTN

179

g169974

Method

NCBI GI BLAST score



4.0e-96 E value 227 Match length % identity 95 NCBI Description Glycine max vspA gene, complete cds 35265 Seq. No. LIB3039-047-Q1-E1-F5 Seq. ID BLASTX Method q3341443 NCBI GI BLAST score 323 5.0e-30 E value Match length 112 56 % identity NCBI Description (AJ223074) acid phosphatase [Glycine max] Seq. No. 35266 LIB3039-047-Q1-E1-G2 Seq. ID Method BLASTN q3318610 NCBI GI BLAST score 42 1.0e-14 E value Match length 86 87 % identity Glycine max mRNA for mitochondrial phosphate transporter, NCBI Description complete cds Seq. No. 35267 Seq. ID LIB3039-047-Q1-E1-H5 Method BLASTN q170091 NCBI GI BLAST score 41 6.0e-14 E value 237 Match length 79 % identity Glycine max vegetative storage protein (vspB) gene, NCBI Description complete cds 35268 Seq. No. LIB3039-048-Q1-E1-A6 Seq. ID BLASTX Method g1374991 NCBI GI 214 BLAST score 2.0e-17 E value 82 Match length 59 % identity

(D83177) furostanol glycoside 26-0-beta-glucosidase (F26G) NCBI Description

[Costus speciosus]

35269 Seq. No.

LIB3039-048-Q1-E1-B10 Seq. ID

BLASTX Method g2623298 NCBI GI 302 BLAST score 9.0e-28 E value 91 Match length 59 % identity

NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis



## thaliana]

```
Seq. No.
                  35270
Seq. ID
                  LIB3039-048-Q1-E1-B3
Method
                  BLASTN
                  q18551
NCBI GI
BLAST score
                  290
                  1.0e-162
E value
                  314
Match length
                  98
% identity
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                  protein
                  35271
Seq. No.
                  LIB3039-048-Q1-E1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q169974
BLAST score
                  146
                   1.0e-76
E value
                   213
Match length
                   92
% identity
NCBI Description Glycine max vspA gene, complete cds
                   35272
Seq. No.
Seq. ID
                   LIB3039-048-Q1-E1-F11
                   BLASTX
Method
NCBI GI
                   q3913008
BLAST score
                   216
                   1.0e-17
E value
Match length
                   73
                   64
% identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                   >qi 3021338 emb CAA06308 (AJ005041) cytosolic
                   fructose-1,6-bisphosphate aldolase [Cicer arietinum]
                   35273
Seq. No.
                   LIB3039-049-Q1-E1-A2
Seq. ID
                   BLASTN
Method
                   g310575
NCBI GI
                   221
BLAST score
E value
                   1.0e-121
                   365
Match length
% identity
                   93
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                   35274
Seq. No.
                   LIB3039-049-Q1-E1-B2
Seq. ID
                   BLASTN
Method
                   g169974
NCBI GI
                   267
BLAST score
                   1.0e-148
E value
Match length
                   363
% identity
                   94
NCBI Description Glycine max vspA gene, complete cds
```

35275 Seq. No.

LIB3039-049-Q1-E1-B4 Seq. ID



```
BLASTX
Method
                  g4049341
NCBI GI
BLAST score
                  292
E value
                  2.0e-26
Match length
                  103
% identity
                  59
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  35276
                  LIB3039-049-Q1-E1-C2
Seq. ID
Method
                  BLASTX
                  g3341443
NCBI GI
BLAST score
                  361
                  2.0e-34
E value
Match length
                  116
% identity
                  63
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                  35277
Seq. No.
                  LIB3039-049-Q1-E1-G6
Seq. ID
Method
                  BLASTX
                  g1717755
NCBI GI
BLAST score
                  135
                  1.0e-10
E value
Match length
                  76
% identity
                  47
                  TROPINONE REDUCTASE HOMOLOG (P29X) >gi_539028 pir__C48674
NCBI Description
                  tropinone reductase homolog - jimsonweed >gi_424158
                  (L20475) 29kDa protein; high homology to aa sequence of
                  tropinone reductases [Datura stramonium]
                  35278
Seq. No.
                  LIB3039-050-Q1-E1-A1
Seq. ID
Method
                  BLASTX
                  g136057
NCBI GI
BLAST score
                  210
                  7.0e-17
E value
                  84
Match length
% identity
                  51
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
                  Coptis japonica >gi 556171 (J04121) triosephosphate
                  isomerase [Coptis japonica]
                  35279
Seq. No.
                  LIB3039-050-Q1-E1-B1
Seq. ID
                  BLASTN
Method
                  g169897
NCBI GI
BLAST score
                  183
E value
                  1.0e-98
Match length
                  346
% identity
                  88
NCBI Description G.max 28 kDa protein, complete cds
```

Seq. No. 35280

LIB3039-050-Q1-E1-B11

Seq. ID LIB3039 Method BLASTX



```
g3128177
NCBI GI
                  146
BLAST score
                  2.0e-09
E value
Match length
                  45
% identity
                  69
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
                  35281
Seq. No.
                  LIB3039-050-Q1-E1-B4
Seq. ID
Method
                  BLASTN
                  g170087
NCBI GI
BLAST score
                  61
                  4.0e-26
E value
                  93
Match length
                  92
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
Seq. No.
                  35282
                  LIB3039-050-Q1-E1-B6
Seq. ID
                  BLASTN
Method
                  q169974
NCBI GI
BLAST score
                  268
                  1.0e-149
E value
                  380
Match length
                  93
% identity
NCBI Description Glycine max vspA gene, complete cds
                  35283
Seq. No.
                  LIB3039-050-Q1-E1-D4
Seq. ID
                  BLASTN
Method
                   g169974
NCBI GI
BLAST score
                   248
                   1.0e-137
E value
                   264
Match length
% identity
                   98
NCBI Description Glycine max vspA gene, complete cds
                   35284
Seq. No.
                   LIB3039-050-Q1-E1-F2
Seq. ID
                   BLASTN
Method
                   g169974
NCBI GI
BLAST score
                   281
                   1.0e-157
E value
                   391
Match length
                   94
% identity
NCBI Description Glycine max vspA gene, complete cds
                   35285
Seq. No.
                   LIB3039-050-Q1-E1-G1
Seq. ID
                   BLASTN
Method
                   g169897
NCBI GI
BLAST score
                   35
                   2.0e-10
E value
                   179
Match length
                   81
% identity
NCBI Description G.max 28 kDa protein, complete cds
```



```
Seq. No.
                  LIB3039-051-Q1-E1-B4
Seq. ID
                  BLASTN
Method
                  q170091
NCBI GI
BLAST score
                  195
E value
                  1.0e-106
                  223
Match length
                  97
% identity
NCBI Description Glycine max vegetative storage protein (vspB) gene,
                  complete cds
                  35287
Seq. No.
Seq. ID
                  LIB3039-051-Q1-E1-D3
                  BLASTN
Method
                  q169974
NCBI GI
BLAST score
                  232
E value
                  1.0e-127
                  336
Match length
% identity
                   92
NCBI Description Glycine max vspA gene, complete cds
                   35288
Seq. No.
                  LIB3039-051-Q1-E1-F3
Seq. ID
                  BLASTX
Method
                   q3292830
NCBI GI
                  139
BLAST score
                   1.0e-10
E value
Match length
                   75
                   43
% identity
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
                   35289
Seq. No.
                   LIB3039-051-Q1-E1-G2
Seq. ID
                   BLASTX
Method
                   g3341443
NCBI GI
BLAST score
                   323
E value
                   4.0e-30
Match length
                   97
                   64
% identity
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                   35290
Seq. No.
                   LIB3039-052-Q1-E1-A6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q18551
BLAST score
                   77
                   2.0e-35
E value
Match length
                   201
% identity
                   85
                   Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                   protein
Seq. No.
                   35291
                   LIB3039-052-Q1-E1-B3
Seq. ID
                   BLASTX
Method
```

5344

g2832657

212

NCBI GI BLAST score

E value

Match length

317



```
4.0e-17
E value
                  95
Match length
% identity
                  (AL021710) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  35292
                  LIB3039-052-Q1-E1-C2
Seq. ID
                  BLASTN
Method
                  q169974
NCBI GI
                  63
BLAST score
                   4.0e-27
E value
Match length
                  218
                  83
% identity
NCBI Description Glycine max vspA gene, complete cds
                   35293
Seq. No.
Seq. ID
                  LIB3039-052-Q1-E1-C3
                  BLASTN
Method
                   q170091
NCBI GI
                   211
BLAST score
                   1.0e-115
E value
                   327
Match length
                   91
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
                   35294
Seq. No.
                   LIB3039-052-Q1-E1-C4
Seq. ID
                   BLASTN
Method
NCBI GI
                   q170087
                   221
BLAST score
                   1.0e-121
E value
                   329
Match length
                   93
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
                   35295
Seq. No.
                   LIB3039-052-Q1-E1-D8
Seq. ID
                   BLASTX
Method
                   g131399
NCBI GI
BLAST score
                   172
                   2.0e-12
E value
Match length
                   81
 % identity
                   48
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE
NCBI Description
                   TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411
                   photosystem II 10K protein precursor - potato
                   >gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum
                   tuberosum]
 Seq. No.
                   35296
                   LIB3039-052-Q1-E1-E2
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g18551
                   234
 BLAST score
                   1.0e-129
```



```
% identity
                   Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                   protein
Seq. No.
                   35297
                   LIB3039-052-Q1-E1-E4
Seq. ID
                   BLASTX
Method
                   q1709449
NCBI GI
                                                                           20.
                   183
BLAST score
                   1.0e-13
E value
Match length
                   86
                   49
% identity
                   PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT
NCBI Description
                   PRECURSOR (PDHE1-A) >gi_1263302 (U51918) pyruvate
                   dehydrogenase El alpha subunit [Pisum sativum]
                   35298
Seq. No.
                   LIB3039-052-Q1-E1-H12
Seq. ID
                   BLASTN
Method
                   g170091
NCBI GI
BLAST score
                   108
                   7.0e-54
E value
                   112
Match length
                   99
% identity
                   Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
                   35299
Seq. No.
                   LIB3039-053-Q1-E1-A9
Seq. ID
Method
                   BLASTX
                   g2462834
NCBI GI
BLAST score
                   207
                   2.0e-16
E value
                   95
Match length
% identity
                   42
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   35300
Seq. No.
                   LIB3039-053-Q1-E1-B12
Seq. ID
                   BLASTX
Method
                   g3183247
NCBI GI
                   237
BLAST score
                   4.0e-20
E value
                   84
Match length
                   51
% identity
                   PUTATIVE GTP-BINDING PROTEIN W08E3.3
NCBI Description
                   >gi_3880615_emb_CAB07131_ (Z92773) predicted using
Genefinder; Similarity to Yeast hypothetical 44.2 KD
                   protein, putative GTP-binding protein (SW:P38219); cDNA EST
                   EMBL:D64516 comes from this gene; cDNA EST EMBL:D65777
                   comes from this gene; cDNA EST EMB
```

 Seq. No.
 35301

 Seq. ID
 LIB3039-053-Q1-E1-F9

 Method
 BLASTN

Method BLASTN NCBI GI g170091 BLAST score 163



```
1.0e-86
E value
Match length
                  275
% identity
                  90
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
Seq. No.
                  35302
                  LIB3039-053-Q1-E1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g343483
BLAST score
                  71
E value
                  1.0e-31
Match length
                  174
% identity
                  89
                  Tobacco chloroplast ATPase subunits I and III gene,
NCBI Description
                  complete cds, and ATPase subunit alpha, 5' end
Seq. No.
                   35303
                  LIB3039-053-Q1-E1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3341443
BLAST score
                   294
                   1.0e-26
E value
                   98
Match length
% identity
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                   35304
Seq. No.
Seq. ID
                   LIB3039-054-Q1-E1-A5
Method
                   BLASTN
NCBI GI
                   g170091
BLAST score
                   278
                   1.0e-155
E value
Match length
                   366
% identity
                   94
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
                   35305
Seq. No.
                   LIB3039-054-Q1-E1-B12
Seq. ID
Method
                   BLASTX
                   g3128206
NCBI GI
BLAST score
                   578
                   7.0e-60
E value
                   129
Match length
% identity
                   81
                  (AC004077) unknown protein [Arabidopsis thaliana]
NCBI Description
                   35306
Seq. No.
                   LIB3039-054-Q1-E1-H12
Seq. ID
                   BLASTX
Method
                   g3075399
NCBI GI
BLAST score
                   162
                   3.0e-11
E value
                   93
Match length
                   43
% identity
```

NCBI Description (AC004484) SF16-like protein [Arabidopsis thaliana]



```
Seq. No. 35307
Seq. ID LIB3040-001-Q1-E1-B7
Method BLASTN
NCBI GI g1055367
BLAST score 228
E value 1.0e-125
Match length 311
% identity 93
NCBI Description Glycine max ribulose
```

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 35308

Seq. ID LIB3040-001-Q1-E1-C12

Method BLASTX
NCBI GI g266945
BLAST score 251
E value 1.0e-21
Match length 85
% identity 62

NCBI Description 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)

>gi\_100065\_pir\_\_S19978 ribosomal protein L9 - garden pea

>gi\_20727\_emb\_CAA46273\_ (X65155) GA [Pisum sativum] >gi\_1279645\_emb\_CAA65987 (X97322) ribosomal protein L9

[Pisum sativum]

Seq. No. 35309

Seq. ID LIB3040-001-Q1-E1-H1

Method BLASTN
NCBI GI g303900
BLAST score 59
E value 6.0e-25
Match length 134
% identity 33

NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No. 35310

Seq. ID LIB3040-002-Q1-E1-A5

Method BLASTN
NCBI GI g2924257
BLAST score 189
E value 1.0e-102
Match length 285
% identity 92

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 35311

Seq. ID LIB3040-002-Q1-E1-D4

Method BLASTX
NCBI GI g2760844
BLAST score 258
E value 2.0e-22
Match length 82
% identity 63

NCBI Description (AC003105) hypothetical protein [Arabidopsis thaliana]

Seq. No. 35312



```
LIB3040-002-Q1-E1-H10
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  36
                  6.0e-11
E value
Match length
                  36
                  100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
Seq. No.
                  35313
                  LIB3040-003-Q1-E1-B5
Seq. ID
Method
                  BLASTX
                  g2129726
NCBI GI
BLAST score
                  178
E value
                  4.0e-13
Match length
                  64
% identity
                  59
                  RNA polymerase II third largest chain RPB35.5A -
NCBI Description
                  Arabidopsis thaliana >gi 514318 (L34770) RNA polymerase II
                  third largest subunit [Arabidopsis thaliana]
                  >qi 4544370 gb AAD22281.1 AC006920 5 (AC006920) RNA
                  polymerase II, third largest subunit [Arabidopsis thaliana]
Seq. No.
                  35314
                  LIB3040-003-Q1-E1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2290120
BLAST score
                  33
E value
                   4.0e-09
Match length
                   69
% identity
                  87
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                   35315
Seq. No.
                  LIB3040-003-Q1-E1-E2
Seq. ID
Method
                   BLASTX
                   g3355468
NCBI GI
BLAST score
                   145
E value
                   1.0e-09
Match length
                   55
                   60
% identity
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                   thaliana]
                   35316
Seq. No.
                   LIB3040-003-Q1-E1-E6
Seq. ID
                   BLASTN
Method
                   g2815245
NCBI GI
                   37
BLAST score
                   2.0e-11
E value
Match length
                   237
                   79
% identity
NCBI Description C.arietinum mRNA for class I type 2 metallothionein (clone:
```

Seq. No. 35317

CanMT-2)



```
LIB3040-003-Q1-E1-G12
Seq. ID
                  BLASTN
Method
                  g2565339
NCBI GI
                  82
BLAST score
                  3.0e-38
E value
                  146
Match length
                  89
% identity
NCBI Description Lupinus luteus ribosomal protein S14 (rps14) mRNA, complete
                  cds
                  35318
Seq. No.
                  LIB3040-004-Q1-E1-B6
Seq. ID
                  BLASTX
Method
                  g3935183
NCBI GI
                  408
BLAST score
                  4.0e-40
E value
                  104
Match length
                  81
% identity
NCBI Description (AC004557) F17L21.26 [Arabidopsis thaliana]
                   35319
Seq. No.
                  LIB3040-004-Q1-E1-G9
Seq. ID
                  BLASTX
Method
                   g2947063
NCBI GI
                   186
BLAST score
                   6.0e-14
E value
                   129
Match length
                   35
% identity
                  (AC002521) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   35320
Seq. No.
                   LIB3040-004-Q1-E1-H11
Seq. ID
                   BLASTX
Method
                   q663070
NCBI GI
                   257
BLAST score
                   2.0e-22
E value
Match length
                   79
 % identity
                  (X77806) histone H4 [Pyrenomonas salina]
NCBI Description
                   35321
 Seq. No.
 Seq. ID
                   LIB3040-005-Q1-E1-A7
 Method
                   BLASTX
                   q3851636
 NCBI GI
                   170
 BLAST score
                   2.0e-12
 E value
                   49
 Match length
 % identity
                   61
                   (AF098519) unknown [Avicennia marina] >gi_4128206
 NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                   35322
 Seq. No.
                   LIB3040-005-Q1-E1-C10
 Seq. ID
                   BLASTN
 Method
```

q18551

269

NCBI GI

BLAST score



```
1.0e-150
E value
Match length
                  395
                  92
% identity
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                  protein
                  35323
Seq. No.
Seq. ID
                  LIB3040-005-Q1-E1-D9
                  BLASTN
Method
NCBI GI
                  g170071
BLAST score
                  63
                  5.0e-27
E value
                  203
Match length
                  83
% identity
NCBI Description Soybean calmodulin (SCaM-2) mRNA, complete cds
Seq. No.
                   35324
Seq. ID
                  LIB3040-005-Q1-E1-F11
                   BLASTN
Method
                   q1806284
NCBI GI
                   52
BLAST score
E value
                   2.0e-20
                   184
Match length
                   82
% identity
NCBI Description S.rostrata mRNA coding for histone H4 homologue
                   35325
Seq. No.
Seq. ID
                   LIB3040-005-Q1-E1-H11
                   BLASTN
Method
NCBI GI
                   g2130559
BLAST score
                   145
E value
                   8.0e-76
Match length
                   265
                   89
% identity
                  Glycine max elongation factor-1 alpha (TefS1) gene, partial
NCBI Description
Seq. No.
                   35326
                   LIB3040-006-Q1-E1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3158476
BLAST score
                   362
E value
                   1.0e-34
Match length
                   99
                   77
% identity
                  (AF067185) aquaporin 2 [Samanea saman]
NCBI Description
Seq. No.
                   35327
                   LIB3040-006-Q1-E1-D10
Seq. ID
Method
                   BLASTN
                   g2687430
NCBI GI
                   43
BLAST score
                   2.0e-15
E value
Match length
                   55
                   95
% identity
                  Acorus gramineus large subunit 26S ribosomal RNA gene,
NCBI Description
```

partial sequence



85

% identity

```
35328
Seq. No.
                  LIB3040-006-Q1-E1-D4
Seq. ID
                  BLASTN
Method
                  g18747
NCBI GI
BLAST score
                  251
                  1.0e-139
E value
                  336
Match length
                  95
% identity
                  G.max mRNA for a protein similar to potato tuber protein
NCBI Description
                  p322 homolgous to Bowman-Birk Proteinase Inhibitor
                  35329
Seq. No.
Seq. ID
                  LIB3040-006-Q1-E1-E5
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  336
                   2.0e-31
E value
Match length
                   79
                   80
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   35330
Seq. No.
Seq. ID
                   LIB3040-006-Q1-E1-F5
Method
                   BLASTN
                   g1336081
NCBI GI
BLAST score
                   178
                   2.0e-95
E value
                   334
Match length
                   89
% identity
                   Glycine max var. Century ascorbate peroxidase 2 (APx2)
NCBI Description
                   mRNA, complete cds
                   35331
Seq. No.
Seq. ID
                   LIB3040-006-Q1-E1-H4
                   BLASTX
Method
NCBI GI
                   g567893
BLAST score
                   156
                   1.0e-10
E value
Match length
                   64
% identity
                   (L37382) beta-galactosidase-complementation protein
NCBI Description
                   [Cloning vector]
Seq. No.
                   35332
                   LIB3040-006-Q1-E1-H8
Seq. ID
Method
                   BLASTN
                   g1370202
NCBI GI
BLAST score
                   122
E value
                   4.0e-62
Match length
                   314
```

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAN1A

% identity

NCBI Description

86

cds



```
Seq. No.
Seq. ID
                  LIB3040-007-Q1-E1-E4
                  BLASTX
Method
                  q266945
NCBI GI
BLAST score
                  195
E value
                   7.0e-16
                   68
Match length
% identity
                   72
                   60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
NCBI Description
                   >qi 100065 pir S19978 ribosomal protein L9 - garden pea
                   >gi 20727 emb CAA46273 (X65155) GA [Pisum sativum]
                   >gi^-12796^-45 emb CAA659^-87 (X97322) ribosomal protein L9
                   [Pisum sativum]
                   35334
Seq. No.
Seq. ID
                   LIB3040-007-Q1-E1-G3
Method
                   BLASTN
NCBI GI
                   q1053044
BLAST score
                   34
                   6.0e-10
E value
Match length
                   46
                   93
% identity
                  Glycine max histone H3 gene, partial cds, clone S1
NCBI Description
Seq. No.
                   35335
                   LIB3040-007-Q1-E1-G7
Seq. ID
Method
                   BLASTN
                   g2606080
NCBI GI
BLAST score
                   42
E value
                   9.0e-15
                   103
Match length
                   92
% identity
                  Glycine max sucrose synthase (SS) mRNA, complete cds
NCBI Description
                   35336
Seq. No.
                   LIB3040-008-Q1-E1-C2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4103476
BLAST score
                   34
E value
                   5.0e-10
Match length
                   42
% identity
                   95
                   Glycine tomentella small subunit ribosomal RNA gene,
NCBI Description
                   partial sequence; internal transcribed spacer 1, 5.8S
                   ribosomal RNA gene and internal transcribed spacer 2,
                   complete sequence; and large subunit ribosomal RNA gene, pa
Seq. No.
                   35337
                   LIB3040-008-Q1-E1-D4
Seq. ID
Method
                   BLASTN
                   g1575730
NCBI GI
                   88
BLAST score
E value
                   9.0e-42
Match length
                   287
```

Glycine max 14-3-3 related protein SGF14D mRNA, complete

NCBI Description



```
35338
Seq. No.
                    LIB3040-008-Q1-E1-F11
Seq. ID
                    BLASTX
Method
                    g3024020
NCBI GI
                    439
BLAST score
                    1.0e-43
E value
                    96
Match length
% identity
                    INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
NCBI Description
                    >gi 2225881 dbj BAA20877 (AB004824) eukaryotic initiation
                    factor 5A3 [Solanum tuberosum]
                    35339
Seq. No.
                    LIB3040-009-Q1-E1-B12
Seq. ID
                    BLASTN
Method
                    g256428
NCBI GI
                    105
BLAST score
                    2.0e-52
E value
                    159
Match length
                    92
% identity
                    KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                    Forrest, mRNA, 1259 nt]
                     35340
Seq. No.
                    LIB3040-009-Q1-E1-E12
Seq. ID
                    BLASTN
Method
                     g170053
NCBI GI
                    178
BLAST score
                     1.0e-95
E value
                     202
Match length
                     97
% identity
NCBI Description Soybean ribosomal protein S11 mRNA, 3' end
                     35341
Seq. No.
Seq. ID
                     LIB3040-009-Q1-E1-E2
                     BLASTX
Method
NCBI GI
                     g3202042
                     119
BLAST score
                     8.0e-15
E value
                     63
Match length
 % identity
                     (AF069324) 26S proteasome regulatory subunit S5A
 NCBI Description
                     [Mesembryanthemum crystallinum]
                     35342
 Seq. No.
 Seq. ID
                     LIB3040-009-Q1-E1-E8
                     BLASTX
 Method
                     g122087
 NCBI GI
 BLAST score
                     344
                     2.0e-32
 E value
 Match length
                     95
                     77
 % identity
                     HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964 (X13673) histone H3 (AA 1-136)
```

[Medicago satīva] >gi\_19609\_emb\_CAA31965\_ (X13674) histone



H3 (AA 1-136) [Medicago sativa] >gi\_21797\_emb\_CAA25451\_ (X00937) H3 histone [Triticum aestivum] >gi\_488565 (U09459) histone H3.1 [Medicago sativa] >gi\_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No. 35343

Seq. ID LIB3040-009-Q1-E1-H4

Method BLASTN
NCBI GI g1695691
BLAST score 84
E value 2.0e-39
Match length 200
% identity 85

NCBI Description Pisum sativum mRNA for diminuto, complete cds

Seq. No. 35344

Seq. ID LIB3040-010-Q1-E1-A8

Method BLASTN
NCBI GI g303900
BLAST score 192
E value 1.0e-104
Match length 307
% identity 31

NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No. 35345

Seq. ID LIB3040-010-Q1-E1-B10

Method BLASTX
NCBI GI g2407800
BLAST score 127
E value 9.0e-09
Match length 56
% identity 68

NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No. 35346

Seq. ID LIB3040-010-Q1-E1-B11

Method BLASTX
NCBI GI g464981
BLAST score 393
E value 3.0e-38
Match length 87
% identity 85

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi\_388207 (L23762)

ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 35347

Seq. ID LIB3040-010-Q1-E1-C10

Method BLASTN
NCBI GI g12245
BLAST score 41
E value 6.0e-14
Match length 73
% identity 89

NCBI Description Spinach chloroplast DNA inversion containing ORF



```
35348
Seq. No.
                  LIB3040-010-Q1-E1-C3
Seq. ID
                  BLASTN
Method
                  g18590
NCBI GI
BLAST score
                  63
E value
                  2.0e-27
                  99
Match length
                  91
% identity
NCBI Description G.max GH3 gene for auxin-regulated protein
                  35349
Seq. No.
Seq. ID
                  LIB3040-010-Q1-E1-E10
                  BLASTN
Method
NCBI GI
                  g531832
                  42
BLAST score
                  1.0e-14
E value
Match length
                  70
                   90
% identity
NCBI Description Cloning vector pSport2, complete sequence
                   35350
Seq. No.
Seq. ID
                  LIB3040-010-Q1-E1-H12
                  BLASTX
Method
                   g2507281
NCBI GI
                  199
BLAST score
                   6.0e-16
E value
                   56
Match length
                   70
% identity
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_
                   (X97380) atran2 [Arabidopsis thaliana]
                   35351
Seq. No.
Seq. ID
                   LIB3040-010-Q1-E1-H3
                   BLASTX
Method
                   q2119279
NCBI GI
                   271
BLAST score
                   3.0e-24
E value
Match length
                   87
% identity
                   57
NCBI Description tubulin beta-2 chain - rice
                   35352
Seq. No.
Seq. ID
                   LIB3040-011-Q1-E1-F12
Method
                   BLASTN
                   q310575
NCBI GI
BLAST score
                   206
                   1.0e-112
E value
Match length
                   324
 % identity
                   93
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                   35353
 Seq. No.
 Seq. ID
                   LIB3040-011-Q1-E1-H8
Method
                   BLASTN
```

g1399379

1.0e-39

84

NCBI GI

E value

BLAST score



Match length 104 % identity 95

NCBI Description Glycine max S-adenosyl-L-methionine:delta24-sterol-C-

methyltransferase mRNA, complete cds

Seq. No. 35354

Seq. ID LIB3040-012-Q1-E1-A3

Method BLASTN
NCBI GI g18551
BLAST score 366
E value 0.0e+00
Match length 396
% identity 98

NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

Seq. No. 35355

Seq. ID LIB3040-012-Q1-E1-E3

Method BLASTN
NCBI GI g18551
BLAST score 94
E value 1.0e-45
Match length 174
% identity 89

NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

Seq. No. 35356

Seq. ID LIB3040-012-Q1-E1-G6

Method BLASTX
NCBI GI g82114
BLAST score 169
E value 5.0e-12
Match length 78
% identity 46

NCBI Description wound-induced protein - tomato (fragment)

>qi 19320 emb CAA42537 (X59882) wound induced protein

[Lycopersicon esculentum]

Seq. No. 35357

Seq. ID LIB3040-012-Q1-E1-H3

Method BLASTX
NCBI GI g1173187
BLAST score 281
E value 1.0e-26
Match length 92
% identity 71

NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi\_1362041\_pir\_\_S56673

ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi\_643074 (U19940) putative 40S ribosomal

protein s12 [Fragaria x ananassa]

Seq. No. 35358

Seq. ID LIB3040-013-Q1-E1-C7

MethodBLASTNNCBI GIg531832BLAST score38



```
E value 4.0e-12

Match length 86
% identity 86

NCBI Description Cloning vector pSport2, complete sequence

Seq. No. 35359
Seq. ID LIB3040-013-Q1-E1-C8
```

Method BLASTX
NCBI GI g730645
BLAST score 166
E value 9.0e-12
Match length 51
% identity 65

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi\_629556\_pir\_\_S43412 ribosomal protein S15 - Arabidopsis thaliana >gi\_313152\_emb\_CAA80679\_

(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi\_313188 emb\_CAA80681\_(Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi\_1903366\_gb\_AAB70449\_(AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb\_R29788,gb\_ATTS0365 come from this gene. [Arabidopsis

thaliana]

 Seq. No.
 35360

 Seq. ID
 LIB3040-014-Q1-E1-B12

 Method
 BLASTX

 NCBI GI
 g3560529

NCBI GI g356052 BLAST score 184 E value 7.0e-14 Match length 84 % identity 49

NCBI Description (AF039598) light harvesting chlorophyll A/B binding protein

[Prunus persica]

Seq. No. 35361

Seq. ID LIB3040-014-Q1-E1-E11

Method BLASTN
NCBI GI g4490324
BLAST score 46
E value 8.0e-17
Match length 66
% identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14

(ESSA project)

Seq. No. 35362

Seq. ID LIB3040-015-Q1-E1-B3

Method BLASTN
NCBI GI g18551
BLAST score 253
E value 1.0e-140
Match length 348
% identity 94

NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

Seq. No. 35363

Seq. ID LIB3040-015-Q1-E1-F1



```
Method
                  BLASTN
NCBI GI
                  g310575
                  144
BLAST score
                   2.0e-75
E value
                   264
Match length
                   92
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                   35364
Seq. No.
Seq. ID
                   LIB3040-016-Q1-E1-A4
                   BLASTX
Method
                   g309673
NCBI GI
                   242
BLAST score
                   1.0e-20
E value
                   71
Match length
% identity
NCBI Description (L19651) light harvesting protein [Pisum sativum]
                   35365
Seq. No.
                   LIB3040-017-Q1-E1-C5
Seq. ID
                   BLASTX
Method
                   g2558962
NCBI GI
                   197
BLAST score
                   3.0e-15
E value
                   89
Match length
                   54
% identity
NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]
                   35366
Seq. No.
Seq. ID
                   LIB3040-017-Q1-E1-G12
                   BLASTN
Method
                   g18644
NCBI GI
BLAST score
                   166
                   2.0e-88
E value
                   278
Match length
                   90
% identity
NCBI Description Soybean mRNA for HMG-1 like protein
                   35367
Seq. No.
                   LIB3040-017-Q1-E1-G7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3687251
BLAST score
                   195
E value
                   3.0e-15
                   84
Match length
% identity
                   (AC005169) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   35368
Seq. ID
                   LIB3040-018-Q1-E1-A6
Method
                   BLASTN
NCBI GI
                   g18551
BLAST score
                   174
E value
                   3.0e-93
Match length
                   274
% identity
                   92
```

5359

NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding



## protein

```
35369
Seq. No.
                  LIB3040-018-Q1-E1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3176098
                  243
BLAST score
                  1.0e-20
E value
                  99
Match length
                  48
% identity
NCBI Description (Y15036) annexin [Medicago truncatula]
Seq. No.
                   35370
                  LIB3040-018-Q1-E1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1362009
BLAST score
                  433
                   5.0e-43
E value
                  105
Match length
                   49
% identity
NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana
Seq. No.
                   35371
                   LIB3040-019-Q1-E1-D5
Seq. ID
                   BLASTN
Method
                   g310575
NCBI GI
BLAST score
                   158
                   1.0e-83
E value
                   262
Match length
                   92
% identity
                  Glycine max nodulin-26 mRNA, complete cds
NCBI Description
Seq. No.
                   35372
Seq. ID
                   LIB3040-019-Q1-E1-G4
Method
                   BLASTN
NCBI GI
                   g11574
BLAST score
                   57
                   2.0e-23
E value
Match length
                   125
                   86
% identity
                  Soybean chloroplast elongator tRNA-Met gene
NCBI Description
Seq. No.
                   35373
                   LIB3040-019-Q1-E1-G6
Seq. ID
                   BLASTN
Method
                   g1143321
NCBI GI
BLAST score
                   49
                   7.0e-19
E value
                   143
Match length
                   89
% identity
                   Glycine max alfa-carboxyltransferase (accA-2) precursor
NCBI Description
                   mRNA, complete cds
```

35374 Seq. No.

LIB3040-019-Q1-E1-H3 Seq. ID

BLASTN Method NCBI GI g170073

5360

% identity

58



```
BLAST score
                  3.0e-25
E value
Match length
                  118
                  89
% identity
                  Soybean calmodulin (SCaM-3) mRNA, complete cds
NCBI Description
                  35375
Seq. No.
                  LIB3040-020-Q1-E1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1848210
BLAST score
                  169
                   6.0e-12
E value
                   64
Match length
                   59
% identity
                  (Y11208) histone H2B1 [Nicotiana tabacum]
NCBI Description
                   35376
Seq. No.
                   LIB3040-020-Q1-E1-D3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2852444
BLAST score
                   46
E value
                   9.0e-17
                   130
Match length
% identity
                   84
                  Salix bakko mRNA for SUI1 homolog, complete cds
NCBI Description
                   35377
Seq. No.
Seq. ID
                   LIB3040-020-Q1-E1-F3
                   BLASTN
Method
NCBI GI
                   q310575
BLAST score
                   158
                   1.0e-83
E value
Match length
                   301
                   90
% identity
                  Glycine max nodulin-26 mRNA, complete cds
NCBI Description
Seq. No.
                   35378
                   LIB3040-021-Q1-E1-A12
Seq. ID
                   BLASTX
Method
                   q267069
NCBI GI
BLAST score
                   247
E value
                   4.0e-21
Match length
                   67
                   72
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   35379
Seq. No.
                   LIB3040-021-Q1-E1-C10
Seq. ID
                   BLASTX
Method
                   g3738259
NCBI GI
                   289
BLAST score
                   5.0e-26
E value
                   103
Match length
```

5361

Seq. ID

Method



```
(AB018411) cytosolic phosphoglycerate kinase 1 [Populus
NCBI Description
                  nigra]
Seq. No.
                  35380
                  LIB3040-021-Q1-E1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3851636
BLAST score
                  196
E value
                  3.0e-15
Match length
                  74
% identity
                  55
NCBI Description
                  (AF098519) unknown [Avicennia marina] >gi 4128206
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
Seq. No.
                  35381
Seq. ID
                  LIB3040-021-Q1-E1-F9
Method
                  BLASTX
NCBI GI
                  g3132470
BLAST score
                  161
E value
                  3.0e-11
Match length
                  87
                  49
% identity
NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]
                  35382
Seq. No.
                  LIB3040-021-Q1-E1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170053
BLAST score
                  190
E value
                  1.0e-103
Match length
                  318
% identity
                  90
NCBI Description Soybean ribosomal protein S11 mRNA, 3' end
                  35383
Seq. No.
                  LIB3040-022-Q1-E1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g414831
BLAST score
                  127
E value
                  2.0e-65
Match length
                  163
% identity
                  94
NCBI Description Glycine max (Rablp) mRNA, complete cds
Seq. No.
                  35384
Seq. ID
                  LIB3040-022-Q1-E1-E2
Method
                  BLASTX
NCBI GI
                  g3687251
BLAST score
                  355
                  1.0e-33
E value
Match length
                  132
                  55
% identity
NCBI Description
                 (AC005169) unknown protein [Arabidopsis thaliana]
Seq. No.
                  35385
```

5362

LIB3040-022-Q1-E1-F9

BLASTN



```
g310575
NCBI GI
BLAST score
                  50
E value
                  2.0e-19
Match length
                  129
% identity
                  88
                  Glycine max nodulin-26 mRNA, complete cds
NCBI Description
                  35386
Seq. No.
                  LIB3040-022-Q1-E1-G1
Seq. ID
Method
                  BLASTN
                  g2924257
NCBI GI
BLAST score
                  112
                  2.0e-56
E value
Match length
                  147
% identity
                  94
NCBI Description Tobacco chloroplast genome DNA
Seq. No.
                  35387
                  LIB3040-023-Q1-E1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q509768
BLAST score
                  69
                   2.0e-30
E value
Match length
                   185
% identity
                  Glycine max seed-specific low molecular weight sulfur-rich
NCBI Description
                  protein
Seq. No.
                   35388
                   LIB3040-023-Q1-E1-A6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2995845
BLAST score
                   42
                   1.0e-14
E value
Match length
                   58
% identity
                   93
                   Trifolium uniflorum 18S ribosomal RNA gene, partial
NCBI Description
                   sequence; internal transcribed spacer 1, 5.8S ribosomal RNA
                   gene and internal transcribed spacer 2, complete sequence;
                   and 26S ribosomal RNA gene, partial sequence
                   35389
Seq. No.
Seq. ID
                   LIB3040-023-Q1-E1-G12
Method
                   BLASTX
                   g4206306
NCBI GI
BLAST score
                   217
                   9.0e-18
E value
                   98
Match length
                   42
% identity
                   (AF049110) prpol [Zea mays]
NCBI Description
                   35390
Seq. No.
                   LIB3040-024-Q1-E1-C5
Seq. ID
```

BLASTX Method g730536 NCBI GI BLAST score 181 E value 7.0e-14

5363



Match length 44 % identity 84

60S RIBOSOMAL PROTEIN L23 >gi\_310933 (L18915) 60S ribosomal NCBI Description

protein subunit L17 [Nicotiana tabacum]

Seq. No. 35391

Seq. ID LIB3040-024-Q1-E1-G12

Method BLASTN NCBI GI g2290120 BLAST score `33 1.0e-09 E value 57 Match length

89 % identity NCBI Description HIV-1 strain MO2 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 35392

Seq. ID LIB3040-025-Q1-E1-A8

Method BLASTX NCBI GI a1173198 BLAST score 174 E value 8.0e-13 Match length 52 % identity 67

40S RIBOSOMAL PROTEIN S13 >gi 480095 pir S36423 ribosomal NCBI Description

protein S13.e - garden pea >gi\_396639\_emb\_CAA80974\_

(Z25509) ribosomal protein S13 [Pisum sativum]

Seq. No.

35393

Seq. ID LIB3040-025-Q1-E1-C5 BLASTN Method

NCBI GI g170053 98 BLAST score E value 7.0e-48 158 Match length % identity 91

NCBI Description Soybean ribosomal protein S11 mRNA, 3' end

Seq. No. 35394

Seq. ID LIB3040-025-Q1-E1-C6

Method BLASTX NCBI GI g1173198 BLAST score 165 E value 2.0e-15 Match length 64 % identity 78

NCBI Description 40S RIBOSOMAL PROTEIN S13 >gi 480095 pir S36423 ribosomal

protein S13.e - garden pea >gi 396639\_emb\_CAA80974\_

(Z25509) ribosomal protein S13 [Pisum sativum]

Seq. No. 35395

LIB3040-025-Q1-E1-D7 Seq. ID

Method BLASTN NCBI GI g310575 BLAST score 65 E value 3.0e-28 Match length 214



```
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                   35396
Seq. No.
Seq. ID
                  LIB3040-025-Q1-E1-D9
Method
                  BLASTX
NCBI GI
                  g2244833
BLAST score
                  169
E value
                   5.0e-12
Match length
                  111
                  35
% identity
```

NCBI Description (Z97337) centromere protein homolog [Arabidopsis thaliana]

35397 Seq. No. Seq. ID LIB3040-025-Q1-E1-E11 Method BLASTX NCBI GI q3687243 BLAST score 256 E value 3.0e-22 Match length 67

% identity (AC005169) putative ribosomal protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 35398 Seq. ID LIB3040-025-Q1-E1-F4 Method BLASTN

NCBI GI g531531 BLAST score 53 5.0e-21 E value Match length 154 % identity 94

NCBI Description P.sativum mitochondrion genes rps10, trnF and trnP gene

Seq. No. 35399 Seq. ID LIB3040-025-Q1-E1-G12 Method BLASTX NCBI GI q2529665

BLAST score 235 E value 6.0e-20Match length 65 % identity 68

(AC002535) putative ribosomal protein L7A [Arabidopsis NCBI Description

thaliana]

Seq. No. 35400

Seq. ID LIB3040-025-Q1-E1-G6

Method BLASTX g1173187 NCBI GI BLAST score 224 E value 1.0e-18 Match length 83 % identity 59

40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir S56673 NCBI Description

ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi\_643074 (U19940) putative 40S ribosomal

protein s12 [Fragaria x ananassa]

BLAST score

E value

99 1.0e-48



```
35401
Seq. No.
                  LIB3040-025-Q1-E1-H11
Seq. ID
                  BLASTX
Method
                  g3176098
NCBI GI
                   167
BLAST score
                   2.0e-14
E value
                   82
Match length
% identity
                   54
NCBI Description (Y15036) annexin [Medicago truncatula]
                   35402
Seq. No.
                   LIB3040-026-Q1-E1-A1
Seq. ID
Method
                   BLASTN
                   g531828
NCBI GI
                   35
BLAST score
                   2.0e-10
E value
                   75
Match length
                   87
% identity
                   Cloning vector pSport1, complete cds
NCBI Description
                   35403
Seq. No.
                   LIB3040-027-Q1-E1-A12
Seq. ID
                   BLASTN
Method
NCBI GI
                   q310575
BLAST score
                   48
                   3.0e-18
E value
                   155
Match length
                   87
% identity
                   Glycine max nodulin-26 mRNA, complete cds
NCBI Description
                   35404
Seq. No.
                   LIB3040-027-Q1-E1-C4
Seq. ID
                   BLASTX
Method
                   g1813329
NCBI GI
                   227
BLAST score
                   7.0e-19
E value
                   70
Match length
                   66
 % identity
                   (AB000637) HMG-1 [Canavalia gladiata]
 NCBI Description
                   35405
 Seq. No.
                   LIB3040-027-Q1-E1-D11
 Seq. ID
                   BLASTN
 Method
                   q303900
 NCBI GI
                   170
 BLAST score
                    9.0e-91
 E value
                    350
 Match length
                    33
 % identity
 NCBI Description Soybean gene for ubiquitin, complete cds
                    35406
 Seq. No.
                    LIB3040-027-Q1-E1-F2
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g2654093
```



```
Match length
                  207
                  87
% identity
                  Glycine max aspartate aminotransferase glyoxysomal isozyme
NCBI Description
                  AAT1 precursor and aspartate aminotransferase cytosolic
                  isozyme AAT2 (AAT) mRNA, complete cds
                  35407
Seq. No.
Seq. ID
                  LIB3040-028-Q1-E1-B6
Method
                  BLASTX
NCBI GI
                  g1813329
BLAST score
                  217
                  1.0e-17
E value
                  73
Match length
% identity
                  63
NCBI Description (AB000637) HMG-1 [Canavalia gladiata]
                  35408
Seq. No.
Seq. ID
                  LIB3040-028-Q1-E1-B8
Method
                  BLASTN
NCBI GI
                  g303900
BLAST score
                  261
E value
                  1.0e-145
                  350
Match length
                                  2
% identity
                  31
NCBI Description Soybean gene for ubiquitin, complete cds
Seq. No.
                  35409
Seq. ID
                  LIB3040-028-Q1-E1-C10
Method
                  BLASTX
NCBI GI
                  q548900
BLAST score
                  147
                  1.0e-09
E value
Match length
                  70
                  49
% identity
NCBI Description SUCROSE-BINDING PROTEIN PRECURSOR (SBP)
                  >gi_322691_pir__JQ1730 62K sucrose-binding protein
                  precursor - soybean >gi 170064 (L06038) glucose binding
                  protein [Glycine max]
Seq. No.
                  35410
Seq. ID
                  LIB3040-028-01-E1-C4
Method
                  BLASTN
NCBI GI
                  g310575
BLAST score
                  44
E value
                  9.0e-16
                  124
Match length
% identity
                  84
NCBI Description Glycine max nodulin-26 mRNA, complete cds
```

Seq. ID LIB3040-029-Q1-E1-D10

Method BLASTN
NCBI GI g18551
BLAST score 49
E value 9.0e-19
Match length 65
% identity 94



```
NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
                  protein
Seq. No.
                  35412
Seq. ID
                  LIB3040-029-Q1-E1-F6
Method
                  BLASTN
                  g473604
NCBI GI
BLAST score
                  46
                  4.0e-17
E value
Match length
                  89
% identity
                  94
NCBI Description Zea mays W-22 histone H2B mRNA, complete cds
                  35413
Seq. No.
Seq. ID
                  LIB3040-029-Q1-E1-G8
Method
                  BLASTN
NCBI GI
                  g3982595
BLAST score
                  94
E value
                  1.0e-45
Match length
                  243
% identity
                  85
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                  35414
                  LIB3040-029-Q1-E1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q506628
BLAST score
                  121
E value
                  6.0e-62
Match length
                  141
% identity
                  96
NCBI Description Glycine max cv. Dare photosystem II type I chlorophyll
                  a/b-binding protein (lhcb1*7) gene, complete cds
Seq. No.
                  35415
Seq. ID
                  LIB3040-030-Q1-E1-A5
Method
                  BLASTX
NCBI GI
                  g3386606
BLAST score
                  432
                  5.0e-43
E value
Match length
                  93
% identity
                  78
NCBI Description (AC004665) putative beta-amylase [Arabidopsis thaliana]
                  35416
Seq. No.
                  LIB3040-030-Q1-E1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g531832
BLAST score
                  44
E value
                  5.0e-16
```

Match length 76 % identity 89

NCBI Description Cloning vector pSport2, complete sequence

Seq. No.

35417

Seq. ID LIB3040-030-Q1-E1-G8

Method BLASTX

E value

4.0e-55



```
q3158476
NCBI GI
BLAST score
                  226
E value
                  6.0e-19
Match length
                  58
% identity
NCBI Description (AF067185) aquaporin 2 [Samanea saman]
Seq. No.
                  35418
                  LIB3040-030-Q1-E1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539332
BLAST score
                  222
E value
                  3.0e-18
Match length
                  78
% identity
                  58
NCBI Description
                  (AL035539) glycosyltransferase like protein (fragment)
                  [Arabidopsis thaliana]
Seq. No.
                  35419
                  LIB3040-031-Q1-E1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006932
BLAST score
                  142
                  8.0e-09
E value
Match length
                  53
% identity
                  57
NCBI Description (AJ011400) NADH: ubiquinone oxidoreductase b17.2 subunit
                  [Bos taurus]
Seq. No.
                  35420
                  LIB3040-031-Q1-E1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170567
BLAST score
                  264
                  2.0e-23
E value
Match length
                  70
% identity
                  70
                  MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
NCBI Description
                  >gi 1085960 pir S52648 INO1 protein - Citrus paradisi
                  >gi 602565 emb CAA83565 (Z32632) INO1 [Citrus x paradisi]
Seq. No.
                  35421
                  LIB3040-031-Q1-E1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2058280
BLAST score
                  146
                  5.0e-21
E value
Match length
                  74
                  73
% identity
NCBI Description (X97381) atran3 [Arabidopsis thaliana]
Seq. No.
                  35422
                  LIB3040-031-Q1-E2-C11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q968986
BLAST score
                  110
```



Match length 206 % identity 89

NCBI Description Glycine max ferritin gene, nuclear gene encoding

chloroplast protein, complete cds

Seq. No. 35423

Seq. ID LIB3040-031-Q1-E2-C5

Method BLASTX
NCBI GI g1174411
BLAST score 207
E value 4.0e-30
Match length 115
% identity 60

NCBI Description MICROSOMAL SIGNAL PEPTIDASE 18 KD SUBUNIT (SPC18)

>gi 206978 (L11319) signal peptidase [Rattus norvegicus]

Seq. No. 35424

Seq. ID LIB3040-031-Q1-E2-D6

Method BLASTX
NCBI GI g4539307
BLAST score 175
E value 1.0e-12
Match length 62
% identity 60

NCBI Description (AL049480) putative acidic ribosomal protein [Arabidopsis

thaliana]

Seq. No. 35425

Seq. ID LIB3040-031-Q1-E2-G8

Method BLASTN
NCBI GI g18551
BLAST score 394
E value 0.0e+00
Match length 394
% identity 100

NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

Seq. No. 35426

Seq. ID LIB3040-032-Q1-E1-G11

Method BLASTX
NCBI GI g730557
BLAST score 239
E value 3.0e-20
Match length 91
% identity 58

NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal

protein L34 - garden pea >gi 498908 (U10047) ribosomal

protein L34 homolog [Pisum sativum]

Seq. No. 35427

Seq. ID LIB3040-032-Q1-E1-H2

Method BLASTN
NCBI GI g18725
BLAST score 34
E value 1.0e-09
Match length 46



% identity NCBI Description Soybean (G. max) mRNA for proliferating cell nuclear antigen (PCNA), partial 35428 Seq. No. LIB3040-033-Q1-E1-F4 Seq. ID BLASTN Method g2935449 NCBI GI 92 BLAST score 3.0e-44E value 160 Match length 89 % identity NCBI Description Malus domestica histone H2B mRNA, partial cds 35429 Seq. No. LIB3040-034-Q1-E1-A2 Seq. ID BLASTN Method g1813328 NCBI GI 66 BLAST score 9.0e-29 E value 198 Match length 83 % identity NCBI Description Canavalia gladiata mRNA for HMG-1, complete cds 35430 Seq. No. LIB3040-034-Q1-E1-D5 Seq. ID BLASTX Method q3928150 NCBI GI 145 BLAST score 1.0e-09 E value 43 Match length 63 % identity NCBI Description (AJ131049) hypothetical protein [Cicer arietinum] 35431 Seq. No. LIB3040-034-Q1-E1-D7 Seq. ID BLASTN Method g310575 NCBI GI BLAST score 41 4.0e-14 E value 165 Match length 83 % identity NCBI Description Glycine max nodulin-26 mRNA, complete cds 35432 Seq. No. LIB3040-034-Q1-E1-E12 Seq. ID BLASTX Method g2894599 NCBI GI 184 BLAST score 1.0e-13 E value Match length 53 70 % identity

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 35433

Seq. ID LIB3040-034-Q1-E1-F11

Method BLASTX



NCBI GI g4455330 BLAST score 154 E value 2.0e-10 Match length 49 % identity 65

NCBI Description (AL035525) contains EST gb:T44002 [Arabidopsis thaliana]

Seq. No. 35434

Seq. ID LIB3040-035-Q1-E1-B1

Method BLASTX
NCBI GI g3377797
BLAST score 160
E value 4.0e-11
Match length 86
% identity 48

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seg. No. 35435

Seq. ID LIB3040-035-Q1-E1-C9

Method BLASTX
NCBI GI g115797
BLAST score 382
E value 6.0e-37
Match length 103
% identity 73

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-215) (LHCP) >gi\_100026\_pir\_\_S16592 chlorophyll

a/b-binding protein - garden pea >gi\_20658\_emb\_CAA40365\_ (X57082) chlorophyll a/b-binding protein [Pisum sativum]

Seq. No. 35436

Seq. ID LIB3040-035-Q1-E1-D9

Method BLASTN
NCBI GI g3309268
BLAST score 53
E value 4.0e-21
Match length 73
% identity 93

NCBI Description Glycine max ferric leghemoglobin reductase-2 precursor

mRNA, complete cds

Seq. No. 35437

Seq. ID LIB3040-035-Q1-E1-G9

Method BLASTN
NCBI GI g169097
BLAST score 36
E value 6.0e-11
Match length 56
% identity 91

NCBI Description Pea histone H2A mRNA

Seq. No. 35438

Seq. ID LIB3040-036-Q1-E1-C6



Method BLASTX NCBI GI q730456 BLAST score 152 E value 4.0e-10 Match length 78 % identity 47 NCBI Description 40S RIBOSOMAL PROTEIN S19

35439

Seg. No. Seq. ID LIB3040-036-Q1-E1-G4 Method BLASTX NCBI GI g131384 BLAST score 248 E value 2.0e-21 Match length 91 % identity 59

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 81934 pir S04132

photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi 20621 emb CAA33408 (X15350) precursor (AA

-81 to 248) [Pisum sativum] >gi\_344004 dbj BAA02554\_ (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi\_226937\_prf\_\_1611461A O2 evolving

complex 33kD protein [Arachis hypogaea]

Seq. No. 35440

LIB3040-037-Q1-E1-A11 Seq. ID

Method BLASTN g1498333 NCBI GI BLAST score 62 E value 2.0e-26 Match length 78 % identity 95

NCBI Description Glycine max actin (Soy57) gene, partial cds

Seq. No. 35441

Seq. ID LIB3040-037-Q1-E1-B1

Method BLASTX NCBI GI q124224 BLAST score 408 E value 4.0e-40 Match length 96 % identity 80

NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)

>gi\_100345\_pir\_\_S21060 translation initiation factor eIF-5A

- common tobacco >gi 19887 emb CAA45105 (X63543)

eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No. 35442

Seq. ID LIB3040-037-Q1-E1-C8

Method BLASTN NCBI GI q310575 BLAST score 121 E value 1.0e-61 Match length 309 % identity 88

Seq. ID

35448

LIB3040-038-Q1-E1-E7

```
NCBI Description Glycine max nodulin-26 mRNA, complete cds
 Seq. No.
                   35443
Seq. ID
                   LIB3040-037-Q1-E1-D6
Method
                   BLASTN
NCBI GI
                   g758643
BLAST score
                   64
E value
                   2.0e-27
Match length
                   179
% identity
                   84
NCBI Description P.sativum mRNA for nucleoside diphosphate kinase II
Seq. No.
                   35444
Seq. ID
                   LIB3040-037-Q1-E1-F4
Method
                   BLASTX
NCBI GI
                   g166867
BLAST score
                   138
E value
                   1.0e-08
Match length
                   60
% identity
                   50
NCBI Description
                   (J05216) ribosomal protein S11 (probable start codon at bp
                   67) [Arabidopsis thaliana]
Seq. No.
                   35445
Seq. ID
                   LIB3040-037-Q1-E1-F5
Method
                   BLASTN
NCBI GI
                   g170053
BLAST score
                   111
E value
                   1.0e-55
Match length
                   163
% identity
                   92
NCBI Description Soybean ribosomal protein S11 mRNA, 3' end
Seq. No.
                   35446
Seq. ID
                  LIB3040-037-Q1-E1-H12
Method
                  BLASTN
NCBI GI
                  q18551
BLAST score
                  330
E value
                  0.0e + 00
Match length
                  363
% identity
                  98
NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
                  protein
Seq. No.
                  35447
Seq. ID
                  LIB3040-038-Q1-E1-B1
Method
                  BLASTN
NCBI GI
                  g3264758
BLAST score
                  58
E value
                  5.0e-24
Match length
                  186
% identity
                  83
NCBI Description Prunus armeniaca 40S ribosomal protein S8 (RPS8) mRNA,
                  complete cds
```

BLAST score

E value

134 2.0e-09



```
BLASTX
Method
                  g1703380
NCBI GI
                  371
BLAST score
                  8.0e-36
E value
                  102
Match length
                  73
% identity
                  ADP-RIBOSYLATION FACTOR >gi 1132483 dbj_BAA04607_ (D17760)
NCBI Description
                  ADP-ribosylation factor [Oryza sativa]
                   35449
Seq. No.
                  LIB3040-039-Q1-E1-C7
Seq. ID
                  BLASTX
Method
                   g309673
NCBI GI
BLAST score
                   273
                   3.0e-24
E value
                   82
Match length
                   76
% identity
                  (L19651) light harvesting protein [Pisum sativum]
NCBI Description
                   35450
Seq. No.
                   LIB3040-039-Q1-E1-D11
Seq. ID
                   BLASTX
Method
                   g4038036
NCBI GI
                   186
BLAST score
                   5.0e-14
E value
                   65
Match length
                   49
% identity
                  (AC005936) unknown protein [Arabidopsis thaliana]
NCBI Description
                   35451
Seq. No.
                   LIB3040-039-Q1-E1-E10
Seq. ID
                   BLASTN
Method
                   g170053
NCBI GI
                   108
BLAST score
                   8.0e-54
E value
                   196
Match length
                   89
% identity
NCBI Description Soybean ribosomal protein S11 mRNA, 3' end
                   35452
Seq. No.
                   LIB3040-039-Q1-E1-G12
Seq. ID
                   BLASTX
Method
                   g1352463
NCBI GI
                   238
BLAST score
                   5.0e-23
E value
Match length
                   95
                   60
% identity
                   MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1161312
NCBI Description
                   (U04876) myo-inositol-1-phosphate synthase [Arabidopsis
                   thaliana]
                   35453
Seq. No.
                   LIB3040-039-Q1-E1-H12
Seq. ID
                   BLASTX
Method
                   g122070
NCBI GI
```



```
69
Match length
                   64
% identity
                   HISTONE H3 >gi 82483 pir_A25564 histone H3 - rice
NCBI Description
                   >gi 169793 (M1\overline{5}664) \overline{histone} 3 [Oryza sativa] >gi_940018
                   (U2\overline{5}664) histone H3 [Oryza sativa]
                   35454
Seq. No.
                   LIB3040-040-Q1-E1-F1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4335723
BLAST score
                   157
                   1.0e-10
E value
Match length
                   41
                   66
% identity
                   (AC006248) putative thioredoxin M [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   35455
                   LIB3040-040-Q1-E1-F12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2905777
BLAST score
                   100
                   5.0e-49
E value
Match length
                   237
                   91
% identity
NCBI Description Glycine max ribosomal protein L41 mRNA, partial cds
                   35456
Seq. No.
                   LIB3040-040-Q1-E1-H2
Seq. ID
Method
                   BLASTN
                   q18747
NCBI GI
BLAST score
                   310
E value
                   1.0e-174
Match length
                   345
                   98
% identity
                   G.max mRNA for a protein similar to potato tuber protein
NCBI Description
                   p322 homolgous to Bowman-Birk Proteinase Inhibitor
                   35457
Seq. No.
                   LIB3040-041-Q1-E1-A5
Seq. ID
                   BLASTX
Method
                   g2335097
NCBI GI
                   253
BLAST score
                   8.0e-30
E value
                   106
Match length
                   65
% identity
                   (AC002339) putative receptor-like protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   35458
Seq. No.
                   LIB3040-041-Q1-E1-B3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g729470
                   283
BLAST score
                   3.0e-25
E value
                   67
Match length
```

% identity 79 NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR

Method

NCBI GI

E value

BLAST score

Match length

% identity

BLASTX

q481285

2.0e-14

189

81 47



(NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)

>gi\_542089\_pir\_\_JQ2272 formate dehydrogenase (EC 1.2.1.2)
precursor, mitochondrial - potato >gi\_297798\_emb\_CAA79702\_
(Z21493) mitochondrial formate dehydrogenase precursor
[Solanum tuberosum]

Seq. No. 35459 Seq. ID LIB3040-041-Q1-E1-E10 Method BLASTX NCBI GI q1053045 BLAST score 252 E value 9.0e-22 Match length 84 % identity 67 NCBI Description (U38424) histone H3 [Glycine max] Seq. No. 35460 LIB3040-041-Q1-E1-F6 Seq. ID Method BLASTN NCBI GI g310575 BLAST score 70 E value 4.0e-31 Match length 216 87 % identity NCBI Description Glycine max nodulin-26 mRNA, complete cds Seq. No. 35461 Seq. ID LIB3040-042-Q1-E1-A11 Method BLASTX NCBI GI q3986296 BLAST score 186 E value 6.0e-14 Match length 72 % identity 51 NCBI Description (AB018419) mitotic checkpoint [Xenopus laevis] Seq. No. 35462 Seq. ID LIB3040-042-Q1-E1-A4 Method BLASTX NCBI GI g1173187 BLAST score 147 E value 3.0e-14 57 Match length 75 % identity NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi\_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa] Seq. No. 35463 Seq. ID LIB3040-042-Q1-E1-C8



NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -NCBI Description Aspergillus niger >qi 408111 emb CAA81550 (Z26938) NADPH cytochrome P450 oxidoreductase [Aspergillus niger] >gi 1582627 prf 2119198A NADPH cytochrome P450 reductase [Aspergillus niger] Seq. No. 35464 Seq. ID LIB3040-042-Q1-E1-D2 Method BLASTN NCBI GI q343344 BLAST score 175 6.0e-94 E value 239 Match length 93 % identity NCBI Description Soybean chloroplast 16S rRNA (3' end), 18S rRNA (5' end), Ile-tRNA, and Ala-tRNA genes Seq. No. 35465 LIB3040-042-Q1-E1-D3 Seq. ID Method BLASTN NCBI GI q310575 BLAST score 79 E value 1.0e-36 199 Match length % identity 89 NCBI Description Glycine max nodulin-26 mRNA, complete cds 35466 Seq. No. LIB3040-042-Q1-E1-E3 Seq. ID Method BLASTN NCBI GI q968986 BLAST score 103 E value 6.0e-51 Match length 166 % identity 96 NCBI Description Glycine max ferritin gene, nuclear gene encoding chloroplast protein, complete cds Seq. No. 35467 LIB3040-042-Q1-E1-G1 Seq. ID Method BLASTX NCBI GI g4417273 BLAST score 421 E value 1.0e-41 Match length 95 % identity 85 (AC007019) ribonucleoside-diphosphate reductase large NCBI Description subunit [Arabidopsis thaliana] Seq. No. 35468

Seq. ID LIB3040-042-Q1-E1-G5

Method BLASTX
NCBI GI g2443836
BLAST score 195
E value 2.0e-15
Match length 55

Match length 55 % identity 71

5378

- <del>- - - -</del> -

NCBI Description



```
(AF020793) tonoplast intrinsic protein homolog MSMCP1
NCBI Description
                   [Medicago sativa]
                  35469
Seq. No.
Seq. ID
                  LIB3040-043-Q1-E1-A6
Method
                  BLASTN
                  q2995841
NCBI GI
                  53
BLAST score
                   6.0e-21
E value
                   57
Match length
% identity
                   Trifolium semipilosum 18S ribosomal RNA gene, partial
NCBI Description
                   sequence; internal transcribed spacer 1, 5.8S ribosomal RNA
                   gene and internal transcribed spacer 2, complete sequence;
                   and 26S ribosomal RNA gene, partial sequence
Seq. No.
                   35470
Seq. ID
                   LIB3040-043-Q1-E1-B9
                   BLASTX
Method
                   g2500354
NCBI GI
                   181
BLAST score
                   1.0e-13
E value
                   73
Match length
                   48
% identity
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
Seq. No.
                   LIB3040-043-Q1-E1-F5
Seq. ID
Method
                   BLASTN
                   q218082
NCBI GI
                   124
BLAST score
E value
                   2.0e-63
                   275
Match length
% identity
                   87
                   Rice mRNA for initiation factor eIF-4D (225 gene), partial
NCBI Description
                   sequence
                   35472
Seq. No.
                   LIB3040-044-Q1-E1-A2
Seq. ID
                   BLASTX
Method
                   g4417266
NCBI GI
BLAST score
                   461
                   3.0e-46
E value
                   122
Match length
                   26
 % identity
                   (AC007019) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   35473
 Seq. No.
                   LIB3040-044-Q1-E1-C10
 Seq. ID
                   BLASTX
 Method
                   g2623199
 NCBI GI
 BLAST score
                   473
                   1.0e-47
 E value
                   105
Match length
                   90
 % identity
```

(AF030290) protein phosphatase X isoform 2 [Arabidopsis



## thaliana]

```
35474
Seq. No.
                  LIB3040-044-Q1-E1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q133867
BLAST score
                  171
                  3.0e-12
E value
                  86
Match length
                  48
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
                  protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
                  ribosomal protein S11 [Zea mays]
                   35475
Seq. No.
                  LIB3040-045-Q1-E1-G3
Seq. ID
                  BLASTX
Method
                  g3184288
NCBI GI
                  159
BLAST score
                   8.0e-11
E value
                   35
Match length
% identity
NCBI Description (AC004136) unknown protein [Arabidopsis thaliana]
                   35476
Seq. No.
                   LIB3040-045-Q1-E1-H3
Seq. ID
                   BLASTX
Method
                   g2443836
NCBI GI
                   274
BLAST score
                   2.0e-24
E value
                   88
Match length
% identity
                   (AF020793) tonoplast intrinsic protein homolog MSMCP1
NCBI Description
                   [Medicago sativa]
                   35477
Seq. No.
                   LIB3040-046-Q1-E1-C8
Seq. ID
                   BLASTX
Method
                   g3687251
NCBI GI
                   157
BLAST score
                   1.0e-10
E value
                   50
Match length
 % identity
                   (AC005169) unknown protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
Seq. ID
                   LIB3040-046-Q1-E1-D1
                   BLASTX
Method
NCBI GI
                   g1173055
                   233
 BLAST score
 E value
                   6.0e-20
                   68
Match length
                   79
 % identity
                   60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__S42497
 NCBI Description
                   ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819
                   RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_
```

(X78284) RL5 ribosomal protein [Medicago sativa]

```
35479
Seq. No.
                  LIB3040-046-Q1-E1-E1
Seq. ID
                  BLASTX
Method
                  g4220519
NCBI GI
                  155
BLAST score
                  2.0e-10
E value
                  108
Match length
                  39
% identity
                  (AL035356) putative protein binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  35480
Seq. No.
                  LIB3040-046-Q1-E1-E8
Seq. ID
                  BLASTN
Method
                  g310575
NCBI GI
                   43
BLAST score
                   2.0e-15
E value
                   107
Match length
                   92
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                   35481
Seq. No.
                   LIB3040-046-Q1-E1-G8
Seq. ID
                   BLASTX
Method
                   g3687243
NCBI GI
                   242
BLAST score
                   1.0e-20
E value
                   61
Match length
                   79
% identity
                   (ACO05169) putative ribosomal protein [Arabidopsis
NCBI Description
                   thaliana]
                   35482
Seq. No.
                   LIB3040-047-Q1-E1-D1
Seq. ID
                   BLASTN
Method
                   g3449334
NCBI GI
BLAST score
                   47
                   2.0e-17
E value
Match length
                   75
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MYH9, complete sequence [Arabidopsis thaliana]
                   35483
Seq. No.
Seq. ID
                   LIB3040-048-Q1-E1-F5
                   BLASTN
Method
                   g498167
NCBI GI
BLAST score
                   84
                   1.0e-39
E value
```

Match length 224 % identity 84

NCBI Description Soybean mRNA for leginsulin, complete cds

Seq. No. 35484

Seq. ID LIB3040-048-Q1-E1-G2

Method BLASTX

BLAST score

E value

2.0e-22



```
q2342735
NCBI GI
                  272
BLAST score
                  4.0e-24
E value
                  83
Match length
% identity
NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]
                  35485
Seq. No.
                  LIB3040-049-Q1-E1-C1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g18644
                  135
BLAST score
                  7.0e-70
E value
                  259
Match length
% identity
NCBI Description Soybean mRNA for HMG-1 like protein
                  35486
Seq. No.
                  LIB3040-050-Q1-E1-A2
Seq. ID
                  BLASTN
Method
                  a602358
NCBI GI
                  54
BLAST score
                  1.0e-21
E value
                  118
Match length
                   87
% identity
NCBI Description P.sativum mRNA for type II chlorophyll a/b binding protein
                   35487
Seq. No.
                   LIB3040-050-Q1-E1-A4
Seq. ID
                   BLASTX
Method
                   q129916
NCBI GI
                   155
BLAST score
                   1.0e-10
E value
                   46
Match length
% identity
                   PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir_
NCBI Description
                   phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                   >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
                   35488
 Seq. No.
                   LIB3040-050-Q1-E1-D10
 Seq. ID
Method
                   BLASTN
                   q1458142
NCBI GI
BLAST score
                   34
                   7.0e-10
E value
                   54
Match length
                   91
 % identity
 NCBI Description Mus musculus histone H2a.2-615 (H2a-615), and histone
                   H3.2-615 (H3-615) genes, complete cds
                   35489
 Seq. No.
                   LIB3040-050-Q1-E1-E4
 Seq. ID
 Method
                   BLASTN
                   q531828
 NCBI GI
                   55
```



```
Match length
                   87
% identity
NCBI Description Cloning vector pSport1, complete cds
                   35490
Seq. No.
Seq. ID
                  LIB3040-050-Q1-E1-G8
Method
                  BLASTX
                   q82065
NCBI GI
                  172
BLAST score
                   1.0e-12
E value
                   56
Match length
                   64
% identity
NCBI Description ribosomal protein S3a - Madagascar periwinkle
                   >gi 217903_dbj_BAA00860_ (D01058) ORF [Catharanthus roseus]
Seq. No.
                   35491
                   LIB3040-051-Q1-E1-B6
Seq. ID
                   BLASTX
Method
                   g122079
NCBI GI
                   169
BLAST score
                   1.0e-14
E value
                   55
Match length
                   85
% identity
NCBI Description HISTONE H3 >gi 84397 pir JQ0757 histone H3 - staghorn
                   coral >gi 1556\overline{40} (M6\overline{0509}) H3 [Acropora formosa] >gi_166308
                   (L11067) histone H3 [Acropora formosa]
                   >gi 455649 bbs 140810 (S67324) histone H3, H3 [Acropora
                   formosa=coral, sperms, Peptide, 136 aa] [Acropora formosa]
                   >gi 450044 prf 1920342A histone H3 [Acropora formosa]
                   35492
Seq. No.
Seq. ID
                   LIB3040-051-Q1-E1-C12
Method
                   BLASTN
NCBI GI
                   g310575
                   53
BLAST score
                   3.0e-21
E value
                   133
Match length
% identity
                   86
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                   35493
Seq. No.
                   LIB3040-051-Q1-E1-D7
Seq. ID
Method
                   BLASTN
NCBI GI
                   q927504
BLAST score
                   43
                   2.0e-15
E value
                   71
Match length
                   90
 % identity
                   P.sativum mRNA for fructose-1, 6-biphosphate aldolase
NCBI Description
                   (clone aldcyt2)
```

Seq. ID LIB3040-052-Q1-E1-B8

Method BLASTX
NCBI GI g1173027
BLAST score 177
E value 8.0e-21



```
89
Match length
% identity
                  60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal
NCBI Description
                  protein L31 [Nicotiana glutinosa]
Seq. No.
                  35495
Seq. ID
                  LIB3040-052-Q1-E1-C1
                  BLASTX
Method
                  q464621
NCBI GI
                  220
BLAST score
                  3.0e-18
E value
                  76
Match length
% identity
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586
NCBI Description
                  ribosomal protein ML16 - common ice plant
                  >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                  [Mesembryanthemum crystallinum]
                  35496
                  LIB3040-052-Q1-E1-D2
                  BLASTX
```

Seq. No. Seq. ID Method NCBI GI g1362103 BLAST score 168 7.0e-12 E value 50 Match length % identity

ubiquitin conjugating enzyme - tomato NCBI Description

>gi\_886679\_emb CAA58111\_ (X82938) ubiquitin conjugating

enzyme [Lycopersicon esculentum]

35497 Seq. No. LIB3040-052-Q1-E1-E9 Seq. ID Method BLASTN q18747 NCBI GI BLAST score 131 2.0e-67 E value 289 Match length 93

% identity G.max mRNA for a protein similar to potato tuber protein NCBI Description

p322 homolgous to Bowman-Birk Proteinase Inhibitor

Seq. No. 35498

Seq. ID LIB3040-053-Q1-E1-A6

Method BLASTX q3947719 NCBI GI 222 BLAST score 3.0e-18 E value Match length 65 75 % identity

(AJ012653) ribosomal protein S28 [Prunus persica] NCBI Description

>gi 3947721 emb\_CAA10102\_ (AJ012654) ribosomal protein S28

[Prunus persica] >gi\_3947723\_emb\_CAA10103\_ (AJ012655)

ribosomal protein S28 [Prunus persica]

35499 Seq. No.

LIB3040-053-Q1-E1-D10 Seq. ID

BLASTX Method



```
g1666173
NCBI GI
                  162
BLAST score
                  2.0e-11
E value
                  76
Match length
% identity
NCBI Description (Y09106) transcription factor [Nicotiana plumbaginifolia]
                  35500
Seq. No.
                  LIB3040-053-Q1-E1-G6
Seq. ID
                  BLASTX
Method
                  g136057
NCBI GI
BLAST score
                  263
                  4.0e-23
E value
                  81
Match length
                  59
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi 99499 pir_ A32187 (S)-tetrahydroberberine oxidase -
                  Coptis japonica >gi_556171 (J04121) triosephosphate
                  isomerase [Coptis japonica]
                  35501
Seq. No.
Seq. ID
                  LIB3040-054-Q1-E1-B3
                  BLASTX
Method
                   g4007863
NCBI GI
                   246
BLAST score
                   4.0e-21
E value
                   64
Match length
                   70
% identity
NCBI Description (AJ131520) alpha-D-xylosidase [Tropaeolum majus]
                   35502
Seq. No.
Seq. ID
                   LIB3040-054-Q1-E1-D2
Method
                   BLASTX
                   q4416302
NCBI GI
                   173
BLAST score
                   8.0e-13
E value
                   76
Match length
% identity
                   51
                   (AF105716) copia-type pol polyprotein [Zea mays]
NCBI Description
                   35503
Seq. No.
                   LIB3040-054-Q1-E1-F12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q18764
BLAST score
                   176
E value
                   2.0e-94
                   228
Match length
                   94
% identity
                   G.max tefS1 gene for elongation factor EF-1a
NCBI Description
                   35504
Seq. No.
                   LIB3040-054-Q1-E1-F9
Seq. ID
Method
                   BLASTN
                   g18764
NCBI GI
                   35
BLAST score
                   3.0e-10
E value
```

5385

83

Match length



```
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-la
Seq. No.
                  35505
                  LIB3040-055-Q1-E1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4102839
BLAST score
                  154
E value
                  3.0e-10
Match length
                  65
% identity
                  48
NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]
Seq. No.
                  35506
                  LIB3040-056-Q1-E1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3785978
BLAST score
                  312
E value
                  9.0e-29
                  100
Match length
% identity
                  65
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
                  35507
Seq. No.
                  LIB3040-056-Q1-E1-F7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g508602
BLAST score
                  52
E value
                  1.0e-20
Match length
                  148
% identity
                  84
                 Glycine max stearoyl-acyl carrier protein desaturase
NCBI Description
                  (SACPD) mRNA, complete cds
Seq. No.
                  35508
Seq. ID
                  LIB3040-057-Q1-E1-B6
Method
                  BLASTN
NCBI GI
                  q18551
BLAST score
                   394
E value
                  0.0e + 00
Match length
                  394
% identity
                  100
NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
                  protein
                  35509
Seq. No.
Seq. ID
                  LIB3040-057-Q1-E1-D2
Method
                  BLASTN
NCBI GI
                  g303900
BLAST score
                  173
                  2.0e-92
E value
Match length
                  224
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
```

Seq. ID LIB3040-057-Q1-E1-D6

Match length

48



```
BLASTN
Method
                  g303900
NCBI GI
                  119
BLAST score
                  2.0e-60
E value
                  239
Match length
                  33
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
                   35511
Seq. No.
                  LIB3040-058-Q1-E1-A8
Seq. ID
                  BLASTN
Method
                   g1277163
NCBI GI
                   176
BLAST score
                   2.0e-94
E value
                   210
Match length
                   96
% identity
NCBI Description Glycine max cysteine proteinase inhibitor mRNA, partial cds
                   35512
Seq. No.
                   LIB3040-058-Q1-E1-C12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g18551
                   357
BLAST score
                   0.0e + 00
E value
                   361
Match length
                   100
% identity
                   Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                   protein
                   35513
Seq. No.
                   LIB3040-058-Q1-E1-C7
Seq. ID
                   BLASTN
Method
                   q11576
NCBI GI
                   109
BLAST score
                   2.0e-54
E value
                   141
Match length
                    94
 % identity
                   Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,
NCBI Description
                   NADH dehydrogenase and ORF
                    35514
 Seq. No.
 Seq. ID
                    LIB3040-058-Q1-E1-E12
 Method
                    BLASTX
 NCBI GI
                    q4115371
                    179
 BLAST score
                    4.0e-13
 E value
                    117
 Match length
                    42
 % identity
                    (AC005967) unknown protein [Arabidopsis thaliana]
 NCBI Description
                    35515
 Seq. No.
 Seq. ID
                    LIB3040-058-Q1-E1-G5
                    BLASTX
 Method
 NCBI GI
                    g3264759
 BLAST score
                    152
                    3.0e-10
 E value
```



```
% identity
                  (AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
NCBI Description
                  35516
Seq. No.
                  LIB3040-060-Q1-E1-A5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1856971
                  283
BLAST score
                   1.0e-25
E value
                   72
Match length
                   75
% identity
                   (D26058) This gene is specifically expressed at the S phase
NCBI Description
                   during the cell cycle in the synchronous culture of
                   periwinkle cells. [Catharanthus roseus]
                   35517
Seq. No.
                   LIB3040-060-Q1-E1-B9
Seq. ID
Method
                   BLASTN
                   q1066304
NCBI GI
                   37
BLAST score
                   1.0e-11
E value
                   57
Match length
                   91
% identity
                   Cloning vector TLF97-1, lambda phage lacZ translational
NCBI Description
                   fusion vector, complete sequence
                   35518
Seq. No.
                   LIB3040-060-Q1-E1-C11
Seq. ID
                   BLASTX
Method
                   g3482967
NCBI GI
                   400
BLAST score
                   5.0e-39
E value
                   98
Match length
% identity
                   76
                   (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                   thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585)
                   protein phosphatase 2C [Arabidopsis thaliana]
                   35519
Seq. No.
                   LIB3040-060-Q1-E1-H4
Seq. ID
                   BLASTN
Method
                   q525331
NCBI GI
                   42
BLAST score
                   2.0e-14
E value
                   70
Match length
                   90
% identity
                   Pisum sativum Alaska alpha-tubulin (TubA1) gene, complete
NCBI Description
                   cds
                   35520
Seq. No.
                   LIB3040-061-Q1-E1-B11
Seq. ID
                   BLASTN
Method
                   g1885368
NCBI GI
                   35
BLAST score
                   2.0e-10
E value
                   43
Match length
```

5388

95

% identity



```
NCBI Description Glycine latrobeana small subunit ribosomal RNA gene,
                  partial sequence, internal transcribed spacer 1, 5.8S
                  ribosomal RNA gene and internal transcribed spacer 2,
                  complete sequence, and large subunit ribosomal RNA gene,
                  part
                  35521
Seq. No.
                  LIB3040-061-Q1-E1-D10
Seq. ID
                  BLASTN
Method
                  q555973
NCBI GI
                  157
BLAST score
                  5.0e-83
E value
                  321
Match length
                  87
% identity
NCBI Description Pisum sativum 14-3-3-like protein mRNA, complete cds
                  35522
Seq. No.
                  LIB3040-061-Q1-E11-A1
Seq. ID
                  BLASTN
Method
                   g310575
NCBI GI
                   157
BLAST score
                   5.0e-83
E value
                   197
Match length
                   95
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                   35523
Seq. No.
                   LIB3040-061-Q1-E11-E6
Seq. ID
                   BLASTN
Method
                   g531828
NCBI GI
                   59
BLAST score
                   1.0e-24
E value
                   167
Match length
                   84
% identity
NCBI Description Cloning vector pSport1, complete cds
                   35524
Seq. No.
                   LIB3040-061-Q1-E11-E7
 Seq. ID
                   BLASTX
Method
 NCBI GI
                   q3980383
                   333
 BLAST score
                   3.0e-31
 E value
                   84
 Match length
                   74
 % identity
                   (AC004561) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   35525
 Seq. No.
                   LIB3049-001-Q1-E1-A3
 Seq. ID
 Method
                   BLASTN
                   g2815245
 NCBI GI
```

NCBI GI g2815245
BLAST score 37
E value 2.0e-11
Match length 101
% identity 85

NCBI Description C.arietinum mRNA for class I type 2 metallothionein (clone:

CanMT-2)



```
35526
Seq. No.
Seq. ID
                   LIB3049-001-Q1-E1-A9
Method
                   BLASTX
                   g134145
NCBI GI
BLAST score
                   155
                   7.0e-11
E value
                   54
Match length
                   63
% identity
                   STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE
NCBI Description
                   PROTEIN A) >gi 99886 pir S08511 28K protein - soybean
                   >gi 169898 (M37530) 28 kDa protein [Glycine max] >gi 169975
                   (M76981) vegetative storage protein [Glycine max]
                   >gi_226867_prf__1609232B 28kD glycoprotein [Glycine max]
>gi_444325_prf__1906374A vegetative storage protein
                   [Glycine max]
Seq. No.
                   35527
Seq. ID
                   LIB3049-001-Q1-E1-C6
Method
                   BLASTX
                   g1053047
NCBI GI
BLAST score
                   326
E value
                   2.0e-30
Match length
                   83
% identity
                   80
NCBI Description
                   (U38425) histone H3 [Glycine max] >qi 1053049 (U38426)
                   histone H3 [Glycine max] >gi 1053051 (U38427) histone H3
                   [Glycine max]
                   35528
Seq. No.
Seq. ID
                   LIB3049-001-Q1-E1-E7
Method
                   BLASTX
NCBI GI
                   q2119011
BLAST score
                   156
E value
                   2.0e-10
Match length
                   83
% identity
                   42
NCBI Description histone H3.2 - long-tailed hamster >gi 516304 emb CAA56580
                   (X80330) histone H3.2 [Cricetulus longicaudatus]
                   35529
Seq. No.
Seq. ID
                   LIB3049-002-Q1-E1-A11
Method
                   BLASTX
NCBI GI
                   g3915039
BLAST score
                   193
                   3.0e-15
E value
Match length
                   53
% identity
                   74
NCBI Description SUGAR CARRIER PROTEIN C > gi 169718 (L08196) sugar carrier
                   protein [Ricinus communis]
                   35530
Seq. No.
Seq. ID
                   LIB3049-002-Q1-E1-A3
```

Method BLASTX
NCBI GI g3982596
BLAST score 242
E value 2.0e-20
Match length 106

NCBI Description



```
% identity
NCBI Description (AF039027) cationic peroxidase 2 [Glycine max]
                  35531
Seq. No.
                  LIB3049-002-Q1-E1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3450842
                  298
BLAST score
                  4.0e-27
E value
                  106
Match length
% identity
                  45
NCBI Description
                  (AF080436) mitogen activated protein kinase kinase [Oryza
                  sativa]
                  35532
Seq. No.
                  LIB3049-002-01-E1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q541943
                  209
BLAST score
                  9.0e-17
E value
                  48
Match length
% identity
                  metallothionein - soybean >gi_228682_prf__1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
Seq. No.
                  35533
                  LIB3049-002-Q1-E1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3341443
                  234
BLAST score
                  1.0e-19
E value
                  101
Match length
% identity
                  51
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
Seq. No.
                   35534
                  LIB3049-002-Q1-E1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076634
                  155
BLAST score
                   2.0e-10
E value
Match length
                  72
% identity
                   46
                  protein-serine/threonine kinase NPK15 - common tobacco
NCBI Description
                   >gi 505146 dbj BAA06538 (D31737) protein-serine/threonine
                   kinase [Nicotiana tabacum]
Seq. No.
                   35535
Seq. ID
                   LIB3049-002-Q1-E1-H2
Method
                  BLASTX
NCBI GI
                   g3914472
                   250
BLAST score
                   9.0e-22
E value
Match length
                   60
                   80
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)
```

>gi 322764\_pir\_\_S32021 photosystem II 10K protein - common



tobacco >gi\_22669\_emb\_CAA49693\_ (X70088) NtpII10 [Nicotiana tabacum]

Seq. No. 35536

Seq. ID LIB3049-002-Q1-E1-H4

Method BLASTX
NCBI GI g4455198
BLAST score 200
E value 1.0e-15
Match length 66
% identity 62

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 35537

Seq. ID LIB3049-003-Q1-E1-D5

Method BLASTN
NCBI GI g493019
BLAST score 68
E value 3.0e-30
Match length 84
% identity 95

NCBI Description Glycine max delta-aminolevulinic acid dehydratase (Alad)

mRNA, complete cds

Seq. No. 35538

Seq. ID LIB3049-003-Q1-E1-H12

Method BLASTN
NCBI GI g310575
BLAST score 57
E value 2.0e-23
Match length 121
% identity 87

NCBI Description Glycine max nodulin-26 mRNA, complete cds

Seq. No. 35539

Seq. ID LIB3049-004-Q1-E1-C12

Method BLASTX
NCBI GI g1922248
BLAST score 153
E value 5.0e-10
Match length 31
% identity 94

NCBI Description (Y10087) hypothetical protein [Arabidopsis thaliana]

Seq. No. 35540

Seq. ID LIB3049-004-Q1-E1-E10

Method BLASTX
NCBI GI g2673905
BLAST score 168
E value 6.0e-12
Match length 108
% identity 35

NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 35541

Seq. ID LIB3049-004-Q1-E1-F11

Method BLASTN



```
NCBI GI
                   q456713
BLAST score
                   253
                   1.0e-140
E value
                   367
Match length
% identity
NCBI Description Glycine max gene for ubiquitin, complete cds
                   35542
Seq. No.
                   LIB3049-004-Q1-E1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q464621
BLAST score
                   324
E value
                   4.0e-30
Match length
                   120
                   46
% identity
                   60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir__S28586
NCBI Description
                   ribosomal protein ML16 - common ice plant
>gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
                   35543
Seq. No.
                   LIB3049-004-Q1-E1-H12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g310575
BLAST score
                   96
                   1.0e-46
E value
                   232
Match length
                   88
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                   35544
Seq. No.
                   LIB3049-005-Q1-E1-E10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3269284
                   246
BLAST score
E value
                   8.0e-25
Match length
                   109
                   55
% identity
                   (AL030978) histone H2A- like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   LIB3049-005-Q1-E1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g464444
BLAST score
                   390
                   6.0e-38
E value
Match length
                   83
% identity
                   88
                   PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                   COMPLEX 30 KD SUBUNIT) >qi 541889 pir S39900 proteasome -
                   Arabidopsis thaliana >gi_166830 (M98495) proteasome
                   [Arabidopsis thaliana]
```

Seq. ID LIB3049-006-Q1-E1-D2

Method BLASTN NCBI GI g3982595



```
BLAST score
                   0.0e + 00
E value
                   390
Match length
                   99
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                   35547
Seq. No.
                   LIB3049-006-Q1-E1-E1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1644288
BLAST score
                   67
E value
                   4.0e-29
Match length
                   151
                   86
% identity
NCBI Description B.juncea mRNA for chlorophyll a/b-binding protein
Seq. No.
                   LIB3049-006-Q1-E1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g133808
BLAST score
                   322
E value
                   7.0e-30
Match length
                   67
% identity
                   97
                   40S RIBOSOMAL PROTEIN S16 >gi_70921 pir__R3YL16 ribosomal
NCBI Description.
                   protein S16, cytosolic - large-leaved lupine >gi 19512 emb CAA36068 (X51766) rps16 gene product (AA
                   1-145) [Lupinus polyphyllus]
                   35549
Seq. No.
Seq. ID
                   LIB3049-007-Q1-E1-D4
Method
                   BLASTN
NCBI GI
                   g18644
                   165
BLAST score
E value
                    8.0e-88
                   233
Match length
                    93
% identity
                   Soybean mRNA for HMG-1 like protein
NCBI Description
                    35550
Seq. No.
                   LIB3049-008-Q1-E1-B8
Seq. ID
                   BLASTX
Method
                    g122007
NCBI GI
                    154
BLAST score
                    1.0e-12
E value
Match length
                    105
% identity
                    44
                   HISTONE H2A >gi 100161 pir S11498 histone H2A - parsley
NCBI Description
                    >gi 20448 emb \overline{CAA37828} (\overline{X53831}) H2A histone protein (AA 1
                    - 149) [Petroselinum crispum]
```

Seq. ID LIB3049-008-Q1-E1-H4

Method BLASTX
NCBI GI g2507421
BLAST score 250
E value 2.0e-21



```
Match length
% identity
                   68
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >qi 1800277
NCBI Description
                   (U81042) translation initiation factor [Arabidopsis
                  thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680)
                  translation initiation factor [Arabidopsis thaliana]
                  35552
Seq. No.
Seq. ID
                  LIB3049-009-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  q1084415
BLAST score
                  197
E value
                  3.0e-15
Match length
                   65
% identity
                   57
                  RNA-binding protein - Wood tobacco >gi_624925_dbj_BAA05170_
NCBI Description
                   (D26182) RNA-binding glycine rich protein (RGP-2)
                   [Nicotiana sylvestris]
Seq. No.
                  35553
Seq. ID
                  LIB3049-010-Q1-E1-F8
Method
                  BLASTN
NCBI GI
                  g18551
BLAST score
                  390
                  0.0e+00
E value
Match length
                  394
% identity
                  100
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                  protein
Seq. No.
                  35554
Seq. ID
                  LIB3049-011-Q1-E1-B12
Method
                  BLASTN
NCBI GI
                  g403326
BLAST score
                  63
E value
                  6.0e-27
Match length
                  123
% identity
NCBI Description T.repens TrMT1A mRNA for metallothionein-like protein
Seq. No.
                   35555
Seq. ID
                  LIB3049-011-Q1-E1-B8
Method
                  BLASTN
NCBI GI
                   q456713
BLAST score
                   142
E value
                   4.0e-74
Match length
                  250
                   37
% identity
NCBI Description Glycine max gene for ubiquitin, complete cds
Seq. No.
                   35556
Seq. ID
                  LIB3049-012-Q1-E1-A2
```

Method BLASTX
NCBI GI g3341443
BLAST score 320
E value 1.0e-29
Match length 119

Seq. ID

35562

LIB3049-013-Q1-E1-B11



```
% identity
NCBI Description (AJ223074) acid phosphatase [Glycine max]
                  35557
Seq. No.
Seq. ID
                  LIB3049-012-Q1-E1-D4
Method
                  BLASTX
                  g3660469
NCBI GI
                  275
BLAST score
                 2.0e-24
E value
                  68
Match length
                  75
% identity
                  (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
NCBI Description
                  thaliana] >gi 4512693 gb AAD21746.1 (AC006569)
                  succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
                  35558
Seq. No.
Seq. ID
                  LIB3049-012-Q1-E1-E2
Method
                  BLASTN
NCBI GI
                  g3982595
                  244
BLAST score
E value
                  1.0e-135
Match length
                  267
% identity
                  98
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                  35559
Seq. No.
Seq. ID
                  LIB3049-012-Q1-E1-F5
Method
                  BLASTX
NCBI GI
                  g3264759
                  306
BLAST score
E value
                  4.0e-28
Match length
                  62
% identity
                  97
NCBI Description (AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
                  35560
Seq. No.
Seq. ID
                  LIB3049-012-Q1-E1-G4
                  BLASTX
Method
                  g3341443
NCBI GI
BLAST score
                  326
E value
                  3.0e-30
Match length
                  94
% identity
                  68
NCBI Description (AJ223074) acid phosphatase [Glycine max]
                  35561
Seq. No.
Seq. ID
                  LIB3049-012-Q1-E1-H9
Method
                  BLASTX
                  g3063695
NCBI GI
                  160
BLAST score
                  5.0e-11
E value
Match length
                  34
% identity
                  (AL022537) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

% identity



```
BLASTN
Method
                  g170071
NCBI GI
BLAST score
                  71
                  6.0e-32
E value
                  111
Match length
% identity
NCBI Description Soybean calmodulin (SCaM-2) mRNA, complete cds
                  35563
Seq. No.
                  LIB3049-013-Q1-E1-C11
Seq. ID
                  BLASTX
Method
                  g4006826
NCBI GI
BLAST score
                  210
E value
                  9.0e-17
                  79
Match length
                  56
% identity
NCBI Description (AC005970) unknown protein [Arabidopsis thaliana]
                  35564
Seq. No.
                  LIB3049-013-Q1-E1-E1
Seq. ID
                  BLASTN
Method
                  g167072
NCBI GI
                  186
BLAST score
                  1.0e-100
E value
                  250
Match length
                  94
% identity
NCBI Description Barley ubiquitin (mub1) gene, complete cds
                  35565
Seq. No.
                  LIB3049-013-Q1-E1-F2
Seq. ID
                  BLASTN
Method
                  g2905771
NCBI GI
                   40
BLAST score
                   3.0e-13
E value
Match length
                   88
                   86
% identity
                  Glycine max glyceraldehyde-3 phosphate dehydrogenase
NCBI Description
                   (GAPDH) mRNA, partial cds
                   35566
Seq. No.
                   LIB3049-014-Q1-E1-A5
Seq. ID
                   BLASTN
Method
                   g547507
NCBI GI
                   99
BLAST score
E value
                   1.0e-48
Match length
                   167
                   90
% identity
                  G.max mRNA for glutamine synthetase
NCBI Description
                   35567
Seq. No.
                   LIB3049-014-Q1-E1-C8
Seq. ID
Method
                   BLASTN
NCBI GI
                   q457569
BLAST score
                   33
E value
                   2.0e-09
Match length
                   113
```

NCBI Description



```
NCBI Description Soybean mRNA for endo-xyloglucan transferase, partial cds
                  35568
Seq. No.
                  LIB3049-014-Q1-E1-D3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g296408
BLAST score
                  147
                   3.0e-77
E value
                   235
Match length
                   91
% identity
NCBI Description G.max ADR12 mRNA
Seq. No.
                   35569
                   LIB3049-015-Q1-E1-A7
Seq. ID
                   BLASTX
Method
                   q3426037
NCBI GI
                   307
BLAST score
                   3.0e-28
E value
Match length
                   101
                   63
% identity
                   (AC005168) putative ABC transporter protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   35570
                   LIB3049-015-Q1-E1-B5
Seq. ID
Method
                   BLASTX
                   q1420887
NCBI GI
                   190
BLAST score
E value
                   1.0e-14
                   74
Match length
                   54
% identity
                   (U34334) non-specific lipid transfer-like protein
NCBI Description
                   [Phaseolus vulgaris]
                   35571
Seq. No.
Seq. ID
                   LIB3049-015-Q1-E1-E7
Method
                   BLASTX
NCBI GI
                   g1076485
BLAST score
                   145
                   3.0e-09
E value
Match length
                   63
                   49
% identity
                   SAM-synthetase - chickpea (fragment)
NCBI Description
                   >gi 732576 emb CAA59508_ (X85252) SAM-synthetase [Cicer
                   arietinum]
Seq. No.
                   35572
                   LIB3049-015-Q1-E1-F7
Seq. ID
                   BLASTN
Method
                   q170067
NCBI GI
                   78
BLAST score
                   4.0e-36
E value
                   174
Match length
                   86
% identity
```

gene, complete cds

Soybean (G.max) proline-rich cell wall protein (SbPRP3)



```
Seq. No.
Seq. ID
                  LIB3049-016-Q1-E1-B7
Method
                  BLASTX
NCBI GI
                  g541943
BLAST score
                  181
E value
                  2.0e-13
                  42
Match length
% identity
                  83
                  metallothionein - soybean >gi 228682 prf 1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
Seq. No.
                   35574
                  LIB3049-016-Q1-E1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2088652
BLAST score
                  236
E value
                   7.0e-20
Match length
                  98
% identity
                   48
NCBI Description
                   (AF002109) 26S proteasome regulatory subunit S12 isolog
                   [Arabidopsis thaliana] >gi_2351376 (U54561) translation
                   initiation factor eIF2 p47 subunit homolog [Arabidopsis
                   thaliana]
Seq. No.
                   35575
Seq. ID
                  LIB3049-016-Q1-E1-F3
Method
                  BLASTN
NCBI GI
                   q1053044
BLAST score
                  84
E value
                   2.0e-39
Match length
                   224
% identity
                   98
NCBI Description Glycine max histone H3 gene, partial cds, clone S1
Seq. No.
                   35576
                   LIB3049-017-Q1-E1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2982259
BLAST score
                   342
E value
                   2.0e-32
                   72
Match length
                   92
% identity
                   (AF051212) probable 60s ribosomal protein L13a [Picea
NCBI Description
                  mariana]
Seq. No.
                   35577
Seq. ID
                   LIB3049-017-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                   q2245040
BLAST score
                   151
E value
                   8.0e-10
                   78
Match length
                   40
% identity
                  (Z97342) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. ID LIB3049-018-Q1-E1-A4



```
BLASTX
Method
                  g115787
NCBI GI
                  246
BLAST score
                  3.0e-21
E value
                  98
Match length
                  56
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-2)D (LHCP) >gi_82461_pir__S03706 chlorophyll
                  a/b-binding protein 2R precursor - rice
                  >qi 20182 emb CAA32109 (X13909) chlorophyll a/b-binding
                  preprotein (AA -28 to 235) [Oryza sativa]
                  35579
Seq. No.
Seq. ID
                  LIB3049-018-Q1-E1-E11
Method
                  BLASTN
                  q3377793
NCBI GI
BLAST score
                  39
                  1.0e-12
E value
                  51
Match length
% identity
                  94
NCBI Description Glycine max proteasome IOTA subunit mRNA, complete cds
Seq. No.
                  35580
                  LIB3049-018-Q1-E1-H3
Seq. ID
Methed
                  BLASTX
                  g3128190
NCBI GI
BLAST score
                  142
                  5.0e-09
E value
                  54
Match length
                  54
% identity
NCBI Description (AC004521) putative beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                  35581
                  LIB3049-019-Q1-E1-C1
Seq. ID
                  BLASTN
Method
                  g166421
NCBI GI
BLAST score
                  51
                  1.0e-19
E value
                  118
Match length
                  86
% identity
                  Medicago sativa ubiquitin carrier protein mRNA, complete
NCBI Description
Seq. No.
                  35582
Seq. ID
                  LIB3049-019-Q1-E1-E5
Method
                  BLASTX
NCBI GI
                  g1707981
BLAST score
                  178
                  5.0e-13
E value
                  100
Match length
                  39
% identity
                  GLUTAREDOXIN >gi 1076561 pir __S54825 glutaredoxin - castor
NCBI Description
                  bean
```

Seq. ID LIB3049-019-Q1-E1-E7

Method BLASTX



```
q1805359
NCBI GI
                  367
BLAST score
                  3.0e-35
E value
                  126
Match length
                  57
% identity
NCBI Description (AB000623) glucosyl transferase [Nicotiana tabacum]
                  35584
Seq. No.
                  LIB3049-019-Q1-E1-H8
Seq. ID
                  BLASTN
Method
                  g303900
NCBI GI
                  127
BLAST score
                  5.0e-65
E value
                  395
Match length
                  47
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
                  35585
Seq. No.
                  LIB3049-020-Q1-E1-G12
Seq. ID
                  BLASTN
Method
                  g3982595
NCBI GI
                  292
BLAST score
                   1.0e-163
E value
                   372
Match length
                   95
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                   35586
Seq. No.
                   LIB3049-020-Q1-E1-G6
Seq. ID
                   BLASTX
Method
                   g3241945
NCBI GI
                   164
BLAST score
                   2.0e-11
E value
                   84
Match length
                   51
% identity
NCBI Description (AC004625) unknown protein [Arabidopsis thaliana]
                   35587
Seq. No.
                   LIB3049-021-Q1-E1-A1
Seq. ID
                   BLASTN
Method
                   q3063391
NCBI GI
                   87
BLAST score
                   3.0e-41
E value
                   231
Match length
                   84
 % identity
NCBI Description Vigna radiata mRNA for Ca2+/H+ exchanger, complete cds
                   35588
 Seq. No.
                   LIB3049-021-Q1-E1-B12
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                   q21264
                   62
 BLAST score
 E value
                   2.0e-26
                   110
 Match length
                   89
 % identity
 NCBI Description Spinach mRNA 23 kDa protein of the photosynthetic
```

oxygen-evolving complex (OEC)



```
Seq. No.
                  35589
Seq. ID
                  LIB3049-021-Q1-E1-D3
Method
                  BLASTX
NCBI GI
                  g485518
                  190
BLAST score
                  6.0e-15
E value
Match length
                  64
% identity
                  61
NCBI Description
                  ubiquitin / ribosomal protein CEP52 - rice
                  >gi 303857_dbj_BAA02154_ (D12629) ubiquitin/ribosomal
                  polyprotein [Oryza sativa]
Seq. No.
                  35590
                  LIB3049-021-Q1-E1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g730536
BLAST score
                  350
                  3.0e-33
E value
Match length
                  98
                  69
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal
                  protein subunit L17 [Nicotiana tabacum]
                  35591
Seq. No.
Seq. ID
                  LIB3049-021-Q1-E1-F3
Method
                  BLASTN
NCBI GI
                  q2815245
BLAST score
                  69
                  2.0e-30
E value
                  252
Match length
                  82
% identity
NCBI Description C.arietinum mRNA for class I type 2 metallothionein (clone:
                  CanMT-2)
                  35592
Seq. No.
                  LIB3049-021-Q1-E1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3947719
BLAST score
                  215
E value
                  2.0e-17
                  50
Match length
% identity
                  86
                  (AJ012653) ribosomal protein S28 [Prunus persica]
NCBI Description
                  >gi 3947721 emb CAA10102 (AJ012654) ribosomal protein S28
                  [Prunus persica] >gi 3947723 emb CAA10103 (AJ012655)
                  ribosomal protein S28 [Prunus persica]
                  35593
Seq. No.
                  LIB3049-022-Q1-E1-B11
Seq. ID
Method
                  BLASTX
                  g1155090
NCBI GI
BLAST score
                  186
E value
                  4.0e-14
Match length
                  65
```

NCBI Description (X94986) beta glucosidase [Manihot esculenta]

52

% identity



```
Seq. No.
                  35594
Seq. ID
                  LIB3049-022-Q1-E1-C12
Method
                  BLASTN
NCBI GI
                  q791097
BLAST score
                  33
                  3.0e-09
E value
Match length
                  57
% identity
                  89
NCBI Description P.vulgaris plsB mRNA
                  35595
Seq. No.
                  LIB3049-022-Q1-E1-D8
Seq. ID
Method
                  BLASTX
                  g115803
NCBI GI
                  299
BLAST score
                  3.0e-27
E value
                  95
Match length
                  62
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-4) (LHCP) >gi_100199_pir__S10857 chlorophyll
                  a/b-binding protein precursor - tomato >gi_170390 (M17558)
                  chlorophyll a/b-binding protein precursor [Lycopersicon
                  esculentum]
                  35596
Seq. No.
Seq. ID
                  LIB3049-022-Q1-E1-E9
Method
                  BLASTX
NCBI GI
                  g3608481
BLAST score
                  513
                  3.0e-52
E value
Match length
                  110
% identity
                  84
NCBI Description (AF088913) ribosomal protein L27a [Petunia x hybrida]
                  35597
Seq. No.
                  LIB3049-022-Q1-E1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4510345
BLAST score
                  160
E value
                  7.0e-11
                  53
Match length
% identity
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.
                  35598
                  LIB3049-022-Q1-E1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2642237
BLAST score
                  92
E value
                  3.0e-44
                  268
Match length
                  84
% identity
```

Seq. No. 35599

NCBI Description Glycine max endoplasmic reticulum HSC70-cognate binding protein precursor (BIP) mRNA, complete cds



```
Seq. ID
                  LIB3049-022-Q1-E1-F8
Method
                  BLASTX
NCBI GI
                  q322750
BLAST score
                  219
E value
                  1.0e-32
Match length
                  107
% identity
NCBI Description
                  ubiquitin / ribosomal protein CEP52 - wood tobacco
                  >qi 170217 (M74100) ubiquitin fusion protein [Nicotiana
                  sylvestris]
                  35600
Seq. No.
                  LIB3049-022-Q1-E1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g136057
BLAST score
                  320
                  1.0e-29
E value
Match length
                  97
% identity
                  63
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
                  Coptis japonica >gi_556171 (J04121) triosephosphate
                  isomerase [Coptis japonica]
Seq. No.
                  35601
Seq. ID
                  LIB3049-022-Q1-E1-G5
Method
                  BLASTX
NCBI GI
                  g2827715
BLAST score
                  324
E value
                  3.0e-30
Match length
                  104
% identity
                  60
NCBI Description
                  (AL021684) receptor protein kinase - like protein
                  [Arabidopsis thaliana]
Seq. No.
                  35602
                  LIB3049-022-Q1-E1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                  217
                  1.0e-17
E value
                  97
Match length
                  43
% identity
NCBI Description (AJ223074) acid phosphatase [Glycine max]
Seq. No.
                  35603
Seq. ID
                  LIB3049-023-Q1-E1-A9
Method
                  BLASTX
NCBI GI
                  g464621
BLAST score
                  159
E value
                  1.0e-15
Match length
                  90
% identity
                  48
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374_pir__S28586
NCBI Description
                  ribosomal protein ML16 - common ice plant
                  >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
```

[Mesembryanthemum crystallinum]



```
35604
Seq. No.
Seq. ID
                  LIB3049-023-Q1-E1-B2
Method
                  BLASTX
NCBI GI
                  q1808656
                  153
BLAST score
                  1.0e-10
E value
                  49
Match length
                  59
% identity
NCBI Description (Y10804) Ubiquitin activating enzyme El [Nicotiana tabacum]
                  35605
Seq. No.
                  LIB3049-023-Q1-E1-D6
Seq. ID
Method
                  BLASTX
                  g4220476
NCBI GI
                  154
BLAST score
                  5.0e-17
E value
Match length
                  82
% identity
                  49
NCBI Description (AC006069) ribophorin I-like protein [Arabidopsis thaliana]
                  35606
Seq. No.
Seq. ID
                  LIB3049-023-Q1-E1-G2
Method
                  BLASTX
NCBI GI
                  q3880282
BLAST score
                  141
                  4.0e-13
E value
Match length
                  75
% identity
                  36
                  (Z82059) similar to ABC transporters (2 domains); cDNA EST
NCBI Description
                  EMBL: D73856 comes from this gene; cDNA EST EMBL: D73975
                  comes from this gene; cDNA EST EMBL: C09722 comes from this
                  gene; cDNA EST yk428c4.5 comes from this gene; cDNA ES...
                  >gi 3881299 emb CAA21772 (AL032665) similar to ABC
                  transporters (2 domains); cDNA EST EMBL: D73856 comes from
                  this gene; cDNA EST EMBL: D73975 comes from this gene; cDNA
                  EST EMBL: C09722 comes from this gene; cDNA EST yk428c4.5
                  comes from this gene; cDNA
Seq. No.
                  35607
Seq. ID
                  LIB3049-023-Q1-E1-G8
Method
                  BLASTX
                  g3582335
NCBI GI
BLAST score
                  341
                  2.0e-32
E value
                  80
Match length
                  79
% identity
NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]
                  35608
Seq. No.
                  LIB3049-023-Q1-E1-H1
Seq. ID
```

Method BLASTN

NCBI GI g3982595 BLAST score 71 E value 3.0e-32 Match length 87 % identity 95



NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. Seq. ID LIB3049-024-Q1-E1-A2 Method BLASTX g541943 NCBI GI BLAST score 210 8.0e-17 E value Match length 52 79 % identity

NCBI Description metallothionein - soybean >gi 228682\_prf \_1808316A

metallothionein-like protein [Glycine max]

35610 Seq. No.

LIB3049-024-Q1-E1-D4 Seq. ID

Method BLASTX q4101564 NCBI GI BLAST score 194 8.0e-15 E value Match length 106 % identity 41

NCBI Description (AF004556) IFA-binding protein [Arabidopsis thaliana]

Seq. No. 35611

LIB3049-024-Q1-E1-G2 Seq. ID

Method BLASTX NCBI GI g116908 195 BLAST score 4.0e-15 E value 74 Match length % identity 57

NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE

(S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID

3-O-METHYLTRANSFERASE) (COMT) >qi 166420 (M63853)

S-adenosyl-L-methionine: caffeic acid 3-0-methyltransferase

[Medicago sativa]

Seq. No. 35612

LIB3049-025-Q1-E1-A7 Seq. ID

Method BLASTN g303900 NCBI GI BLAST score 316 1.0e-178 E value Match length 396 % identity

NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No. 35613

Seq. ID LIB3049-025-Q1-E1-B8

Method BLASTX NCBI GI g1666096 BLAST score 255 E value 1.0e-22 62 Match length 77 % identity

NCBI Description (Y09113) dioxygenase [Marah macrocarpus]

Method

NCBI GI

BLASTX

g4191796



```
Seq. No.
                   LIB3049-025-Q1-E1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3386613
BLAST score
                   175
                   2.0e-14
E value
                   77
Match length
                   66
% identity
NCBI Description (AC004665) putative ATP-dependent RNA helicase [Arabidopsis
                   thaliana]
                   35615
Seq. No.
                   LIB3049-025-Q1-E1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                  g126409
BLAST score
                   195
E value
                   2.0e-15
Match length
                   50
                   74
% identity
NCBI Description LIPOXYGENASE 1 >gi_100005_pir__S22153 lipoxygenase (EC 1.13.11.12) - kidney bean >gi_21017_emb_CAA45088_ (X63525)
                   lipoxygenase [Phaseolus vulgaris]
Seq. No.
                   35616
Seq. ID
                   LIB3049-025-Q1-E1-H3
Method
                   BLASTX
NCBI GI
                   q3935167
BLAST score
                   120
                   1.0e-11
E value
                   120
Match length
% identity
                   47
NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]
Seq. No.
                   35617
                   LIB3049-026-Q1-E1-A1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3982595
BLAST score
                   320
E value
                   1.0e-180
Match length
                   336
% identity
                   99
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                   35618
                   LIB3049-026-Q1-E1-B6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3982595
BLAST score
                   341
E value
                   0.0e + 00
Match length
                   357
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                   35619
                   LIB3049-026-Q1-E1-E3
Seq. ID
```

5407



```
BLAST score
                  185
E value
                  2.0e-14
                  62
Match length
                  56
% identity
NCBI Description (AC005917) putative senescence-associated protein 5
                  [Arabidopsis thaliana]
                  35620
Seq. No.
Seq. ID
                  LIB3049-026-Q1-E1-G6
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                  279
                  6.0e-25
E value
Match length
                  101
% identity
                  57
NCBI Description (AJ223074) acid phosphatase [Glycine max]
Seq. No.
                  35621
Seq. ID
                  LIB3049-027-Q1-E1-A2
Method
                  BLASTN
NCBI GI
                  g3982595
                  80
BLAST score
E value
                  4.0e-37
Match length
                  196
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                  35622
Seq. ID
                  LIB3049-027-Q1-E1-A6
                  BLASTN
Method
NCBI GI
                  g3982595
BLAST score
                  265
E value
                  1.0e-147
                  391
Match length
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                  35623
Seq. ID
                  LIB3049-027-Q1-E1-A7
Method
                  BLASTN
NCBI GI
                  g3982595
BLAST score
                  150
E value
                  6.0e-79
                  213
Match length
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                  35624
Seq. ID
                  LIB3049-027-Q1-E1-A8
Method
                  BLASTN
NCBI GI
                  g3982595
BLAST score
                  54
E value
                  1.0e-21
Match length
                  166
% identity
                  84
```

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds



```
Seq. No.
                  35625
                  LIB3049-027-Q1-E1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3183088
BLAST score
                  210
                  5.0e-17
E value
Match length
                  94
% identity
                  48
NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
                  (LTP) >gi_629658_pir__S47084 lipid transfer like protein -
                  cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer
                  like protein [Vigna unguiculata]
                  35626
Seq. No.
                  LIB3049-027-Q1-E1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2924772
BLAST score
                  142
E value
                  4.0e-09
Match length
                  58
% identity
                  55
NCBI Description (AC002334) unknown protein [Arabidopsis thaliana]
Seq. No.
                  35627
Seq. ID
                  LIB3049-027-Q1-E1-D9
Method
                  BLASTX
NCBI GI
                  q2829923
BLAST score
                  426
E value
                  4.0e-42
Match length
                  121
% identity
                  72
                  (AC002291) Similar to uridylyl transferases [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  35628
Seq. ID
                  LIB3049-027-Q1-E1-G3
Method
                  BLASTN
NCBI GI
                  g3982595
BLAST score
                  272
                  1.0e-151
E value
Match length
                  288
                  99
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                  35629
Seq. ID
                  LIB3049-027-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  g3738257
BLAST score
                  212
                  4.0e-17
E value
```

Match length 71 % identity 62

(AB018410) cytosolic phosphoglycerate kinase 1 [Populus NCBI Description

nigra]

35630 Seq. No.

LIB3049-027-Q1-E1-H2 Seq. ID

NCBI GI

BLAST score



```
Method
                  BLASTX
                  g3868758
NCBI GI
BLAST score
                  327
                  4.0e-37
E value
                  133
Match length
                  62
% identity
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                  35631
Seq. No.
                  LIB3049-028-Q1-E1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738334
BLAST score
                  186
                  6.0e-14
E value
                  122
Match length
% identity
                  40
NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]
Seq. No.
                  35632
Seq. ID
                  LIB3049-028-Q1-E1-B6
Method
                  BLASTX
NCBI GI
                  q549061
BLAST score
                  140
                  1.0e-08
E value
Match length
                  59
% identity
                  53
                  T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA)
NCBI Description
                  (CCT-ZETA-1) >gi 631655 pir S43063 CCT (chaperonin
                  containing TCP-1) zeta chain - mouse
                  >gi 468554 emb CAA83432 (Z31557) CCT (chaperonin
                  containing TCP-1) zeta subunit [Mus musculus]
Seq. No.
                  35633
Seq. ID
                  LIB3049-028-Q1-E1-D10
Method
                  BLASTN
NCBI GI
                  q3021372
BLAST score
                  180
                  9.0e-97
E value
Match length
                  276
% identity
                  92
NCBI Description Glycine max mRNA for profilin, PRO2
Seq. No.
                  35634
                  LIB3049-028-Q1-E1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g927428
BLAST score
                  269
E value
                  1.0e-23
Match length
                  107
% identity
                  48
NCBI Description (X86733) fis1 [Linum usitatissimum]
Seq. No.
                  35635
                  LIB3049-028-Q1-E1-E10
Seq. ID
Method
                  BLASTX
```

g1420887

207



2.0e-16 E value Match length 69 % identity 57 NCBI Description (U34334) non-specific lipid transfer-like protein [Phaseolus vulgaris] Seq. No. 35636 LIB3049-029-Q1-E1-A2 Seq. ID Method BLASTX NCBI GI g3023819 BLAST score 188 3.0e-14 E value Match length 90 % identity 44 NCBI Description CELL DIVISION PROTEIN FTSJ HOMOLOG >gi 2127806 pir G64471 cell division protein J - Methanococcus jannaschii >gi 1592021 (U67577) cell division protein FtsJ [Methanococcus jannaschii] Seq. No. 35637 Seq. ID LIB3049-029-Q1-E1-C3 Method BLASTX NCBI GI g3158476 BLAST score 247 E value 2.0e-21 Match length 85 % identity 67 NCBI Description (AF067185) aguaporin 2 [Samanea saman] 35638 Seq. No. Seq. ID LIB3049-029-Q1-E1-D11 Method BLASTX g2623296 NCBI GI BLAST score 181 2.0e-13 E value Match length 54 67 % identity NCBI Description (AC002409) hypothetical protein [Arabidopsis thaliana] Seq. No. 35639 Seq. ID LIB3049-029-Q1-E1-D6 Method BLASTX NCBI GI q3024020 BLAST score 402 E value 2.0e-39 93 Match length

80 % identity

NCBI Description INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)

>gi\_2225881\_dbj\_BAA20877\_ (AB004824) eukaryotic initiation

factor 5A3 [Solanum tuberosum]

Seq. No. 35640

Seq. ID LIB3049-029-Q1-E1-D7

Method BLASTX NCBI GI g1350983 BLAST score 242 E value 1.0e-20



```
Match length
                  90
                  57
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                  35641
Seq. No.
                  LIB3049-029-Q1-E1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3868758
BLAST score
                  171
E value
                  3.0e-12
Match length
                  69
% identity
                  51
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                  35642
Seq. No.
                  LIB3049-030-Q1-E1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g730456
BLAST score
                  144
                  2.0e-09
E value
                  39
Match length
% identity
                  69
NCBI Description 40S RIBOSOMAL PROTEIN S19
                  35643
Seq. No.
Seq. ID
                  LIB3049-030-Q1-E1-E8
                  BLASTN
Method
                  g1208702
NCBI GI
                  79
BLAST score
E value
                  1.0e-36
Match length
                  127
                  100
% identity
NCBI Description Glycine max histone H3 gene, partial cds, clone H3-DMAX
Seq. No.
                  35644
                  LIB3049-031-Q1-E1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3132476
BLAST score
                  214
E value
                  2.0e-17
Match length
                  81
                  58
% identity
NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]
                  35645
Seq. No.
                  LIB3049-031-Q1-E1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2431771
BLAST score
                  182
E value
                  2.0e-13
Match length
                  72
% identity
NCBI Description (U62753) acidic ribosomal protein P2b [Zea mays]
```

Seq. No. 35646

Seq. ID LIB3049-031-Q1-E1-E12

Method BLASTX



```
q2507421
NCBI GI
                  144
BLAST score
                  3.0e-09
E value
                  36
Match length
                  75
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277
NCBI Description
                   (U81042) translation initiation factor [Arabidopsis
                  thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680)
                  translation initiation factor [Arabidopsis thaliana]
                   35647
Seq. No.
                  LIB3049-031-Q1-E1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2583118
                   261
BLAST score
                   6.0e-23
E value
                   96
Match length
                   59
% identity
                  (AC002387) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   35648
Seq. No.
                   LIB3049-031-Q1-E1-G11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1362093
BLAST score
                   325
                   3.0e-30
E value
                   73
Match length
                   81
% identity
                   hypothetical protein (clone TPP15) - tomato (fragment)
NCBI Description
                   >gi_924632 (U20595) unknown [Solanum lycopersicum]
                   35649
Seq. No.
                   LIB3049-031-Q1-E1-H1
Seq. ID
Method
                   BLASTX
                   q1076485
NCBI GI
BLAST score
                   153
E value
                   3.0e-10
                   59
Match length
                   58
 % identity
                   SAM-synthetase - chickpea (fragment)
NCBI Description
                   >gi 732576 emb_CAA59508_ (X85252) SAM-synthetase [Cicer
                   arietinum]
                   35650
 Seq. No.
                   LIB3049-032-Q1-E1-B2
 Seq. ID
                   BLASTN
 Method
                   g945086
 NCBI GI
                   40
 BLAST score
                   2.0e-13
 E value
                   76
 Match length
 % identity
                   88
```

Seq. No. 35651

NCBI Description

Seq. ID LIB3049-032-Q1-E1-C5

Method BLASTX NCBI GI g1848212

Glycine max transcription factor TFIIB mRNA, complete cds

% identity



```
BLAST score
                   2.0e-17
E value
                   53
Match length
                   39
% identity
                   (Y11209) protein disulfide-isomerase precursor [Nicotiana
NCBI Description
                   tabacum]
                   35652
Seq. No.
                   LIB3049-032-Q1-E1-C6
Seq. ID
Method
                   BLASTX
                   g3355468
NCBI GI
BLAST score
                   312
                   7.0e-29
E value
                   79
Match length
                   85
% identity
                   (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                   thaliana]
                   35653
Seq. No.
                   LIB3049-032-Q1-E1-D10
Seq. ID
Method
                   BLASTN
                   g1666172
NCBI GI
BLAST score
                   38
E value
                   4.0e-12
                   134
Match length
                   82
% identity
NCBI Description N.plumbaginifolia mRNA for BTF3-like transcription factor
Seq. No.
                   35654
                   LIB3049-032-Q1-E1-D5
Seq. ID
Method
                   BLASTX
                   g1053059
NCBI GI
BLAST score
                   187
                   2.0e-14
E value
Match length
                   61
% identity
                   64
                  (U38423) histone H3 [Triticum aestivum]
NCBI Description
                   35655
Seq. No.
                   LIB3049-032-Q1-E1-E7
Seq. ID
                   BLASTN
Method
                   g3193282
NCBI GI
BLAST score
                   33
                   5.0e-09
E value
                   53
Match length
                   91
% identity
NCBI Description Arabidopsis thaliana BAC T14P8
                   35656
Seq. No.
                   LIB3049-032-Q1-E1-F11
Seq. ID
                   BLASTN
Method
                   g2764805
NCBI GI
BLAST score
                   138
                   8.0e-72
E value
                   250
Match length
                    90
```

NCBI Description G.max gene encoding epoxide hydrolase



```
Seq. No.
                  LIB3049-032-Q1-E1-H4
Seq. ID
                  BLASTN
Method
                  q1107486
NCBI GI
                  42
BLAST score
                  1.0e-14
E value
Match length
                  94
                  86
% identity
NCBI Description A.thaliana mRNA for 60S ribosomal protein L27a
                  35658
Seq. No.
                  LIB3049-032-Q1-E1-H7
Seq. ID
Method
                  BLASTN
                  g927504
NCBI GI
                  87
BLAST score
                  2.0e-41
E value
                  163
Match length
                  88
% identity
                  P.sativum mRNA for fructose-1, 6-biphosphate aldolase
NCBI Description
                   (clone aldcyt2)
                   35659
Seq. No.
                  LIB3049-033-Q1-E1-A3
Seq. ID
Method
                  BLASTX
                   g3582339
NCBI GI
                   240
BLAST score
                   1.0e-20
E value
                   62
Match length
                   65
% identity
                  (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
                   35660
Seq. No.
                   LIB3049-033-Q1-E1-B10
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2618602
BLAST score
                   33
                   4.0e-09
E value
Match length
                   68
                   88
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSJ1, complete sequence [Arabidopsis thaliana]
                   35661
Seq. No.
                   LIB3049-033-Q1-E1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3080439
BLAST score
                   200
E value
                   1.0e-15
Match length
                   59
 % identity
                   69
                   (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
                   35662
Seq. No.
                   LIB3049-033-Q1-E1-C6
Seq. ID
```

BLASTN

g2815245

Method

NCBI GI



```
BLAST score
                  2.0e-33
E value
Match length
                  242
                  83
% identity
                  C.arietinum mRNA for class I type 2 metallothionein (clone:
NCBI Description
                  CanMT-2)
                  35663
Seq. No.
                  LIB3049-033-Q1-E1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q456567
BLAST score
                   66
E value
                   9.0e-29
                   161
Match length
                   88
% identity
                  Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
NCBI Description
                  cds
                   35664
Seq. No.
                   LIB3049-034-Q1-E1-B5
Seq. ID
                   BLASTN
Method
                   q303900
NCBI GI
BLAST score
                   272
E value
                   1.0e-151
                   344
Match length
                   31
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
                   35665
Seq. No.
                   LIB3049-034-Q1-E1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1619602
BLAST score
                   280
                   5.0e-25
E value
Match length
                   81
% identity
                   73
NCBI Description (Y08726) MtN3 [Medicago truncatula]
                   35666
Seq. No.
                   LIB3049-034-Q1-E1-G9
Seq. ID
                   BLASTX
Method
                   g1490271
NCBI GI
BLAST score
                   197
                   2.0e-15
E value
                   87
Match length
                   49
% identity
NCBI Description (Z69744) ALL-1 protein [Homo sapiens]
                   35667
Seq. No.
                   LIB3049-035-Q1-E1-A9
Seq. ID
                   BLASTX
Method
                   g322750
NCBI GI
                   399
BLAST score
                   6.0e-39
E value
                   82
Match length
                   95
% identity
NCBI Description ubiquitin / ribosomal protein CEP52 - wood tobacco
```

NCBI Description



>gi\_170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]

```
35668
Seq. No.
Seq. ID
                  LIB3049-035-Q1-E1-B10
                  BLASTX
Method
                  g541943
NCBI GI
                  190
BLAST score
                  1.0e-14
E value
                  44
Match length
                  80
% identity
                  metallothionein - soybean >gi 228682 prf 1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
                  35669
Seq. No.
Seq. ID
                  LIB3049-035-Q1-E1-B8
Method
                  BLASTX
                  g135410
NCBI GI
BLAST score
                  237
                  4.0e-20
E value
                  60
Match length
% identity
                  68
                  TUBULIN ALPHA-2 CHAIN >gi 85173_pir B26488 tubulin alpha-2
NCBI Description
                  chain - fruit fly (Drosophila melanogaster) >gi_158733
                   (M14644) alpha-tubulin 2 [Drosophila melanogaster]
                  35670
Seq. No.
                  LIB3049-035-Q1-E1-D12
Seq. ID
                  BLASTN
Method
                  g3982595
NCBI GI
BLAST score
                  101
E value
                  1.0e-49
                  228
Match length
                  86
% identity
                  Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
NCBI Description
                  35671
Seq. No.
Seq. ID
                  LIB3049-035-Q1-E1-D5
                  BLASTX
Method
                  q122078
NCBI GI
BLAST score
                  160
                   2.0e-16
E value
Match length
                   83
                   69
% identity
                  HISTONE H3.4 (EMBRYONIC) >gi_51298 emb CAA24131 (V00754)
NCBI Description
                  reading frame histone H3 [Mus musculus]
                   35672
Seq. No.
                   LIB3049-035-Q1-E1-E10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3947719
BLAST score
                   188
                   3.0e-14
E value
Match length
                   65
% identity
                   66
```

(AJ012653) ribosomal protein S28 [Prunus persica]

>gi\_3947721\_emb\_CAA10102\_ (AJ012654) ribosomal protein S28



[Prunus persica] >gi\_3947723\_emb\_CAA10103\_ (AJ012655) ribosomal protein S28 [Prunus persica]

 Seq. No.
 35673

 Seq. ID
 LIB3049-035-Q1-E1-E9

 Method
 BLASTX

 NCBI GI
 g1173187

 BLAST score
 168

 E value
 3.0e-12

Match length 48 % identity 73

NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi\_1362041\_pir\_\_ S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden

strawberry >gi\_643074 (U19940) putative 40S ribosomal

protein s12 [Fragaria x ananassa]

Seq. No. 35674

Seq. ID LIB3049-035-Q1-E1-F11

Method BLASTN
NCBI GI g2055227
BLAST score 230
E value 1.0e-126
Match length 234
% identity 100

NCBI Description Glycine max mRNA for SRC1, complete cds

Seq. No. 35675

Seq. ID LIB3049-035-Q1-E1-G5

Method BLASTX
NCBI GI g4038045
BLAST score 505
E value 2.0e-51
Match length 112
% identity 81

NCBI Description (AC005936) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 35676

Seq. ID LIB3049-035-Q1-E1-H1

Method BLASTX
NCBI GI g2598597
BLAST score 159
E value 6.0e-11
Match length 81
% identity 48

NCBI Description (Y15371) MtN5 [Medicago truncatula]

Seq. No. 35677

Seq. ID LIB3049-036-Q1-E1-A11

Method BLASTX
NCBI GI g2347088
BLAST score 146
E value 1.0e-09
Match length 56
% identity 54

NCBI Description (U72765) non-specific lipid transfer protein PvLTP-24

[Phaseolus vulgaris]



```
35678
Seq. No.
                  LIB3049-036-Q1-E1-B11
Seq. ID
                  BLASTN
Method
                  q886099
NCBI GI
                  59
BLAST score
                  2.0e-24
E value
                  71
Match length
                  96
% identity
                  Glycine max putative water channel protein (Pip1) mRNA,
NCBI Description
                  complete cds
                  35679
Seq. No.
                  LIB3049-036-Q1-E1-C5
Seq. ID
                  BLASTN
Method
                  a1053044
NCBI GI
                   37
BLAST score
                   7.0e-12
E value
                   65
Match length
                   89
% identity
NCBI Description Glycine max histone H3 gene, partial cds, clone S1
                   35680
Seq. No.
                   LIB3049-036-Q1-E1-D10
Seq. ID
                   BLASTN
Method
                   q168492
NCBI GI
                   45
BLAST score
                   2.0e-16
E value
                   121
Match length
% identity
NCBI Description Corn histone H3 (H3C3) gene, complete cds
                   35681
Seq. No.
                   LIB3049-036-Q1-E1-D12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1053215
BLAST score
                   309
                   1.0e-173
E value
                   347
Match length
 % identity
                   98
                   Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                   nuclear gene encoding chloroplast protein, complete cds
                   35682
 Seq. No.
                   LIB3049-037-Q1-E1-C9
 Seq. ID
                   BLASTX
Method
                   g541943
 NCBI GI
                   205
 BLAST score
                   3.0e-16
 E value
 Match length
                   51
                   76
 % identity
                   metallothionein - soybean >gi_228682_prf__1808316A
 NCBI Description
```

Seq. No. 35683

Seq. ID LIB3049-037-Q1-E1-D9

Method BLASTX

metallothionein-like protein [Glycine max]



```
q3850582
NCBI GI
                  151
BLAST score
                  6.0e-10
E value
                  45
Match length
                  64
% identity
                  (AC005278) F15K9.14 [Arabidopsis thaliana]
NCBI Description
                  35684
Seq. No.
                  LIB3049-037-Q1-E1-F10
Seq. ID
                  BLASTX
Method
                  g1870700
NCBI GI
BLAST score
                  217
                  9.0e-18
E value
                  70
Match length
% identity
                  69
                  (U84116) cleavage stage histone H3 [Psammechinus miliaris]
NCBI Description
                  35685
Seq. No.
                  LIB3049-037-Q1-E1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4336747
BLAST score
                  157
                  4.0e-11
E value
                  57
Match length
                  29
% identity
                  (AF104924) unconventional myosin heavy chain [Zea mays]
NCBI Description
Seq. No.
                   35686
                  LIB3049-037-Q1-E1-H9
Seq. ID
                  BLASTX
Method
                  g4336747
NCBI GI
BLAST score
                   251
                   1.0e-21
E value
                   93
Match length
                   52
% identity
                  (AF104924) unconventional myosin heavy chain [Zea mays]
NCBI Description
                   35687
Seq. No.
                  LIB3049-038-Q1-E1-B5
Seq. ID
                   BLASTX
Method
                   g2662469
NCBI GI
BLAST score
                   183
                   7.0e-14
E value
                   71
Match length
                   54
% identity
                  (AF034217) ribosomal protein S6 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   35688
Seq. ID
                   LIB3049-038-Q1-E1-B7
                   BLASTX
Method
                   g135406
NCBI GI
BLAST score
                   147
E value
                   7.0e-10
                   48
Match length
% identity
                   TUBULIN ALPHA-3/ALPHA-5 CHAIN >qi 99768 pir A32712 tubulin
NCBI Description
```

alpha-5 chain - Arabidopsis thaliana >gi\_166912 (M17189)



alpha-tubulin [Arabidopsis thaliana] >gi\_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

35689 Seq. No. LIB3049-038-Q1-E1-F12 Seq. ID Method BLASTN NCBI GI q170053 165 BLAST score E value 8.0e-88 189 Match length 97 % identity Soybean ribosomal protein S11 mRNA, 3' end NCBI Description 35690 Seq. No. LIB3049-038-Q1-E1-F6 Seq. ID BLASTN Method q456713 NCBI GI BLAST score 203 1.0e-110 E value Match length 353 32 % identity Glycine max gene for ubiquitin, complete cds NCBI Description Seq. No. 35691 LIB3049-039-Q1-E1-B1 Seq. ID BLASTN Method g296408 NCBI GI BLAST score 181 2.0e-97 E value 293 Match length % identity 90 NCBI Description G.max ADR12 mRNA Seq. No. 35692 LIB3049-039-Q1-E1-B12 Seq. ID Method BLASTX g1351014 NCBI GI 329 BLAST score 7.0e-31 E value Match length 82 77 % identity 40S RIBOSOMAL PROTEIN S8 >gi\_968902\_dbj\_BAA07207\_ (D38010) NCBI Description ribosomal protein S8 [Oryza sativa] Seq. No. 35693 LIB3049-039-Q1-E1-H1 Seq. ID Method BLASTX g4455787 NCBI GI 152 BLAST score 3.0e-10 E value 66 Match length 39 % identity

Seq. No. 35694

NCBI Description

Seq. ID LIB3049-040-Q1-E1-C2

[Schizosaccharomyces pombe]

(AL035536) putative DNA polymerase accessory protein

BLAST score

E value

211 5.0e-17



```
BLASTX
Method
                  g1707642
NCBI GI
                  257
BLAST score
                  3.0e-22
E value
                  118
Match length
                  19
% identity
                  (Y07748) TMK [Oryza sativa]
NCBI Description
                  35695
Seq. No.
                  LIB3049-040-Q1-E1-C4
Seq. ID
                  BLASTX
Method
                  g3482972
NCBI GI
                   143
BLAST score
                   7.0e-09
E value
                   61
Match length
                   44
% identity
                  (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                   35696
Seq. No.
                  LIB3049-040-Q1-E1-D9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2340166
                   197
BLAST score
                   1.0e-15
E value
                   79
Match length
                   49
% identity
                   (AF008124) glutathione S-conjugate transporting ATPase
NCBI Description
                   [Arabidopsis thaliana] >gi 2459949 (AF008125) multidrug
                   resistance-associated protein homolog [Arabidopsis
                   thaliana]
Seq. No.
                   35697
                   LIB3049-041-Q1-E1-C3
Seq. ID
                   BLASTN
Method
                   g1813328
NCBI GI
BLAST score
                   45
                   3.0e-16
E value
                   89
Match length
                   88
% identity
                   Canavalia gladiata mRNA for HMG-1, complete cds
NCBI Description
Seq. No.
                   35698
Seq. ID
                   LIB3049-041-Q1-E1-D7
Method
                   BLASTN
                   q3982595
NCBI GI
                   208
BLAST score
                   1.0e-113
E value
                   252
Match length
% identity
                   Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
NCBI Description
Seq. No.
                   35699
                   LIB3049-041-Q1-E1-E10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4559358
```



```
Match length
                  66
% identity
                  59
                  (AC006585) putative steroid binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  35700
Seq. No.
                  LIB3049-041-Q1-E1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1363492
                  532
BLAST score
                  1.0e-54
E value
                  119
Match length
% identity
                  85
NCBI Description
                  outer envelope membrane protein OEP75 precursor - garden
                  pea >gi_576507 (L36858) outer membrane protein [Pisum
                  sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic
                  outer envelope membrane protein (OEP75) [Pisum sativum]
Seq. No.
                  35701
Seq. ID
                  LIB3049-042-Q1-E1-A1
Method
                  BLASTX
NCBI GI
                  g2570342
BLAST score
                  280
E value
                  3.0e-31
Match length
                  80
% identity
                  86
                  (U90929) glyoxalase II cytoplasmic isozyme [Arabidopsis
NCBI Description
                  thaliana]
                  35702
Seq. No.
Seq. ID
                  LIB3049-042-Q1-E1-A3
Method
                  BLASTN
                  g1420886
NCBI GI
                  63
BLAST score
                  6.0e-27
E value
Match length
                  144
% identity
                 Phaseolus vulgaris non-specific lipid transfer-like protein
NCBI Description
                  mRNA, complete cds
Seq. No.
                  35703
Seq. ID
                  LIB3049-042-Q1-E1-C4
Method
                  BLASTN
NCBI GI
                  g3982595
BLAST score
                  257
E value
                  1.0e-142
Match length
                  269
                  99
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
```

Seq. No. 35704

Seq. ID LIB3049-042-Q1-E1-C5 Method BLASTX NCBI GI g3282523 BLAST score 309 E value 1.0e-28

77 Match length



```
% identity
NCBI Description (AF025433) tyrosine/dopa decarboxylase [Papaver somniferum]
                  35705
Seq. No.
                  LIB3049-042-Q1-E1-D3
Seq. ID
                  BLASTN
Method
                  g2104678
NCBI GI
                  43
BLAST score
                  2.0e-15
E value
                  71
Match length
% identity
NCBI Description V. faba mRNA for transcription factor containing HMG-box
                  35706
Seq. No.
                  LIB3049-042-Q1-E1-D6
Seq. ID
                  BLASTN
Method
                  g18644
NCBI GI
                  218
BLAST score
                  1.0e-119
E value
                  326
Match length
                  91
% identity
NCBI Description Soybean mRNA for HMG-1 like protein
                  35707
Seq. No.
                  LIB3049-042-Q1-E1-F4
Seq. ID
                  BLASTX
Method
                   q475257
NCBI GI
                   156
BLAST score
                   1.0e-14
E value
                   51
Match length
% identity
                  (M95065) similar to ribosomal protein L19 [Zea mays]
NCBI Description
                   35708
Seq. No.
                   LIB3049-042-Q1-E1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3183088
                   175
BLAST score
                   1.0e-12
E value
Match length
                   82
                   43
 % identity
                   PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
NCBI Description
                   (LTP) >gi_629658_pir__S47084 lipid transfer like protein -
                   cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer
                   like protein [Vigna unguiculata]
                   35709
 Seq. No.
                   LIB3049-042-Q1-E1-G3
 Seq. ID
 Method
                   BLASTN
                   q669002
 NCBI GI
                   162
 BLAST score
                   4.0e-86
 E value
                   166
 Match length
                   99
 % identity
 NCBI Description Glycine max calnexin mRNA, complete cds
```

35710

Seq. No.



```
LIB3049-043-Q1-E1-G5
Seq. ID
                  BLASTN
Method
NCBI GI
                  q303900
                  92
BLAST score
                  2.0e-44
E value
                  181
Match length
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
                  35711
Seq. No.
                  LIB3049-043-Q1-E1-G7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q170071
BLAST score
                  287
                  1.0e-160
E value
                   310
Match length
                   99
% identity
NCBI Description Soybean calmodulin (SCaM-2) mRNA, complete cds
                   35712
Seq. No.
                   LIB3049-043-Q1-E1-G8
Seq. ID
                  BLASTX
Method
                   q1053045
NCBI GI
BLAST score
                   223
                   2.0e-18
E value
Match length
                   81
                   60
% identity
NCBI Description (U38424) histone H3 [Glycine max]
                   35713
Seq. No.
                   LIB3049-044-Q1-E1-A11
Seq. ID
                   BLASTX
Method
                   g3201554
NCBI GI
 BLAST score
                   152
                   3.0e-20
 E value
 Match length
                   97
                   54
 % identity
 NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]
                   35714
 Seq. No.
                   LIB3049-044-Q1-E1-D9
 Seq. ID
                   BLASTX
 Method
                   g3377797
 NCBI GI
 BLAST score
                   292
                   2.0e-26
 E value
                   100
 Match length
                   61
 % identity
                   (AF075597) Similar to 60S ribosome protein L19; coded for
 NCBI Description
                   by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
                   A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                   R90691 [Ara
                   35715
 Seq. No.
                   LIB3049-044-Q1-E1-E9
 Seq. ID
```

BLASTX

g1703375

Method

NCBI GI



```
BLAST score
                  2.0e-24
E value
Match length
                  88
                  73
% identity
                  ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
NCBI Description
                  DcARF1 [Daucus carota]
                  35716
Seq. No.
                  LIB3049-044-Q1-E1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1255951
BLAST score
                  228
E value
                  5.0e-19
                  72
Match length
                  72
% identity
                  (X96932) PS60 [Nicotiana tabacum]
NCBI Description
                   35717
Seq. No.
                  LIB3049-045-Q1-E1-C8
Seq. ID
Method
                  BLASTX
                  g2213877
NCBI GI
                   239
BLAST score
E value
                   3.0e-20
Match length
                   86
% identity
                  (AF003197) glutamine synthetase [Hevea brasiliensis]
NCBI Description
                   35718
Seq. No.
                   LIB3049-045-Q1-E1-D4
Seq. ID
Method
                   BLASTX
                   g541943
NCBI GI
                   223
BLAST score
E value
                   2.0e-18
Match length
                   55
                   73
% identity
                  metallothionein - soybean >gi_228682_prf__1808316A
NCBI Description
                   metallothionein-like protein [Glycine max]
Seq. No.
                   35719
                   LIB3049-046-Q1-E1-A10
Seq. ID
                   BLASTN
Method
                   g1336081
NCBI GI
                   78
BLAST score
                   4.0e-36
E value
                   82
Match length
                   99
% identity
                   Glycine max var. Century ascorbate peroxidase 2 (APx2)
NCBI Description
                   mRNA, complete cds
                   35720
Seq. No.
                   LIB3049-046-Q1-E1-A12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g541943
BLAST score
                   163
                   2.0e-11
E value
                   78
Match length
```

% identity



NCBI Description metallothionein - soybean >gi\_228682\_prf\_\_1808316A metallothionein-like protein [Glycine max]

Seq. No. 35721

Seq. ID LIB3049-046-Q1-E1-C12

Method BLASTX
NCBI GI g2129562
BLAST score 190
E value 8.0e-15
Match length 75
% identity 55

NCBI Description class III ADH, glutathione-dependent formaldehyde

dehydrogenase. - Arabidopsis thaliana

>gi\_1143388\_emb\_CAA57973\_ (X82647) class III ADH, glutathione-dependent formaldehyde dehydrogenase.

[Arabidopsis thaliana]

Seq. No. 35722

Seq. ID LIB3049-046-Q1-E1-C8

Method BLASTX
NCBI GI g4325342
BLAST score 161
E value 3.0e-11
Match length 50
% identity 62

NCBI Description (AF128393) No definition line found [Arabidopsis thaliana]

Seq. No. 35723

Seq. ID LIB3049-048-Q1-E1-D6

Method BLASTN
NCBI GI g2407789
BLAST score 50
E value 3.0e-19
Match length 119
% identity 91

NCBI Description Glycine max grr1 (grr1) mRNA, complete cds

Seq. No. 35724

Seq. ID LIB3049-048-Q1-E1-F12

Method BLASTX
NCBI GI g3075394
BLAST score 355
E value 6.0e-34
Match length 104
% identity 63

NCBI Description (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead

protein [Arabidopsis Thaliana]

Seq. No. 35725

Seq. ID LIB3049-048-Q1-E1-F5

Method BLASTX
NCBI GI g1708424
BLAST score 230
E value 2.0e-19
Match length 86
% identity 55

NCBI Description

Seq. No.

Seq. ID

35731

LIB3049-050-Q1-E1-F5



```
ISOFLAVONE REDUCTASE HOMOLOG >gi 1230614 (U48590)
NCBI Description
                  isoflavone reductase-like protein [Lupinus albus]
                  35726
Seq. No.
                  LIB3049-049-Q1-E1-E5
Seq. ID
Method
                  BLASTX
                  g2499114
NCBI GI
                  282
BLAST score
                  2.0e-25
E value
Match length
                  103
% identity
                  53
                  VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi_1839240
NCBI Description
                  (U86663) aVps41p [Arabidopsis thaliana]
Seq. No.
                  35727
                  LIB3049-049-Q1-E1-F4
Seq. ID
Method
                  BLASTX
                  g2267593
NCBI GI
                  142
BLAST score
                  2.0e-09
E value
                  54
Match length
% identity
                  52
                  (AF009411) glycine-rich RNA-binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  LIB3049-049-Q1-E1-G8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3021374
BLAST score
                  55
                  4.0e-22
E value
                  103
Match length
% identity
                  88
NCBI Description Glycine max mRNA for profilin, PRO1
Seq. No.
                   35729
                  LIB3049-050-Q1-E1-A5
Seq. ID
                  BLASTX
Method
                  g2500354
NCBI GI
                   233
BLAST score
                   9.0e-20
E value
                   61
Match length
                   69
% identity
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj_BAA19462_
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
                   35730
Seq. No.
Seq. ID
                  LIB3049-050-Q1-E1-B4
                  BLASTX
Method
                   q2961300
NCBI GI
                   239
BLAST score
E value
                   2.0e-20
                   72
Match length
% identity
                   67
```

5428

(AJ225027) ribosomal protein L24 [Cicer arietinum]

BLAST score

E value

139

1.0e-08



```
BLASTN
Method
                  q1208702
NCBI GI
                  75
BLAST score
                  3.0e-34
E value
                  126
Match length
                  99
% identity
                  Glycine max histone H3 gene, partial cds, clone H3-DMAX
NCBI Description
                  35732
Seq. No.
                  LIB3049-051-Q1-E1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3341443
                   254
BLAST score
                  5.0e-22
E value
                  85
Match length
                   59
% identity
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                   35733
Seq. No.
                  LIB3049-051-Q1-E1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3900979
BLAST score
                   40
                   3.0e-13
E value
                   129
Match length
                   88
% identity
                  Eichhornia crassipes mRNA for metallothionein-like protein,
NCBI Description
                   clone A
                   35734
Seq. No.
Seq. ID
                   LIB3049-051-Q1-E1-G4
                   BLASTX
Method
                   g2244876
NCBI GI
                   327
BLAST score
                   1.0e-30
E value
                   95
Match length
                   63
% identity
                   (Z97338) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   35735
Seq. No.
Seq. ID
                   LIB3049-052-Q1-E1-A8
                   BLASTN
Method
                   g441456
NCBI GI
                   40
BLAST score
                   3.0e-13
E value
                   68
Match length
% identity
                   L.esculentum mRNA for ubiquitin conjugating enzyme E2
NCBI Description
                   >gi 2296161 emb A39963.1 A39963 Sequence 7 from Patent
                   WO9421794
Seq. No.
                   35736
Seq. ID
                   LIB3049-052-Q1-E1-H7
                   BLASTX
Method
NCBI GI
                   q2194143
```



```
Match length
                  64
% identity
                  (AC002062) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  35737
Seq. ID
                  LIB3049-053-Q1-E1-A11
                  BLASTX
Method
NCBI GI
                  g4263722
BLAST score
                  260
                  1.0e-22
E value
Match length
                  93
                  57
% identity
                  (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
                  35738
Seq. No.
Seq. ID
                  LIB3049-053-Q1-E1-B10
Method
                  BLASTX
                  g3687239
NCBI GI
BLAST score
                  321
                  8.0e-30
E value
                  93
Match length
% identity
                  72
                  (AC005169) putative clathrin coat assembly protein
NCBI Description
                  [Arabidopsis thaliana]
                  35739
Seq. No.
Seq. ID
                  LIB3049-053-Q1-E1-B6
Method
                  BLASTN
                  g857398
NCBI GI
BLAST score
                  210
                  1.0e-114
E value
Match length
                  370
                  89
% identity
NCBI Description Glycine max mRNA for mitotic cyclin b1-type, complete cds
                  35740
Seq. No.
Seq. ID
                  LIB3049-053-Q1-E1-C10
                  BLASTN
Method
NCBI GI
                  g1129144
BLAST score
                  90
                   4.0e-43
E value
Match length
                  170
% identity
                  M.indica (Manila) THMF5 mRNA for 3-ketoacyl-coA thiolase B
NCBI Description
Seq. No.
                   35741
Seq. ID
                  LIB3049-053-01-E1-E6
Method
                  BLASTX
NCBI GI
                  q1856971
BLAST score
                   385
                   3.0e-37
E value
```

Match length 98 72 % identity

(D26058) This gene is specifically expressed at the S phase NCBI Description

during the cell cycle in the synchronous culture of

periwinkle cells. [Catharanthus roseus]



```
35742
Seq. No.
                  LIB3049-053-Q1-E1-F4
Seq. ID
                  BLASTX
Method
                  g3608128
NCBI GI
                  276
BLAST score
                  2.0e-24
E value
                  104
Match length
                  61
% identity
                  (AC005314) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4263794 gb AAD15454_ (AC006068) hypothetical protein
                   [Arabidopsis thaliana]
                  35743
Seq. No.
                  LIB3049-053-Q1-E1-G4
Seq. ID
                  BLASTN
Method
                  g1421750
NCBI GI
                  34
BLAST score
                  1.0e-09
E value
                  46
Match length
                   93
% identity
                  Pisum sativum S-adenosylmethionine decarboxylase mRNA,
NCBI Description
                  complete cds
                  35744
Seq. No.
                  LIB3049-054-Q1-E1-A6
Seq. ID
Method *
                  BLASTX
                   q4539351
NCBI GI
                   320
BLAST score
                   1.0e-29
E value
                   120
Match length
                   49
% identity
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   35745
Seq. No.
                   LIB3049-054-Q1-E1-D5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3169719
                   199
BLAST score
                   2.0e-15
E value
                   61
Match length
                   64
% identity
                  (AF007109) similar to yeast dcp1 [Arabidopsis thaliana]
NCBI Description
                   35746
Seq. No.
                   LIB3049-054-Q1-E1-D7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4056497
BLAST score
                   249
                   3.0e-21
E value
                   107
Match length
                   54
% identity
                  (AC005896) putative histone H2B [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 35747

Seq. ID LIB3049-054-Q1-E1-E3

Method BLASTX NCBI GI g3158476

BLAST score

E value

251 9.0e-22



```
BLAST score
                     9.0e-32
  E value
                     105
  Match length
                     72
  % identity
                     (AF067185) aquaporin 2 [Samanea saman]
  NCBI Description
                     35748
  Seq. No.
                     LIB3049-054-Q1-E1-H11
  Seq. ID
                     BLASTX
  Method
                     g730583
  NCBI GI
                     154
  BLAST score
                     3.0e-10
  E value
                     68
  Match length
                     51
  % identity
                     60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 551267 emb CAA55047
  NCBI Description
                     (X78213) 60s acidic ribosomal protein P2 [Parthenium
                     argentatum]
  Seq. No.
                     35749
                     LIB3049-055-Q1-E1-A12
   Seq. ID
  Method
                     BLASTN
  NCBI GI
                     g18551
  BLAST score
                     219
💸 E value
                     1.0e-120
                     324
  Match length
                     92
   % identity
                     Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
   NCBI Description
                     protein
                     35750
   Seq. No.
                     LIB3049-055-Q1-E1-C9
   Seq. ID
                     BLASTX
   Method
                     g3024020
   NCBI GI
                     193
   BLAST score
                     2.0e-15
   E value
                     50
   Match length
                     78
   % identity
                     INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
   NCBI Description
                     >gi 2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation
                      factor 5A3 [Solanum tuberosum]
                      35751
   Seq. No.
   Seq. ID
                     LIB3049-055-Q1-E1-D10
                     BLASTN
   Method
                     g1370195
   NCBI GI
                      52
   BLAST score
                      3.0e-20
   E value
                      92
   Match length
                      89
   % identity
                     L.japonicus mRNA for small GTP-binding protein, RAB8D
   NCBI Description
                      35752
   Seq. No.
   Seq. ID
                      LIB3049-055-Q1-E1-F5
                      BLASTX
   Method
   NCBI GI
                      q1076485
```



```
Match length
                  69
% identity
                  SAM-synthetase - chickpea (fragment)
NCBI Description
                  >gi 732576 emb_CAA59508_ (X85252) SAM-synthetase [Cicer
                  arietinum]
                  35753
Seq. No.
                  LIB3049-055-Q1-E1-G10
Seq. ID
                  BLASTN
Method
NCBI GI
                  q310575
                  223
BLAST score
                  1.0e-122
E value
                  347
Match length
                  94
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                  35754
Seq. No.
Seq. ID
                  LIB3049-055-Q1-E1-H1
                  BLASTX
Method
NCBI GI
                  g3980254
BLAST score
                  359
                  3.0e-34
E value
                  98
Match length
                  70
% identity
                  (AJ006053) peroxisomal membrane protein [Arabidopsis
NCBI Description
                  thaliana]
                  35755
Seq. No.
Seq. ID
                  LIB3049-056-Q1-E1-A9
                  BLASTX
Method
NCBI GI
                  g3204134
                  497
BLAST score
                  2.0e-50
E value
Match length
                  131
                  71
% identity
                  (AJ006771) beta-galactosidase [Cicer arietinum]
NCBI Description
                  35756
Seq. No.
                  LIB3049-056-Q1-E1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1710587
                  126
BLAST score
E value
                  1.0e-12
                   62
Match length
                   69
% identity
                  60S ACIDIC RIBOSOMAL PROTEIN PO >gi 1196897 (L46848) acidic
NCBI Description
                  ribosomal protein PO [Glycine max]
                   35757
Seq. No.
                  LIB3049-056-Q1-E1-C5
Seq. ID
                  BLASTX
Method
```

Method BLASTX
NCBI GI 94325382
BLAST score 241
E value 2.0e-20
Match length 72
% identity 67

NCBI Description (AF129075) T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)



## [Homo sapiens]

```
35758
Seq. No.
                  LIB3049-056-Q1-E1-D12
Seq. ID
                  BLASTN
Method
                  q456713
NCBI GI
BLAST score
                  172
                  6.0e-92
E value
                  264
Match length
                  27
% identity
                  Glycine max gene for ubiquitin, complete cds
NCBI Description
                  35759
Seq. No.
                  LIB3049-056-Q1-E1-E4
Seq. ID
                  BLASTX
Method
                  g3880527
NCBI GI
                  129
BLAST score
                  3.0e-09
E value
                  65
Match length
                  62
% identity
                  (Z74476) similar to Core histones H2A, H2B, H3 and H4; cDNA
NCBI Description
                  EST EMBL:T01147 comes from this gene; cDNA EST EMBL:C08843
                  comes from this gene; cDNA EST EMBL:D74607 comes from this
                  gene; cDNA EST EMBL: C07474 comes from this gene;
                  35760
Seq. No.
Seq. ID
                  LIB3049-056-Q1-E1-E5
                  BLASTN
Method
                  g1143318
NCBI GI
                  118
BLAST score
                   8.0e-60
E value
Match length
                   238
% identity
                  Glycine max biotin carboxyl carrier protein precursor
NCBI Description
                   (accB-1) mRNA, complete cds
                   35761
Seq. No.
                   LIB3049-056-Q1-E1-F11
Seq. ID
                   BLASTX
Method
                   q1172811
NCBI GI
BLAST score
                   257
                   3.0e-41
E value
Match length
                   92
                   91
% identity
                   60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)
NCBI Description
                   >gi_1076751_pir__S49575 ribosomal protein L10.e, cytosolic
                   - rice >gi 575355 emb CAA57339 (X81691) putative tumor
                   suppresser [Oryza sativa]
Seq. No.
                   35762
                   LIB3049-056-Q1-E1-G10
Seq. ID
Method
                   BLASTX
                   q3043428
NCBI GI
BLAST score
                   388
```

1.0e-37

91 76

E value Match length

% identity

Method

NCBI GI

BLASTX

q4185511



```
NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
                  35763
Seq. No.
                  LIB3049-056-Q1-E1-G11
Seq. ID
                  BLASTX
Method
                  g1370287
NCBI GI
                  425
BLAST score
                  5.0e-42
E value
                  105
Match length
                  77
% identity
                  (Z73553) core protein [Pisum sativum]
NCBI Description
                   35764
Seq. No.
                  LIB3049-056-Q1-E1-G2
Seq. ID
                  BLASTX
Method
                   q1419088
NCBI GI
BLAST score
                   141
                   9.0e-09
E value
                   68
Match length
                   49
% identity
                   (Z71395) calreticulin [Nicotiana plumbaginifolia]
NCBI Description
Seq. No.
                   35765
                   LIB3050-001-Q1-E1-A5
Seq. ID
                   BLASTX
Method
                   g1707364
NCBI GI
                   264
BLAST score
                   2.0e-23
E value
                   76
Match length
                   74
% identity
                   (X94626) AATP2 [Arabidopsis thaliana]
NCBI Description
                   35766
Seq. No.
                   LIB3050-001-Q1-E1-B10
Seq. ID
                   BLASTN
Method
                   q18764
NCBI GI
BLAST score
                   89
                   2.0e-42
E value
                   181
Match length
                   87
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
                   35767
Seq. No.
Seq. ID
                   LIB3050-001-Q1-E1-D11
Method
                   BLASTN
                   g170023
NCBI GI
BLAST score
                   66
                   9.0e-29
E value
                   278
Match length
                   82
% identity
                   Glycine max maturation-associated protein (MAT9) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   35768
Seq. ID
                   LIB3050-001-Q1-E1-E1
```

5435



```
BLAST score
                   1.0e-34
E value
Match length
                   87
                   79
% identity
                   (AF102822) actin depolymerizing factor 4 [Arabidopsis
NCBI Description
                   thaliana]
                   35769
Seq. No.
                   LIB3050-001-Q1-E1-G3
Seq. ID
                   BLASTX
Method
                   g1350548
NCBI GI
                   175
BLAST score
                   1.0e-12
E value
                   71
Match length
                   49
% identity
NCBI Description (L47609) heat shock-like protein [Picea glauca]
                   35770
Seq. No.
                   LIB3050-002-Q1-E1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2995951
                   316
BLAST score
                   3.0e-29
E value
                   79
Match length
                   80
% identity
                   (AF053564) auxin-induced protein [Mesembryanthemum
NCBI Description
                   crystallinum]
                   35771
Seq. No.
                   LIB3050-002-Q1-E1-C5
Seq. ID
                   BLASTN
Method
NCBI GI
                   q169980
                   388
BLAST score
                   0.0e + 00
E value
                   418
Match length
                   100
% identity
                   Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
NCBI Description
                   35772
Seq. No.
Seq. ID
                   LIB3050-002-Q1-E1-D12
Method
                   BLASTX
                   q498707
NCBI GI
BLAST score
                   274
                   2.0e-24
E value
                   118
Match length
                   47
 % identity
                   (X78422) HYP1 [Arabidopsis thaliana]
NCBI Description
                   35773
 Seq. No.
                   LIB3050-002-Q1-E1-D4
 Seq. ID
                   BLASTN
Method
                   g1204128
 NCBI GI
 BLAST score
                   100
 E value
                   5.0e-49
                   227
 Match length
                   88
 % identity
 NCBI Description M.sativa MMK2 mRNA for protein kinase
```



```
35774
Seq. No.
Seq. ID
                  LIB3050-002-Q1-E1-E2
                  BLASTX
Method
NCBI GI
                  g4510398
                  325
BLAST score
                  3.0e-30
E value
                  96
Match length
% identity
NCBI Description (AC006587) hypothetical protein [Arabidopsis thaliana]
                  35775
Seq. No.
                  LIB3050-002-Q1-E1-F1
Seq. ID
                  BLASTX
Method
                  g3924597
NCBI GI
                  173
BLAST score
                  2.0e-12
E value
                  101
Match length
% identity
                  41
NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.
                  35776
                  LIB3050-003-Q1-E1-C11
Seq. ID
                  BLASTN
Method
                  q169980
NCBI GI
                  303
BLAST score
                  1.0e-170
E value
                  351
Match length
                  99
% identity
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.
                  35777
                  LIB3050-003-Q1-E1-D9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3021374
                  163
BLAST score
E value
                  1.0e-86
                  171
Match length
                  99
% identity
NCBI Description Glycine max mRNA for profilin, PRO1
Seq. No.
                  35778
Seq. ID
                  LIB3050-003-Q1-E1-H2
Method
                  BLASTX
NCBI GI
                  g1781322
                  210
BLAST score
                  7.0e-17
E value
                  104
Match length
                  44
% identity
                  (Y10462) peroxidase [Spinacia oleracea]
NCBI Description
```

Seq. No. 35779

Seq. ID LIB3050-004-Q1-E1-A7

Method BLASTN
NCBI GI g1208702
BLAST score 79
E value 1.0e-36



```
Match length
                  100
% identity
NCBI Description Glycine max histone H3 gene, partial cds, clone H3-DMAX
                  35780
Seq. No.
Seq. ID
                  LIB3050-004-Q1-E1-C9
Method
                  BLASTN
                  g531828
NCBI GI
BLAST score
                  46
E value
                  3.0e-17
                  78
Match length
                  90
% identity
NCBI Description Cloning vector pSport1, complete cds
                  35781
Seq. No.
Seq. ID
                  LIB3050-004-Q1-E1-D12
                  BLASTX
Method
NCBI GI
                  g4545262
BLAST score
                  150
E value
                  3.0e-10
Match length
                  39
                  67
% identity
                  (AF118230) metallothionein-like protein [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  35782
Seq. ID
                  LIB3050-004-Q1-E1-D5
Method
                  BLASTX
NCBI GI
                  g3935167
BLAST score
                  168
E value
                  4.0e-12
Match length
                  67
% identity
                  49
                  (AC004557) F17L21.10 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  35783
                  LIB3050-004-Q1-E1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2894379
BLAST score
                  223
E value
                   3.0e-18
Match length
                  132
% identity
NCBI Description
                  (Y14573) ring finger protein [Hordeum vulgare]
Seq. No.
                  35784
                  LIB3050-004-Q1-E1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169980
```

Method BLASTN
NCBI GI g169980
BLAST score 35
E value 2.0e-10
Match length 55
% identity 91

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No. 35785

Seq. ID LIB3050-004-Q1-E1-G8



```
BLASTX
Method
                  q4218010
NCBI GI
                   426
BLAST score
                   5.0e-42
E value
                  131
Match length
                   67
% identity
                   (AC006135) putative sugar transporter [Arabidopsis
NCBI Description
                  thaliana] >gi_4309720_gb_AAD15490_ (AC006439) putative
                   sugar transporter [Arabidopsis thaliana]
                   35786
Seq. No.
                  LIB3050-005-Q1-K1-B8
Seq. ID
                  BLASTX
Method
                   q863000
NCBI GI
                   222
BLAST score
                   1.0e-18
E value
Match length
                   55
                   76
% identity
                   (U27348) S-adenosyl-L-methionine synthetase [Populus
NCBI Description
                   deltoides]
Seq. No.
                   35787
                   LIB3050-005-Q1-K1-D1
Seq. ID
Method
                   BLASTX
                   g3860263
NCBI GI
                   200
BLAST score
                   6.0e-16
E value
Match length
                   75
                   55
% identity
                   (AC005824) putative cytochrome p450 protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   35788
                   LIB3050-005-Q1-K1-D10
Seq. ID
Method
                   BLASTX
                   g730456
NCBI GI
                   205
BLAST score
                   2.0e-16
E value
                   78
Match length
                   55
% identity
                   40S RIBOSOMAL PROTEIN S19
NCBI Description
                   35789
Seq. No.
Seq. ID
                   LIB3050-005-Q1-K1-D11
                   BLASTX
Method
                   g1742965
NCBI GI
BLAST score
                   230
                   3.0e-19
E value
                   99
Match length
                   47
% identity
                   (Y09562) HAPp48,5 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   35790
Seq. ID
                   LIB3050-005-Q1-K1-D5
Method
                   BLASTN
```

q1055367

64

NCBI GI BLAST score



```
8.0e-28
E value
                  156
Match length
                  85
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
                  35791
Seq. No.
                  LIB3050-005-Q1-K1-E1
Seq. ID
                  BLASTX
Method
                  g3738302
NCBI GI
                  179
BLAST score
                  3.0e-13
E value
                  92
Match length
                  45
% identity
                  (AC005309) tubby-like protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4249398 (AC006072) putative tubby protein [Arabidopsis
                  thaliana]
                   35792
Seq. No.
                  LIB3050-005-Q1-K1-F11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g992916
BLAST score
                  112
                   3.0e-56
E value
                  248
Match length
                   86
% identity
                  Glycine max (clones 513 and 1221) acetyl coA carboxylase
NCBI Description
                   (ACCase-A) gene, complete cds
                   35793
Seq. No.
Seq. ID
                   LIB3050-005-Q1-K1-G1
                   BLASTX
Method
                   q1709002
NCBI GI
                   298
BLAST score
                   1.0e-27
E value
                   67
Match length
                   84
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_1033190
                   (U38186) S-adenosyl methionine synthetase [Pinus banksiana]
Seq. No.
                   35794
Seq. ID
                   LIB3050-005-Q1-K1-G11
Method
                   BLASTX
NCBI GI
                   q1326022
                   309
BLAST score
E value
                   9.0e-29
Match length
                   80
% identity
```

(X01474) polyubiquitin precursor fragment [Saccharomyces NCBI Description

cerevisiae]

35795 Seq. No.

LIB3050-005-Q1-K1-G2 Seq. ID

Method BLASTX NCBI GI g3618320 BLAST score 187

Match length

% identity

368

32



```
3.0e-14
E value
                  80
Match length
                  50
% identity
                  (AB001888) zinc finger protein [Oryza sativa]
NCBI Description
                  35796
Seq. No.
                  LIB3050-005-Q1-K1-G7
Seq. ID
                  BLASTX
Method
                  g2760362
NCBI GI
BLAST score
                  189
                  1.0e-14
E value
                  71
Match length
% identity
                   (AF016511) 15.9 kDa subunit of RNA polymerase II
NCBI Description
                   [Arabidopsis thaliana]
                  35797
Seq. No.
                  LIB3050-005-Q1-K1-H9
Seq. ID
                  BLASTX
Method
                  g2181190
NCBI GI
                   192
BLAST score
E value
                   3.0e-15
Match length
                   62
                   68
% identity
                   (Y12531) serine/threonine kinase [Brassica oleracea]
NCBI Description
                   35798
Seq. No.
                   LIB3050-006-Q1-E1-A1
Seq. ID
                   BLASTN
Method
                   g170048
NCBI GI
                   84
BLAST score
E value
                   1.0e-39
                   216
Match length
                   71
% identity
                   Glycine max SbPRP1 gene encoding a proline-rich protein,
NCBI Description
                   complete cds
                   35799
Seq. No.
                   LIB3050-006-Q1-E1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g267072
                   239
BLAST score
                   3.0e-20
E value
                   88
Match length
% identity
                   TUBULIN BETA-1 CHAIN >gi 100072 pir S20868 tubulin beta-1
NCBI Description
                   chain - garden pea >gi 20758 emb CAA38613 (X54844)
                   beta-tubulin 1 [Pisum sativum]
Seq. No.
                   35800
                   LIB3050-006-Q1-E1-G5
Seq. ID
Method
                   BLASTN
NCBI GI
                   q456713
BLAST score
                   241
                   1.0e-133
E value
```



NCBI Description Glycine max gene for ubiquitin, complete cds

Seq. No. 35801

Seq. ID LIB3050-006-Q1-E1-G9

Method BLASTX
NCBI GI g3695408
BLAST score 149
E value 1.0e-09
Match length 79
% identity 53

NCBI Description (AF096373) contains similarity to Solanum lycopersicum

(tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi 4538956 emb CAB39780.1 (AL049488) probable

wound-induced protein [Arabidopsis thaliana]

Seq. No. 35802

Seq. ID LIB3050-007-Q1-E1-B4

Method BLASTX
NCBI GI g3033389
BLAST score 233
E value 2.0e-19
Match length 133
% identity 6

NCBI Description (AC004238) Cf-2.1-like protein [Arabidopsis thaliana]

Seq. No. 35803

Seq. ID LIB3050-007-Q1-E1-B5

Method BLASTX
NCBI GI g2982311
BLAST score 383
E value 4.0e-37
Match length 94
% identity 74

NCBI Description (AF051240) probable ubiquitin-conjugating enzyme E2 [Picea

mariana]

Seq. No. 35804

Seq. ID LIB3050-007-Q1-E1-C10

Method BLASTX
NCBI GI g3290020
BLAST score 208
E value 1.0e-16
Match length 65
% identity 68

NCBI Description (AF044172) cysteine synthase; CS-A; O-acetylserine (thiol)

lyase; cytosolic isoform [Solanum tuberosum]

Seq. No. 35805

Seq. ID LIB3050-007-Q1-E1-C3

Method BLASTX
NCBI GI g2181184
BLAST score 333
E value 3.0e-31
Match length 102
% identity 62

NCBI Description (Y13577) JR3 protein [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                  LIB3050-007-Q1-E1-D3
                  BLASTX
Method
                  g3402750
NCBI GI
                  379
BLAST score
                  2.0e-36
E value
Match length
                  128
                  56
% identity
                  (AL031187) putative protein [Arabidopsis thaliana]
NCBI Description
                  35807
Seq. No.
Seq. ID
                  LIB3050-007-Q1-E1-D5
                  BLASTX
Method
                  g2623310
NCBI GI
                  332
BLAST score
                   4.0e-31
E value
                   95
Match length
                   66
% identity
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3402721 (AC004261) unknown protein [Arabidopsis
                  thaliana]
                   35808
Seq. No.
                  LIB3050-007-Q1-E1-F3
Seq. ID
                  BLASTX
Method
                   q3738299
NCBI GI
BLAST score
                   334
                   2.0e-31
E value
                   87
Match length
                   75
% identity
                   (AC005309) putative glutaredoxin [Arabidopsis thaliana]
NCBI Description
                   >gi 4249395 (AC006072) putative glutaredoxin [Arabidopsis
                   thaliana]
                   35809
Seq. No.
Seq. ID
                   LIB3050-008-Q1-E1-B1
                   BLASTX
Method
                   g118493
NCBI GI
BLAST score
                   160
                   3.0e-11
E value
                   87
Match length
                   45
% identity
                   ALDEHYDE DEHYDROGENASE, CYTOSOLIC (CLASS 1)
NCBI Description
                   >gi_104527_pir__S14629 aldehyde dehydrogenase (NAD+) (EC
                   1.2.1.3) 1, cytosolic - chicken >gi 63033 emb_CAA41679_
                   (X58869) aldehyde dehydrogenase (NAD+) [Gallus gallus]
Seq. No.
                   35810
Seq. ID
                   LIB3050-008-Q1-E1-D5
                   BLASTX
Method
                   g1730081
NCBI GI
BLAST score
                   278
                   9.0e-25
E value
                   99
Match length
                   59
% identity
```

PROTEIN L1R18B (LLPR10.1B) >gi 1039336 emb\_CAA56299

(X79975) L1R18B [Lupinus luteus] >gi\_2183277 (AF002278)

NCBI GI

E value Match length

BLAST score



## L1PR10.1B [Lupinus luteus]

Seq. No. 35811 LIB3050-008-Q1-E1-E12 Seq. ID Method BLASTX NCBI GI q124230 247 BLAST score 1.0e-21 E value Match length 64 % identity 73 NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D) >gi\_72894\_pir\_\_FIAAA translation initiation factor eIF-5A - alfalfa >gi 19601 emb CAA42065 (X59441) eukaryotic translation initiation factor 4D [Medicago sativa] 35812 Seq. No. Seq. ID LIB3050-008-Q1-E1-E3 Method BLASTN g609224 NCBI GI BLAST score 151 E value 2.0e-79 Match length 294 88 % identity P.sativum mRNA for SAMS-2 >gi 609558 gb L36681 PEADENSYNB NCBI Description Pisum sativum S-adenosylmethionine synthase mRNA, complete 35813 Seq. No. Seq. ID LIB3050-008-Q1-E1-F7 Method BLASTX NCBI GI g2281637 BLAST score 268 E value 1.0e-23 90 Match length % identity NCBI Description (AF003099) AP2 domain containing protein RAP2.6 [Arabidopsis thaliana] 35814 Seq. No. LIB3050-008-Q1-E1-G5 Seq. ID Method BLASTX NCBI GI q3426064 BLAST score 237 E value 8.0e-25 Match length 113 54 % identity NCBI Description (AJ007588) monooxygenase [Arabidopsis thaliana] >qi 4467141 emb CAB37510 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana] Seq. No. 35815 Seq. ID LIB3050-009-Q1-E1-A11 Method BLASTX

g2245683

101 3.0e-09

93



```
% identity
NCBI Description (AF007211) peroxidase precursor [Glycine max]
                  35816
Seq. No.
Seq. ID
                  LIB3050-009-Q1-E1-A12
                  BLASTN
Method
                  g2245682
NCBI GI
                  52
BLAST score
                  2.0e-20
E value
                  140
Match length
                  85
% identity
                  Glycine max peroxidase precursor (GMIPER1) mRNA, complete
NCBI Description
                  cds
                  35817
Seq. No.
                  LIB3050-009-Q1-E1-D2
Seq. ID
Method
                  BLASTN
                  g3021374
NCBI GI
                  108
BLAST score
                  1.0e-53
E value
                  200
Match length
% identity
                  89
NCBI Description Glycine max mRNA for profilin, PRO1
                  35818
Seq. No.
                  LIB3050-009-Q1-E1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g730536
BLAST score
                  163
                  8.0e-12
E value
                  47
Match length
                  70
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L23 >gi 310933 (L18915) 60S ribosomal
                  protein subunit L17 [Nicotiana tabacum]
                  35819
Seq. No.
Seq. ID
                  LIB3050-009-Q1-E1-F2
                  BLASTX
Method
                  g3378650
NCBI GI
                  206
BLAST score
                  2.0e-17
E value
                  74
Match length
% identity
                  72
NCBI Description (X97606) abscisic acid activated [Medicago sativa]
                  35820
Seq. No.
Seq. ID
                  LIB3050-009-Q1-E1-G2
Method
                  BLASTX
NCBI GI
                  q3063701
BLAST score
                   310
                   2.0e-28
E value
Match length
                  114
% identity
                   55
                  (AL022537) putative protein [Arabidopsis thaliana]
```

Seq. No. 35821

NCBI Description

Seq. ID LIB3050-010-Q1-E1-B4



```
BLASTX
Method
NCBI GI
                  g466330
BLAST score
                  243
E value
                  6.0e-21
                  77
Match length
                  68
% identity
NCBI Description (L31352) hexose carrier [Ricinus communis]
                  35822
Seq. No.
Seq. ID
                  LIB3050-010-Q1-E1-B5
Method
                  BLASTN
                  g18725
NCBI GI
                  69
BLAST score
                  1.0e-30
E value
                  185
Match length
                  86
% identity
                  Soybean (G. max) mRNA for proliferating cell nuclear
NCBI Description
                  antigen (PCNA), partial
                  35823
Seq. No.
Seq. ID
                  LIB3050-010-Q1-E1-B9
                  BLASTN
Method
                  g3264758
NCBI GI
                  55
BLAST score
                  2.0e-22
E value
                  135
Match length
                   87
% identity
                  Prunus armeniaca 40S ribosomal protein S8 (RPS8) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   35824
                  LIB3050-010-Q1-E1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q485518
                   218
BLAST score
E value
                   9.0e-18
                   60
Match length
                   77
% identity
                  ubiquitin / ribosomal protein CEP52 - rice
NCBI Description
                   >gi 303857 dbj BAA02154 (D12629) ubiquitin/ribosomal
                   polyprotein [Oryza sativa]
Seq. No.
                   35825
Seq. ID
                   LIB3050-010-Q1-E1-C11
                   BLASTN
Method
NCBI GI
                   q3021374
BLAST score
                   99
                   2.0e-48
E value
Match length
                   155
                   91
% identity
NCBI Description Glycine max mRNA for profilin, PRO1
Seq. No.
                   35826
Seq. ID
                   LIB3050-010-Q1-E1-D11
Method
                   BLASTN
```

q456567

46

NCBI GI BLAST score

% identity

NCBI Description

95



```
8.0e-17
E value
                  125
Match length
% identity
                  Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
NCBI Description
                  cds
                  35827
Seq. No.
                  LIB3050-010-Q1-E1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4204269
                  171
BLAST score
                  2.0e-12
E value
                  101
Match length
                  15
% identity
                  (AC005223) 64111 [Arabidopsis thaliana]
NCBI Description
                   35828
Seq. No.
                   LIB3050-011-Q1-E1-A10
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3702335
BLAST score
                   211
E value
                   6.0e-17
Match length
                   69
                   58
% identity
                   (AC005397) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   35829
Seq. No.
                   LIB3050-011-Q1-E1-B12
Seq. ID
                   BLASTX
Method
                   g3411177
NCBI GI
BLAST score
                   193
                   9.0e-15
E value
                   110
Match length
% identity
NCBI Description (AF076240) MocC [Rhizobium leguminosarum bv. viciae]
                   35830
Seq. No.
Seq. ID
                   LIB3050-011-Q1-E1-B6
                   BLASTX
Method
NCBI GI
                   q4455365
BLAST score
                   156
                   2.0e-10
E value
Match length
                   63
% identity
                   52
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   35831
Seq. No.
                   LIB3050-011-Q1-E1-C7
Seq. ID
Method
                   BLASTN
                   g169980
NCBI GI
BLAST score
                   296
                   1.0e-166
E value
Match length
                   376
```

Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

BLAST score

E value

183 9.0e-14



```
35832
Seq. No.
                  LIB3050-011-Q1-E1-E2
Seq. ID
                  BLASTN
Method
                  g169980
NCBI GI
                  301
BLAST score
                  1.0e-169
E value
                  329
Match length
                  98
% identity
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
NCBI Description
                  35833
Seq. No.
                  LIB3050-011-Q1-E1-E3
Seq. ID
                  BLASTN
Method
                  g169980
NCBI GI
                  53
BLAST score
                  2.0e-21
E value
                  105
Match length
                   88
% identity
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
NCBI Description
                   35834
Seq. No.
                  LIB3050-011-Q1-E1-F6
Seq. ID
                  BLASTX
Method
                   g2832675
NCBI GI
                   238
BLAST score
                   4.0e-20
E value
                   49
Match length
                   80
% identity
                  (AL021712) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   35835
Seq. No.
                   LIB3050-011-Q1-E1-F9
Seq. ID
                   BLASTX
Method
                   q4538913
NCBI GI
                   243
BLAST score
E value
                   1.0e-20
Match length
                   109
                   54
% identity
                  (ALO49482) putative protein [Arabidopsis thaliana]
NCBI Description
                   35836
Seq. No.
                   LIB3050-011-Q1-E1-G11
Seq. ID
Method
                   BLASTN
                   q2815245
NCBI GI
                   37
BLAST score
                   2.0e-11
E value
Match length
                   97
                   86
% identity
                   C.arietinum mRNA for class I type 2 metallothionein (clone:
NCBI Description
                   CanMT-2)
Seq. No.
                   35837
                   LIB3050-012-Q1-E1-B4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3947985
```



```
Match length
                  55
% identity
NCBI Description (U78948) MADS-box protein 2 [Malus domestica]
                  35838
Seq. No.
Seq. ID
                  LIB3050-012-Q1-E1-C2
                  BLASTX
Method
                  g4336205
NCBI GI
                  215
BLAST score
                  2.0e-17
E value
                  61
Match length
                   61
% identity
                  (AF077372) cytochrome b5 reductase [Zea mays]
NCBI Description
                   35839
Seq. No.
                  LIB3050-012-Q1-E1-E8
Seq. ID
                  BLASTX
Method
                   g2388565
NCBI GI
                   403
BLAST score
                   2.0e-39
E value
                   93
Match length
                   75
% identity
                   (AC000098) Similar to Prunus pectinesterase (gb_X95991).
NCBI Description
                   [Arabidopsis thaliana]
                   35840
Seq. No.
                   LIB3050-012-Q1-E1-F12
Seq. ID
Method
                   BLASTN
                   g2463568
NCBI GI
                   256
BLAST score
                   1.0e-142
E value
Match length
                   281
                   97
% identity
                   Glycine max mRNA for squalene synthase, complete cds
NCBI Description
                   35841
Seq. No.
                   LIB3050-012-Q1-E1-G3
Seq. ID
                   BLASTX
Method
                   g2500354
NCBI GI
BLAST score
                   492
                   8.0e-50
E value
                   95
Match length
                   94
% identity
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462_
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
                   35842
Seq. No.
Seq. ID
                   LIB3050-013-Q1-E1-A10
                   BLASTX
Method
                   q2132842
NCBI GI
                   326
BLAST score
                   2.0e-30
E value
                   122
Match length
                   52
% identity
                   probable membrane protein YOL077c - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >qi 1419909 emb CAA99087 (Z74819) ORF YOL077c
```

[Saccharomyces cerevisiae]

Seq. ID Method



```
35843
Seq. No.
                  LIB3050-013-Q1-E1-C10
Seq. ID
                  BLASTX
Method
                  g2982324
NCBI GI
                  99
BLAST score
                  7.0e-11
E value
                  55
Match length
                  61
% identity
                  (AF051247) defender against cell death 1 homolog [Picea
NCBI Description
                  mariana]
                  35844
Seq. No.
                  LIB3050-013-Q1-E1-D4
Seq. ID
                  BLASTX
Method
                  g3329368
NCBI GI
                  158
BLAST score
                  8.0e-11
E value
                  75
Match length
                   44
% identity
                  (AF031244) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
                   35845
Seq. No.
                  LIB3050-013-Q1-E1-D8
Seq. ID
                  BLASTN
Method
                   g18660
NCBI GI
                   77
BLAST score
                   3.0e-35
E value
                   202
Match length
                   88
% identity
                  G.max hsp22 gene for low MW heat shock protein
NCBI Description
                   35846
Seq. No.
                   LIB3050-013-Q1-E1-E2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g408791
BLAST score
                   60
                   2.0e-25
E value
                   196
Match length
                   83
% identity
                   Glycine soja chloroplast omega-3 fatty acid desaturase
NCBI Description
                   (Fadd) mRNA, complete cds
Seq. No.
                   35847
Seq. ID
                   LIB3050-013-Q1-E1-G2
                   BLASTN
Method
NCBI GI
                   q3449322
                   45
BLAST score
                   3.0e-16
E value
                   193
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXC17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   35848
```

LIB3050-014-Q1-E1-A9

BLASTX

% identity

54



```
g2245093
NCBI GI
BLAST score
                  136
                  5.0e-13
E value
Match length
                  72
                  65
% identity
                  (Z97343) membrane channel protein [Arabidopsis thaliana]
NCBI Description
                  35849
Seq. No.
Seq. ID
                  LIB3050-014-Q1-E1-C10
Method
                  BLASTN
                  g2055227
NCBI GI
                  46
BLAST score
                  9.0e-17
E value
                  132
Match length
                  88
% identity
NCBI Description Glycine max mRNA for SRC1, complete cds
                  35850
Seq. No.
                  LIB3050-014-Q1-E1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4115918
                  152
BLAST score
                  2.0e-10
E value
                  49
Match length
                  65
% identity
                  (AF118222) similar to nascent polypeptide associated
NCBI Description
                  complex alpha chain [Arabidopsis thaliana]
                  35851
Seq. No.
Seq. ID
                  LIB3050-014-Q1-E1-G1
                  BLASTX
Method
                  g4263722
NCBI GI
BLAST score
                  327
                  8.0e-31
E value
                  79
Match length
                  75
% identity
                  (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  35852
                  LIB3050-014-Q1-E1-G8
Seq. ID
Method
                  BLASTX
                  q4056425
NCBI GI
BLAST score
                  238
                  4.0e-20
E value
                  95
Match length
                  49
% identity
NCBI Description
                  (AC005322) ESTs qb H36249, qb AA59732 and qb AA651219 come
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  35853
Seq. ID
                  LIB3050-014-Q1-E1-H8
Method
                  BLASTX
NCBI GI
                  q4406820
BLAST score
                  166
E value
                   6.0e-18
Match length
                  110
```



```
(AC006201) putative ras superfamily member [Arabidopsis
NCBI Description
                  thaliana]
                  35854
Seq. No.
                  LIB3050-015-Q1-E1-A7
Seq. ID
Method
                  BLASTX
                  g3122357
NCBI GI
BLAST score
                  221
E value
                  3.0e-18
                  59
Match length
                  73
% identity
                  PUTATIVE LIPOATE-PROTEIN LIGASE B (LIPOATE BIOSYNTHESIS
NCBI Description
                  PROTEIN B) >gi 2494127 (AC002376) Contains similarity to
                  Mycobacterium LIPB gene (gb_Q104041). [Arabidopsis
                  thaliana]
                  35855
Seq. No.
Seq. ID
                  LIB3050-015-Q1-E1-B1
Method
                  BLASTX
NCBI GI
                  g4103635
BLAST score
                  145
                  4.0e-09
E value
                  92
Match length
                  39
% identity
                  (AF026538) ABA-responsive protein [Hordeum vulgare]
NCBI Description
                  35856
Seq. No.
                  LIB3050-015-Q1-E1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3893081
BLAST score
                  463
                  2.0e-46
E value
                  105
Match length
                  79
% identity
                  (AJ012747) MLH1 protein [Arabidopsis thaliana]
NCBI Description
                  35857
Seq. No.
                  LIB3050-015-Q1-E1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q548437
BLAST score
                  151
                  6.0e-10
E value
Match length
                  111
                  37
% identity
NCBI Description
                  OSH1 PROTEIN >qi 1078479 pir S53463 SWH1 protein (version
                  1) - yeast (Saccharomyces cerevisiae) >gi 456143 (L28920)
                  Oshlp [Saccharomyces cerevisiae]
Seq. No.
                  35858
                  LIB3050-015-Q1-E1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1432056
BLAST score
                  174
E value
                  1.0e-12
Match length
                  54
                  57
% identity
```

(U56834) WRKY3 [Petroselinum crispum]



```
35859
Seq. No.
Seq. ID
                  LIB3050-015-Q1-E1-F8
Method
                  BLASTX
NCBI GI
                  g3935167
BLAST score
                  107
                   6.0e-10
E value
Match length
                   71
% identity
                   52
NCBI Description
                  (AC004557) F17L21.10 [Arabidopsis thaliana]
                   35860
Seq. No.
Seq. ID
                  LIB3050-015-Q1-E1-F9
Method
                  BLASTX
NCBI GI
                   g121345
BLAST score
                   244
                   5.0e-33
E value
                   109
Match length
                   70
% identity
NCBI Description
                  GLUTAMINE SYNTHETASE PR-2 (ISOZYME ALPHA)
                   (GLUTAMATE--AMMONIA LIGASE) >gi 68593 pir AJFBQA
                   glutamate--ammonia ligase (EC 6.3.1.2) alpha, cytosolic -
                   kidney bean >gi_21013_emb_CAA27632_ (X04002) glutamine
                   synthetase subunit (aa 1-356) [Phaseolus vulgaris]
                   >gi 225068 prf 1208270B synthetase R2,Gln [Phaseolus
                   vulgaris]
Seq. No.
                   35861
Seq. ID
                  LIB3050-016-Q1-E1-B4
Method
                  BLASTN
NCBI GI
                   g1370177
BLAST score
                   45
                   3.0e-16
E value
Match length
                  125
% identity
                   84
                  L.japonicus mRNA for small GTP-binding protein, RAB5A
NCBI Description
Seq. No.
                   35862
Seq. ID
                  LIB3050-016-Q1-E1-C5
Method
                   BLASTN
NCBI GI
                   g169980
BLAST score
                   374
E value
                   0.0e + 00
Match length
                   390
                   99
% identity
NCBI Description
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.
                   35863
Seq. ID
                   LIB3050-016-Q1-E1-G11
Method
                   BLASTX
NCBI GI
                   g66009
BLAST score
                   153
E value
                   3.0e-10
Match length
                  73
% identity
                   49
```

glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C, cytosolic - maize >gi 22238 emb CAA30151 (X07156) GADPH



## (AA 1-337) [Zea mays]

```
Seq. No.
                  35864
                  LIB3050-017-Q1-E1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1498053
BLAST score
                  154
E value
                   4.0e-19
                  87
Match length
% identity
                   67
                  (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
                  35865
Seq. No.
                  LIB3050-017-Q1-E1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3402672
BLAST score
                   215
                  1.0e-17
E value
Match length
                   84
                   54
% identity
                  (AC004697) putative white protein [Arabidopsis thaliana]
NCBI Description
                   35866
Seq. No.
Seq. ID
                  LIB3050-017-Q1-E1-D8
                  BLASTX
Method
NCBI GI
                   g399014
BLAST score
                   170
E value
                   2.0e-12
                   60
Match length
                   53
% identity
NCBI Description
                  ADP, ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE
                   NUCLEOTIDE TRANSLOCATOR) (ANT) >gi 99444 pir_A41677
                   ADP, ATP carrier protein - Chlorella kessleri >gi 516597
                   (M76669) ATP/ADP translocator [Chlorella kessleri]
Seq. No.
                   35867
                   LIB3050-017-Q1-E1-E5
Seq. ID
Method
                   BLASTX
                   g3980393
NCBI GI
BLAST score
                   320
E value
                   8.0e-30
Match length
                   102
% identity
                   (AC004561) putative glutathione S-transferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   35868
Seq. ID
                   LIB3050-017-Q1-E1-G3
                   BLASTX
Method
NCBI GI
                   q3426064
BLAST score
                   231
                   3.0e-19
E value
Match length
                   75
% identity
                   60
```

[Arabidopsis thaliana]

(AJ007588) monooxygenase [Arabidopsis thaliana]

>gi 4467141 emb CAB37510 (AL035540) monooxygenase 2 (MO2)



```
Seq. No.
                  35869
Seq. ID
                  LIB3050-017-Q1-E1-H8
Method
                  BLASTX
NCBI GI
                  g4220480
BLAST score
                  204
                  4.0e-16
E value
                  122
Match length
% identity
                  (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                  35870
Seq. No.
                  LIB3050-018-Q1-E1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3881189
                  167
BLAST score
                  9.0e-12
E value
Match length
                  56
% identity
                  50
NCBI Description
                  (Z99281) similar to ADP-ribosylation factor; cDNA EST
                  EMBL: C08179 comes from this gene; cDNA EST EMBL: C08337
                  comes from this gene; cDNA EST EMBL: C09829 comes from this
                  gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4
Seq. No.
                  35871
                  LIB3050-018-Q1-E1-A4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2565339
BLAST score
                  56
E value
                  1.0e-22
Match length
                  180
% identity
                  84
                  Lupinus luteus ribosomal protein S14 (rps14) mRNA, complete
NCBI Description
Seq. No.
                  35872
Seq. ID
                  LIB3050-018-Q1-E1-A7
Method
                  BLASTN
NCBI GI
                  g303900
BLAST score
                  250
E value
                  1.0e-138
Match length
                  347
% identity
                  32
NCBI Description
                  Soybean gene for ubiquitin, complete cds
Seq. No.
                  35873
Seq. ID
                  LIB3050-018-Q1-E1-A9
Method
                  BLASTX
NCBI GI
                  g4510348
BLAST score
                  259
E value
                  1.0e-22
Match length
                  99
% identity
                  51
```

Seq. No. 35874

NCBI Description

Seq. ID LIB3050-018-Q1-E1-B3

(AC006921) unknown protein [Arabidopsis thaliana]



Method BLASTX NCBI GI g416650 BLAST score 236 6.0e-20 E value Match length 101 48 % identity NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN PGNT35/PCNT111) >gi 100304 pir S16268 auxin-induced protein (clone pGNT35) - common tobacco >qi 19797 emb CAA39706 (X56265) auxin-induced protein [Nicotiana tabacum] >gi 19801 emb\_CAA39710\_ (X56269) auxin-induced protein [Nicotiana tabacum] Seq. No. 35875 Seq. ID LIB3050-018-Q1-E1-B8 Method BLASTX NCBI GI q632734 BLAST score 485 E value 4.0e-49 Match length 103 % identity 79 NCBI Description (S72452) CBP20=pathogen- and wound-inducible antifungal protein {clone cbp20-52, pathogen- and wound-inducible} [Nicotiana tabacum=tobacco, Samsun NN, leaves, Peptide, 211 aa] [Nicotiana tabacum] 35876 Seq. No. Seq. ID LIB3050-018-Q1-E1-D6 Method BLASTN NCBI GI q3334662 BLAST score 54 E value 9.0e-22 Match length 166 83 % identity NCBI Description G.max mRNA for putative cytochrome P450, clone CP4 Seq. No. 35877 Seq. ID LIB3050-018-Q1-E1-E12 Method BLASTX

Method BLASTX
NCBI GI g1346765
BLAST score 171
E value 3.0e-12
Match length 53
% identity 72

NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP1

>gi\_1084368\_pir\_\_S52371 phosphoprotein phosphatase (EC
3.1.3.16) PP1 - kidney bean >gi\_2129870\_pir\_\_S60053

phosphoprotein phosphatase 1 - kidney bean

>gi\_667049\_emb\_CAA88254\_ (Z48221) protein phosphatase PP1

[Phaseolus vulgaris]

Seq. No. 35878

Seq. ID LIB3050-018-Q1-E1-E3

Method BLASTN
NCBI GI g403328
BLAST score 36
E value 7.0e-11



```
Match length
                  89
% identity
NCBI Description
                  T.repens TrMT1B mRNA for metallothionein-like protein
                  35879
Seq. No.
Seq. ID
                  LIB3050-018-Q1-E1-E5
Method
                  BLASTX
NCBI GI
                  g4218116
BLAST score
                  141
                  9.0e-09
E value
Match length
                  37
                  65
% identity
NCBI Description
                  (AL035353) putative protein [Arabidopsis thaliana]
Seq. No.
                  35880
                  LIB3050-018-Q1-E1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832658
BLAST score
                  140
E value
                  6.0e-14
Match length
                  68
% identity
                  63
                  (AL021710) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  35881
Seq. ID
                  LIB3050-018-Q1-E1-F10
Method
                  BLASTN
NCBI GI
                  g11748
BLAST score
                  96
E value
                  1.0e-46
Match length
                  228
% identity
                  86
                  Nicotiana debneyi chloroplast DNA for tRNA-Ile and
NCBI Description
                  ribosomal protein L2
Seq. No.
                  35882
Seq. ID
                  LIB3050-018-Q1-E1-G10
Method
                  BLASTX
NCBI GI
                  g127046
BLAST score
                  247
E value
                  3.0e-21
Match length
                  97
% identity
                  53
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >qi 304637
                   (M61882) S-adenosylmethionine synthetase [Dianthus
                  caryophyllus] >gi 228314 prf 1802406A Met(S-adenosyl)
                  synthetase [Dianthus caryophyllus]
                  35883
Seq. No.
Seq. ID
                  LIB3050-018-Q1-E1-G3
```

Method BLASTX
NCBI GI g464981
BLAST score 164
E value 6.0e-12
Match length 50
% identity 62



NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi\_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 35884

Seq. ID LIB3050-018-Q1-E1-H11

Method BLASTX
NCBI GI 94158230
BLAST score 289
E value 6.0e-26
Match length 126
% identity 48

NCBI Description (Y18625) amylogenin [Triticum aestivum]

Seq. No. 35885

Seq. ID LIB3050-018-Q1-E1-H4

Method BLASTN
NCBI GI g169980
BLAST score 324
E value 0.0e+00
Match length 335
% identity 99

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No. 35886

Seq. ID LIB3050-018-Q1-E1-H8

Method BLASTX
NCBI GI g1370180
BLAST score 344
E value 2.0e-32
Match length 109
% identity 70

NCBI Description (Z73939) RAB5B [Lotus japonicus]

Seq. No. 35887

Seq. ID LIB3050-019-Q1-K1-A6

Method BLASTX
NCBI GI 94038042
BLAST score 395
E value 1.0e-38
Match length 98
% identity 73

NCBI Description (AC005936) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 35888

Seq. ID LIB3050-019-Q1-K1-D11

Method BLASTX
NCBI GI g3738194
BLAST score 165
E value 6.0e-12
Match length 75
% identity 44

NCBI Description (AL031854) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 35889

Seq. ID LIB3050-019-Q1-K1-E12

E value Match length

% identity

61 70



```
Method
                  BLASTN
NCBI GI
                  g303900
BLAST score
                  172
                  5.0e-92
E value
Match length
                  271
% identity
                  30
NCBI Description Soybean gene for ubiquitin, complete cds
Seq. No.
                  35890
                  LIB3050-019-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2317901
BLAST score
                  168
E value
                  5.0e-12
Match length
                  82
% identity
                  50
                  (U89959) Similar to vesicle transport protein, PIR
NCBI Description
                  Accession Number A55931 [Arabidopsis thaliana]
Seq. No.
                  35891
Seq. ID
                  LIB3050-019-Q1-K1-F2
Method
                  BLASTN
NCBI GI
                  g18655
                  78
BLAST score
E value
                  4.0e-36
Match length
                  130
% identity
                  90
NCBI Description Soybean heat-shock gene hs6871 sequence
Seq. No.
                  35892
Seq. ID
                  LIB3050-019-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g2829887
BLAST score
                  234
E value
                  7.0e-20
Match length
                  84
% identity
NCBI Description
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  35893
Seq. ID
                  LIB3050-019-Q1-K1-H8
Method
                  BLASTN
NCBI GI
                  g829118
BLAST score
                  62
                  1.0e-26
E value
Match length
                  114
% identity
                  89
NCBI Description P.vulgaris gene for cyclophilin
Seq. No.
                  35894
Seq. ID
                  LIB3050-020-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  g2213783
BLAST score
                  232
                  2.0e-19
```

5459

carota]



```
(U89256) Pti5 [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  35895
Seq. ID
                  LIB3050-020-Q1-K1-B10
Method
                  BLASTN
NCBI GI
                  g3452082
BLAST score
                  186
                  1.0e-100
E value
Match length
                  190
                  99
% identity
NCBI Description
                  Glycine max mRNA for polyubiquitin, partial
                  35896
Seq. No.
Seq. ID
                  LIB3050-020-Q1-K1-C12
Method
                  BLASTX
                  g2961348
NCBI GI
BLAST score
                  138
E value
                  7.0e-09
Match length
                  63
% identity
                  48
                  (AL022140) putative protein [Arabidopsis thaliana]
NCBI Description
                  35897
Seq. No.
                  LIB3050-020-Q1-K1-D5
Seq. ID
Method
                  BLASTN
                  q886099
NCBI GI
BLAST score
                  132
                  3.0e-68
E value
Match length
                  204
% identity
                  91
NCBI Description
                  Glycine max putative water channel protein (Pip1) mRNA,
                  complete cds
Seq. No.
                  35898
Seq. ID
                  LIB3050-020-01-K1-F12
Method
                  BLASTX
NCBI GI
                  g266945
BLAST score
                  149
E value
                  4.0e-10
Match length
                  39
% identity
                  79
NCBI Description
                  60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
                  >gi 100065 pir S19978 ribosomal protein L9 - garden pea
                  >qi 20727 emb CAA46273 (X65155) GA [Pisum sativum]
                  >gi 1279645 emb CAA65987 (X97322) ribosomal protein L9
                   [Pisum sativum]
Seq. No.
                  35899
                  LIB3050-020-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2224911
BLAST score
                  380
E value
                  6.0e-37
                  97
Match length
                  72
% identity
```

(U93048) somatic embryogenesis receptor-like kinase [Daucus



```
Seq. No.
                    35900
 Seq. ID
                    LIB3050-020-Q1-K1-G7
 Method
                    BLASTX
 NCBI GI
                    g4455159
 BLAST score
                    295
                    5.0e-27
 E value
 Match length
                    75
 % identity
                    75
                   (AL021687) putative protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    35901
 Seq. ID
                    LIB3050-020-Q1-K1-G8
 Method
                    BLASTN
 NCBI GI
                    g456713
 BLAST score
                    38
                    3.0e-12
 E value
 Match length
                    86
 % identity
                    66
 NCBI Description
                   Glycine max gene for ubiquitin, complete cds
 Seq. No.
                    35902
 Seq. ID
                    LIB3050-020-Q1-K1-H2
 Method
                    BLASTX
NCBI GI
                    q3860250
 BLAST score
                    158
                    8.0e-11
 E value
 Match length
                    89
 % identity
                    43
 NCBI Description
                    (AC005824) putative chloroplast prephenate dehydratase
                    [Arabidopsis thaliana]
 Seq. No.
                    35903
 Seq. ID
                    LIB3050-021-Q1-K1-C8
 Method
                    BLASTN
 NCBI GI
                    g170071
 BLAST score
                    80
 E value
                    3.0e-37
 Match length
                    191
 % identity
                    86
 NCBI Description
                   Soybean calmodulin (SCaM-2) mRNA, complete cds
 Seq. No.
                    35904
 Seq. ID
                    LIB3050-021-Q1-K1-D10
 Method
                    BLASTX
 NCBI GI
                    g1084334
 BLAST score
                    179
                    3.0e-13
 E value
 Match length
                    42
 % identity
                    83
 NCBI Description
                   calcium-dependent protein kinase (EC 2.7.1.-) 1 -
                    Arabidopsis thaliana >gi 604880 dbj BAA04829 (D21805)
                    calcium-dependent protein kinase [Arabidopsis thaliana]
```

Seq. No. 35905

Seq. ID LIB3050-021-Q1-K1-D12

Method BLASTN

5461

% identity

NCBI Description

54



```
g3021374
NCBI GI
BLAST score
                  77
E value
                  2.0e-35
Match length
                  177
% identity
                  86
NCBI Description
                  Glycine max mRNA for profilin, PRO1
Seq. No.
                  35906
Seq. ID
                  LIB3050-021-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  q3928150
                  177
BLAST score
                  3.0e-13
E value
Match length
                  45
% identity
                  69
                  (AJ131049) hypothetical protein [Cicer arietinum]
NCBI Description
Seq. No.
                  35907
                  LIB3050-021-Q1-K1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g531531
BLAST score
                  153
                  1.0e-80
E value
Match length
                  222
% identity
                  92
NCBI Description P.sativum mitochondrion genes rps10, trnF and trnP gene
Seq. No.
                  35908
Seq. ID
                  LIB3050-021-Q1-K1-E8
Method
                  BLASTN
NCBI GI
                  g18642
BLAST score
                  78
                  3.0e-36
E value
Match length
                  118
% identity
                  92
NCBI Description G.max mRNA from stress-induced gene (H4)
                  35909
Seq. No.
                  LIB3050-022-Q1-K1-B12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169980
BLAST score
                  306
                  1.0e-172
E value
Match length
                  389
                  96
% identity
NCBI Description
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                  35910
Seq. No.
                  LIB3050-022-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2979565
BLAST score
                  153
                  3.0e-10
E value
Match length
                  59
```

5462

[Arabidopsis thaliana]

(AC003680) putative sin3 associated polypeptide (SAP18)



```
Seq. No.
                    35911
 Seq. ID
                    LIB3050-022-Q1-K1-F2
 Method
                    BLASTX
                    q2651314
 NCBI GI
 BLAST score
                    209
                    3.0e-17
 E value
Match length
                    60
% identity
                    63
 NCBI Description
                    (AC002336) putative ribosomal protein S26 [Arabidopsis
                    thaliana]
                    35912
 Seq. No.
 Seq. ID
                    LIB3050-022-Q1-K1-F8
                    BLASTX
 Method
 NCBI GI
                    g3876716
 BLAST score
                    274
 E value
                    3.0e-24
                    87
 Match length
 % identity
                    51
                    (Z46242) similar to Zinc finger, C3HC4 type (RING finger)
 NCBI Description
                    [Caenorhabditis elegans]
 Seq. No.
                    35913
 Seq. ID
                    LIB3050-022-Q1-K1-G6
 Method
                    BLASTN
                    q170065
 NCBI GI
                    152
 BLAST score
                    4.0e-80
 E value
 Match length
                    165
 % identity
                    42
 NCBI Description
                    Soybean (G.max) proline-rich cell wall protein (SbPRP2)
                    gene, complete cds
 Seq. No.
                    35914
 Seq. ID
                    LIB3050-022-Q1-K1-H4
 Method
                    BLASTX
 NCBI GI
                    g2370459
 BLAST score
                    118
                    4.0e-14
 E value
 Match length
                    54
                    69
 % identity
 NCBI Description
                   (Y11987) FPF1 protein [Sinapis alba]
 Seq. No.
                    35915
 Seq. ID
                    LIB3050-023-Q1-K1-C3
 Method
                    BLASTX
 NCBI GI
                    g1053047
 BLAST score
                    147
                    2.0e-09
 E value
 Match length
                    96
 % identity
                    39
 NCBI Description
                    (U38425) histone H3 [Glycine max] >qi 1053049 (U38426)
                    histone H3 [Glycine max] >gi 1053051 (U38427) histone H3
```

Seq. No. 35916

[Glycine max]



Seq. ID LIB3050-023-Q1-K1-C4 Method BLASTX NCBI GI g1778143 BLAST score 406 E value 6.0e-40Match length 104 % identity 73 NCBI Description (U66401) phosphate/phosphoenolpyruvate translocator precursor [Nicotiana tabacum] Seq. No. 35917 Seq. ID LIB3050-023-Q1-K1-F4 Method BLASTN NCBI GI q169980 BLAST score 120 E value 6.0e-61 Match length 236 % identity 88 NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds Seq. No. 35918 Seq. ID LIB3050-023-Q1-K1-F7 Method BLASTN NCBI GI g169980 BLAST score 102 4.0e-50 E value Match length 338 % identity 83 NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds Seq. No. 35919 Seq. ID LIB3050-024-Q1-K1-A11 Method BLASTN NCBI GI g2267582 BLAST score 50 E value 3.0e-19 Match length 122 85 % identity NCBI Description Gossypium hirsutum vacuolar H+-ATPase subunit E mRNA, complete cds Seq. No. 35920 Seq. ID LIB3050-024-Q1-K1-H1 Method BLASTX NCBI GI q3688181 BLAST score 100 E value 1.0e-08 Match length 78 % identity 51 NCBI Description (AL031804) putative protein (fragment) [Arabidopsis thaliana]

Seq. No. 35921

Seq. ID LIB3050-024-Q1-K1-H10

Method BLASTX NCBI GI g3881189 BLAST score 148

38.4



1.0e-09 E value Match length 53

55 % identity

NCBI Description (Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL: C09829 comes from this

gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4

35922 Seq. No.

Seq. ID LIB3050-024-Q1-K1-H12

Method BLASTN NCBI GI g169980 BLAST score 273 1.0e-152 E value 325 Match length 96 % identity

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

35923 Seq. No.

Seq. ID LIB3050-025-Q1-K1-A4

BLASTN Method NCBI GI g169980 BLAST score 297 E value 1.0e-166 349 Match length 96 % identity

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

35924 Seq. No.

LIB3050-025-Q1-K1-A5 Seq. ID

Method BLASTX NCBI GI q456568 BLAST score 165 1.0e-11 E value Match length 53

% identity 64

NCBI Description (L29077) ubiquitin conjugating enzyme [Pisum sativum]

Seq. No. 35925

Seq. ID LIB3050-025-Q1-K1-B7

Method BLASTX NCBI GI q3980387 BLAST score 158 E value 6.0e-11 Match length 78 % identity 42

NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis

thaliana]

35926 Seq. No.

Seq. ID LIB3050-025-Q1-K1-C2

Method BLASTX NCBI GI g3377797 BLAST score 188 2.0e-14 E value Match length 80 54 % identity



NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No. 35927 Seq. ID LIB3050-025-Q1-K1-E1 Method BLASTY

Method BLASTX
NCBI GI g3122785
BLAST score 102
E value 4.0e-10
Match length 64
% identity 67

NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi\_2565340 (AF026079) ribosomal

protein S14 [Lupinus luteus]

Seq. No. 35928

Seq. ID LIB3050-025-Q1-K1-F7

Method BLASTN
NCBI GI g3452143
BLAST score 136
E value 2.0e-70
Match length 136
% identity 100

NCBI Description Glycine max mRNA for chalcone isomerase, partial

Seq. No. 35929

Seq. ID LIB3050-025-Q1-K1-G3

Method BLASTN
NCBI GI g169980
BLAST score 197
E value 1.0e-107
Match length 281
% identity 93

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No. 35930

Seq. ID LIB3050-026-Q1-K1-F6

Method BLASTX
NCBI GI g4580469
BLAST score 209
E value 1.0e-16
Match length 96
% identity 51

NCBI Description (AC006081) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 35931

Seq. ID LIB3050-026-Q1-K1-H5

Method BLASTX
NCBI GI g4531444
BLAST score 143
E value 6.0e-09
Match length 110
% identity 34

NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No.

Seq. ID

35937

LIB3050-028-Q1-E1-E8



```
Seq. No.
                  35932
Seq. ID
                  LIB3050-027-Q1-E1-C12
Method
                  BLASTN
                  q169980
NCBI GI
BLAST score
                  390
E value
                  0.0e + 00
Match length
                  422
% identity
                  100
NCBI Description
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.
                  35933
Seq. ID
                  LIB3050-027-Q1-E1-C3
Method
                  BLASTX
NCBI GI
                  q1169383
BLAST score
                  88
E value
                  1.0e-08
Match length
                  58
                  55
% identity
NCBI Description
                  DNAJ PROTEIN HOMOLOG ATJ >qi 535588 (L36113) putative
                  [Arabidopsis thaliana] >gi 1582356 prf 2118338A AtJ2
                  protein [Arabidopsis thaliana]
Seq. No.
                  35934
Seq. ID
                  LIB3050-027-Q1-E1-D10
Method
                  BLASTX
NCBI GI
                  q4455351
BLAST score
                  218
E value
                  1.0e-17
Match length
                  66
% identity
                  67
NCBI Description
                  (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                  35935
Seq. ID
                  LIB3050-027-01-E1-F12
Method
                  BLASTX
NCBI GI
                  g4206787
BLAST score
                  173
E value
                  2.0e-12
Match length
                  40
% identity
                  82
NCBI Description
                  (AF112863) syntaxin-related protein Nt-syr1 [Nicotiana
                  tabacum]
Seq. No.
                  35936
Seq. ID
                  LIB3050-028-Q1-E1-E6
Method
                  BLASTX
NCBI GI
                  g3763927
BLAST score
                  197
E value
                  2.0e-15
Match length
                  107
% identity
                  35
NCBI Description
                  (AC004450) putative carboxyphosphoenolpyruvate mutase
                  [Arabidopsis thaliana]
```

Method BLASTN NCBI GI g169980 BLAST score 220 E value 1.0e-120 Match length 344 % identity 91 NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds Seq. No. 35938 Seq. ID LIB3050-028-Q1-E1-F1 Method BLASTX NCBI GI q3157951 BLAST score 218 E value 1.0e-17 Match length 82 62 % identity (AC002131) Contains similarity to vesicle trafficking NCBI Description protein qb U91538 from Mus musculus. ESTs qb F15494 and gb F14097 come from this gene. [Arabidopsis thaliana] Seq. No. Seq. ID LIB3050-028-Q1-E1-H3 Method BLASTX NCBI GI q3150404 BLAST score 168 E value 5.0e-12 Match length 72 57 % identity NCBI Description (AC004165) putative mitochondrial carrier protein [Arabidopsis thaliana] 35940 LIB3051-001-Q1-E1-D10 Seq. ID Method BLASTN NCBI GI q170023 BLAST score 255 1.0e-141 E value

Seq. No.

Match length 331 % identity 85

NCBI Description Glycine max maturation-associated protein (MAT9) mRNA,

complete cds

Seq. No. 35941

LIB3051-001-Q1-E1-D11 Seq. ID

Method BLASTX NCBI GI q3702325 BLAST score 175 E value 7.0e-13 Match length 91 % identity 41

(AC005397) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 35942

LIB3051-001-Q1-E1-F10 Seq. ID

BLASTN Method g531828 NCBI GI BLAST score 37

Seq. No.

35948



```
E value
                   2.0e-11
Match length
                   105
% identity
NCBI Description
                  Cloning vector pSport1, complete cds
Seq. No.
                   35943
Seq. ID
                   LIB3051-001-Q1-E1-G3
Method
                   BLASTX
NCBI GI
                   g1350548
BLAST score
                   142
E value
                   9.0e-09
Match length
                   71
% identity
                   42
NCBI Description
                  (L47609) heat shock-like protein [Picea glauca]
Seq. No.
                   35944
Seq. ID
                   LIB3051-002-Q1-E1-A6
Method
                   BLASTX
NCBI GI
                   g3980398
BLAST score
                   167
E value
                   1.0e-11
Match length
                   111
% identity
                   56
NCBI Description
                   (AC004561) putative tropinone reductase [Arabidopsis
                   thaliana]
Seq. No.
                   35945
                   LIB3051-002-Q1-E1-C12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q22075
BLAST score
                   55
E value
                   2.0e-22
Match length
                   87
% identity
                   91
NCBI Description Vigna unguiculata cDNA for stored cotyledon mRNA
Seq. No.
                   35946
Seq. ID
                  LIB3051-002-Q1-E1-C5
Method
                   BLASTX
NCBI GI
                   q3033382
BLAST score
                   403
E value
                   2.0e-39
Match length
                  110
% identity
                  70
NCBI Description
                  (AC004238) unknown protein [Arabidopsis thaliana]
Seq. No.
                  35947
Seq. ID
                  LIB3051-002-Q1-E1-H6
Method
                  BLASTX
NCBI GI
                  g3786009
BLAST score
                  322
E value
                  8.0e-30
Match length
                  70
% identity
                  87
                  (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
```



```
LIB3051-003-Q1-E1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2924777
BLAST score
                  193
                  7.0e-15
E value
Match length
                  103
% identity
NCBI Description
                  (AC002334) putative receptor protein kinase [Arabidopsis
                  thaliana]
                  35949
Seq. No.
                  LIB3051-003-Q1-E1-F5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  35
                  3.0e-10
E value
Match length
                  36
                  60
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  35950
Seq. ID
                  LIB3051-003-Q1-E1-G2
                  BLASTN
Method
                 g18743
NCBI GI
BLAST score
                  163
E value
                  1.0e-86
                  250
Match length
                  92
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
Seq. No.
                  35951
                  LIB3051-003-Q1-E1-H12
Seq. ID
Method
                  BLASTX
                  q4371285
NCBI GI
BLAST score
                  270
E value
                  1.0e-23
Match length
                  84
                  62
% identity
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  35952
Seq. ID
                  LIB3051-004-Q1-E1-B10
Method
                  BLASTX
NCBI GI
                  q2655098
BLAST score
                  169
E value
                  3.0e-24
Match length
                  82
% identity
                  70
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]
Seq. No.
                  35953
                  LIB3051-004-Q1-E1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2055229
BLAST score
                  124
```

3.0e-63

348

E value Match length

% identity

NCBI Description

28



```
% identity
NCBI Description Soybean mRNA for SRC2, complete cds
Seq. No.
                  35954
Seq. ID
                  LIB3051-004-Q1-E1-D6
Method
                  BLASTX
NCBI GI
                  g3668089
                  259
BLAST score
                  2.0e-22
E value
Match length
                  100
% identity
                  51
                  (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  35955
                  LIB3051-004-Q1-E1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1944341
BLAST score
                  79
E value
                  6.0e-37
Match length
                  118
% identity
                  92
                  Glycine max DNA for cysteine proteinase inhibitor, complete
NCBI Description
                  cds
                  35956
Seq. No.
Seq. ID
                  LIB3051-004-Q1-E1-G5
Method
                  BLASTX
NCBI GI
                  g2435519
BLAST score
                  309
E value
                  3.0e-28
Match length
                  86
                  73
% identity
                  (AF024504) similar to mouse MEM3 (GB:U47024 and S.
NCBI Description
                  cerevisiae vacuolar sorting protein 35 (SW; P34110)
                   [Arabidopsis thaliana]
Seq. No.
                  35957
Seq. ID
                  LIB3051-005-Q1-E1-C3
Method
                  BLASTX
NCBI GI
                  q2598589
BLAST score
                  447
                  2.0e-44
E value
Match length
                  119
                  71
% identity
NCBI Description
                  (Y15367) MtN19 [Medicago truncatula]
Seq. No.
                  35958
Seq. ID
                  LIB3051-005-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                  g2132480
BLAST score
                  147
                  2.0e-09
E value
Match length
                  134
```

5471

[Saccharomyces cerevisiae]

probable membrane protein YDR205w - yeast (Saccharomyces

cerevisiae) >gi 1122333 emb CAA92344 (Z68194) unknown

Method

NCBI GI BLAST score BLASTX g1699024

247

```
35959
Seq. No.
Seq. ID
                  LIB3051-005-Q1-E1-F3
Method
                  BLASTN
NCBI GI
                  g454847
BLAST score
                  86
                  1.0e-40
E value
                  143
Match length
% identity
NCBI Description Glycine max ribosomal protein S11 gene, complete cds
                  35960
Seq. No.
                  LIB3051-006-Q1-E1-C10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g452593
                  234
BLAST score
                  2.0e-19
E value
                  132
Match length
                  46
% identity
                 (D21814) ORF [Lilium longiflorum]
NCBI Description
                  35961
Seq. No.
Seq. ID
                  LIB3051-006-Q1-E1-D11
                  BLASTN
Method
NCBI GI
                  q18764
BLAST score
                  175
E value
                  1.0e-93
                  347
Match length
                  88
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-la
                  35962
Seq. No.
                  LIB3051-006-Q1-E1-E11
Seq. ID
Method
                  BLASTX
                  q2765091
NCBI GI
BLAST score
                  182
                  8.0e-21
E value
Match length
                  102
                  58
% identity
                 (Y10982) putative cytochrome P450 [Glycine max]
NCBI Description
                  35963
Seq. No.
Seq. ID
                  LIB3051-006-Q1-K1-C10
                  BLASTN
Method
NCBI GI
                  g2062691
BLAST score
                  36
E value
                  9.0e-11
Match length
                  39
                  65
% identity
NCBI Description Human sodium phosphate transporter (NPT4) mRNA, complete
                  cds
                  35964
Seq. No.
Seq. ID
                  LIB3051-006-Q1-K1-C4
```

5472

Match length

% identity

108

62



```
3.0e-21
E value
Match length
                  67
                  60
% identity
                  (U78866) gene1000 [Arabidopsis thaliana] >gi 1699057
NCBI Description
                  (U78870) unknown [Arabidopsis thaliana]
                  35965
Seq. No.
                  LIB3051-006-Q1-K1-D11
Seq. ID
Method
                  BLASTN
                  a18764
NCBI GI
BLAST score
                  94
                  2.0e-45
E value
                  110
Match length
                  96
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-la
                  35966
Seq. No.
Seq. ID
                  LIB3051-006-Q1-K1-G10
Method
                  BLASTN
NCBI GI
                  g2465018
                  67
BLAST score
                  3.0e-29
E value
                  142
Match length
                   92
% identity
                  Fragaria vesca partial mRNA for putative cystathionine
NCBI Description
                  gamma synthase
                   35967
Seq. No.
Seq. ID
                  LIB3051-007-Q1-E1-A1
Method
                   BLASTX
NCBI GI
                   q3882321
                   176
BLAST score
                   9.0e-13
E value
Match length
                   117
% identity
NCBI Description
                  (AB018343) KIAA0800 protein [Homo sapiens]
Seq. No.
                   35968
                   LIB3051-007-Q1-E1-B11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g567893
                   150
BLAST score
E value
                   7.0e-10
                   78
Match length
% identity
                   (L37382) beta-galactosidase-complementation protein
NCBI Description
                   [Cloning vector]
                   35969
Seq. No.
                   LIB3051-007-Q1-E1-B12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1169200
BLAST score
                   313
                   8.0e-29
E value
```

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR



>gi\_421829\_pir\_\_S33706 DNA-damage resistance protein Arabidopsis thaliana >gi\_166694 (M98455) [Arabidopsis
thaliana recombination and DNA-damage resistance protein
(DRT111) mRNA, complete cds.], gene product [Arabidopsis
thaliana]

```
35970
   Seq. No.
   Seq. ID
                      LIB3051-007-Q1-E1-B5
                      BLASTX
   Method
NCBI GI
                      q461944
   BLAST score
                      189
   E value
                      1.0e-14
   Match length
                      75
                      51
   % identity
                     DNAJ PROTEIN HOMOLOG (DNAJ-1) >gi 18260 emb CAA47925
   NCBI Description
                      (X67695) cs DnaJ-1 [Cucumis sativus]
                      35971
   Seq. No.
   Seq. ID
                      LIB3051-007-Q1-E1-F10
                      BLASTX
   Method
   NCBI GI
                      q4415912
   BLAST score
                      314
                      7.0e-29
   E value
                      90
   Match length
                      69
   % identity
                     (AC006282) putative protease [Arabidopsis thaliana]
   NCBI Description
                      35972
   Seq. No.
   Seq. ID
                      LIB3051-007-Q1-E1-G10
   Method
                      BLASTX
   NCBI GI
                      q1403522
                      223
   BLAST score
                      2.0e-32
   E value
                      92
   Match length
   % identity
                      69
   NCBI Description
                     (X57187) chitinase [Phaseolus vulgaris]
                      35973
   Seq. No.
                      LIB3051-007-Q1-E1-G5
   Seq. ID
                      BLASTN
   Method
   NCBI GI
                      q2062691
   BLAST score
                      34
   E value
                      7.0e-10
                      46
   Match length
   % identity
                      67
                      Human sodium phosphate transporter (NPT4) mRNA, complete
   NCBI Description
                      cds
   Seq. No.
                      35974
                      LIB3051-008-Q1-E1-B2
   Seq. ID
   Method
                      BLASTN
                      g170065
   NCBI GI
   BLAST score
                      136
   E value
                      2.0e-70
   Match length
                      373
   % identity
                      18
```

NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP2)



## gene, complete cds

```
Seq. No.
                  35975
Seq. ID
                  LIB3051-008-Q1-E1-C6
Method
                  BLASTN
NCBI GI
                  g2739043
                  380
BLAST score
                  0.0e + 00
E value
                  384
Match length
                  100
% identity
                  Glycine max polyphosphoinositide binding protein Sshlp
NCBI Description
                   (SSH1) mRNA, complete cds
Seq. No.
                   35976
Seq. ID
                  LIB3051-008-Q1-E1-C7
Method
                  BLASTN
NCBI GI
                  g2739043
BLAST score
                   91
                   1.0e-43
E value
Match length
                   139
% identity
                  Glycine max polyphosphoinositide binding protein Sshlp
NCBI Description
                   (SSH1) mRNA, complete cds
Seq. No.
                   35977
                  LIB3051-008-Q1-E1-D11
Seq. ID
                   BLASTN
Method
                   g3265097
NCBI GI
BLAST score
                   57
                   3.0e-23
E value
Match length
                   106
                   91
% identity
                  Reseda alba 18S ribosomal RNA gene, partial sequence
NCBI Description
                   35978
Seq. No.
Seq. ID
                   LIB3051-008-Q1-E1-E10
Method
                   BLASTX
NCBI GI
                   g1362073
BLAST score
                   338
E value
                   1.0e-31
Match length
                   126
% identity
                   54
                  basic chitinase class 3 - cowpea >gi 871764 emb CAA61279
NCBI Description
                   (X88801) basic chitinase class 3 [Vigna unguiculata]
Seq. No.
                   35979
                   LIB3051-008-Q1-E1-F7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3850817
BLAST score
                   80
E value
                   5.0e-37
Match length
                   180
% identity
                   86
                  Oryza sativa mRNA for U2 snRNP auxiliary factor, small
NCBI Description
```

Seq. No. 35980

subunit 35a

Seq. ID

Method



```
LIB3051-008-Q1-E1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1172977
BLAST score
                  161
E value
                  5.0e-11
                  70
Match length
                  51
% identity
                  60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
NCBI Description
                  ribosomal protein L18 [Arabidopsis thaliana]
                  35981
Seq. No.
Seq. ID
                  LIB3051-008-Q1-E1-H12
                  BLASTN
Method
                  g18743
NCBI GI
BLAST score
                  198
                  1.0e-107
E value
                  206
Match length
                  99
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
Seq. No.
                  35982
Seq. ID
                  LIB3051-008-Q1-E1-H5
Method
                  BLASTX
NCBI GI
                  q541546
BLAST score
                  191
                  8.0e-15
E value
                  93
Match length
                  10
% identity
                  ubiquitin precursor - Volvox carteri
NCBI Description
                  >gi_395295_emb_CAA52290_ (X74214) polyubiquitin [Volvox
                  carteri]
Seq. No.
                  35983
Seq. ID
                  LIB3051-008-Q1-E1-H8
                  BLASTN
Method
NCBI GI
                  g2920665
BLAST score
                  297
                  1.0e-166
E value
Match length
                  301
                  100
% identity
                  Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                   (GSTa) mRNA, complete cds
Seq. No.
                  35984
Seq. ID
                  LIB3051-009-Q1-E1-A7
Method
                  BLASTX
NCBI GI
                  q3901012
BLAST score
                  189
                  3.0e-14
E value
                  102
Match length
% identity
NCBI Description
                  (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
                  sylvatica]
Seq. No.
                  35985
```

LIB3051-009-Q1-E1-E1

BLASTX

% identity



```
g2244771
NCBI GI
BLAST score
                  140
                  3.0e-14
E value
Match length
                  87
% identity
                  59
NCBI Description (Z97335) kinesin homolog [Arabidopsis thaliana]
Seq. No.
                  35986
Seq. ID
                  LIB3051-009-Q1-E1-G10
Method
                  BLASTX
NCBI GI
                  q2829912
                  158
BLAST score
                  1.0e-10
E value
Match length
                  40
% identity
                  70
                  (ACO02291) Similar ATP-dependent RNA Helicase [Arabidopsis
NCBI Description
                  thaliana]
                  35987
Seq. No.
Seq. ID
                  LIB3051-009-Q1-E1-H4
Method
                  BLASTN
NCBI GI
                  q4218188
BLAST score
                  62
E value
                  3.0e-26
Match length
                  141
% identity
                  87
                  Glycine max cytosolic glutamine synthetase (gs15) gene
NCBI Description
                  promoter
Seq. No.
                  35988
Seq. ID
                  LIB3051-010-Q1-E1-D7
Method
                  BLASTX
NCBI GI
                  g3080530
BLAST score
                  177
                  8.0e-13
E value
Match length
                  119
                  37
% identity
                  (AL022600) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                  35989
Seq. ID
                  LIB3051-010-Q1-E1-F4
Method
                  BLASTX
NCBI GI
                  q4210449
BLAST score
                  220
                   6.0e-18
E value
Match length
                  90
% identity
                  50
                  (AB016471) ARR1 protein [Arabidopsis thaliana]
NCBI Description
                  35990
Seq. No.
Seq. ID
                  LIB3051-010-Q1-E1-G1
Method
                  BLASTN
NCBI GI
                  g456713
BLAST score
                  376
                  0.0e+00
E value
Match length
                  416
```



```
NCBI Description Glycine max gene for ubiquitin, complete cds

Seq. No. 35991
Seq. ID LIB3051-010-Q1-E1-G2
```

Method BLASTX
NCBI GI g4455223
BLAST score 227
E value 7.0e-19
Match length 83
% identity 57

NCBI Description (AL035440) putative DNA binding protein [Arabidopsis

thaliana]

 Seq. No.
 35992

 Seq. ID
 LIB3051-010-Q1-E1-G6

 Method
 BLASTN

NCBI GI g210811
BLAST score 95
É value 5.0e-46
Match length 293

% identity 84
NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 35993

Seq. ID LIB3051-011-Q1-E1-B8

Method BLASTX
NCBI GI g2980641
BLAST score 260
E value 1.0e-22
Match length 142
% identity 40

NCBI Description (Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No. 35994

Seq. ID LIB3051-011-Q1-E1-C1

Method BLASTX
NCBI GI g3885340
BLAST score 237
E value 6.0e-20
Match length 115
% identity 48

NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

Seq. No. 35995

Seq. ID LIB3051-011-Q1-E1-E4

Method BLASTN
NCBI GI g4097879
BLAST score 73
E value 6.0e-33
Match length 229
% identity 83

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 35996

Seq. ID LIB3051-011-Q1-E1-E9

NCBI GI

E value

BLAST score



```
Method
                   BLASTX
NCBI GI
                   g2105430
BLAST score
                   424
E value
                   7.0e-42
Match length
                   132
% identity
                   62
NCBI Description
                   (U97079) U5-116kD [Mus musculus]
Seq. No.
                   35997
Seq. ID
                   LIB3051-011-Q1-E1-F12
Method
                   BLASTX
NCBI GI
                   g4336436
BLAST score
                   163
E value
                   3.0e-11
Match length
                   62
% identity
                   53
NCBI Description
                  (AF092432) protein phosphatase type 2C [Lotus japonicus]
Seq. No.
                   35998
Seq. ID
                   LIB3051-011-Q1-E1-F4
Method
                   BLASTN
NCBI GI
                   g2739005
BLAST score
                   62
                   2.0e-26
E value
Match length
                   126
% identity
                   87
NCBI Description
                   Glycine max cytochrome P450 monooxygenase CYP93C1p
                   (CYP93C1) mRNA, complete cds
Seq. No.
                   35999
Seq. ID
                   LIB3051-011-Q1-E1-G4
Method
                   BLASTX
                   q99992
NCBI GI
BLAST score
                   140
E value
                   3.0e-14
Match length
                   91
                   54
% identity
NCBI Description
                  protein disulfide-isomerase (EC 5.3.4.1) precursor -
                   alfalfa (clone B2) >gi_166418 (M82973) putative
                   endomembrane protein; putative [Medicago sativa]
Seq. No.
                   36000
Seq. ID
                   LIB3051-011-Q1-E1-H7
Method
                   BLASTX
NCBI GI
                   g2262178
BLAST score
                   336
E value
                   2.0e-31
Match length
                   138
% identity
NCBI Description
                   (AC002329) putative Mlo-like protein [Arabidopsis thaliana]
Seq. No.
                   36001
Seq. ID
                   LIB3051-012-Q1-E1-B10
Method
                   BLASTX
```

200

1.0e-13

g3080411

183

```
Match length
% identity
                   40
NCBI Description
                   (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                   36002
Seq. ID
                   LIB3051-012-Q1-E1-C11
Method
                   BLASTX
NCBI GI
                   q541943
BLAST score
                   327
E value
                   1.0e-30
Match length
                   79
                   73
% identity
NCBI Description
                  metallothionein - soybean >gi_228682_prf__1808316A
                   metallothionein-like protein [Glycine max]
Seq. No.
                   36003
Seq. ID
                   LIB3051-012-Q1-E1-D6
Method
                   BLASTX
NCBI GI
                   g3322882
BLAST score
                   315
E value
                   3.0e-29
Match length
                   97
% identity
                   60
NCBI Description
                   (AE001234) leucyl-tRNA synthetase (leuS) [Treponema
                  pallidum]
Seq. No.
                   36004
Seq. ID
                  LIB3051-012-Q1-E1-E4
Method
                  BLASTN
NCBI GI
                   g2661020
BLAST score
                   176
E value
                   2.0e-94
                  272
Match length
% identity
                  91
NCBI Description
                  Glycine max catalase (cat4) mRNA, complete cds
Seq. No.
                  36005
Seq. ID
                  LIB3051-012-Q1-E1-H5
Method
                  BLASTX
NCBI GI
                  g4262222
BLAST score
                  361
E value
                  1.0e-34
Match length
                  108
% identity
                  62
NCBI Description
                  (AC006200) putative RNA helicase A, 3' partial [Arabidopsis
                  thaliana]
Seq. No.
                  36006
```

Seq. ID LIB3051-013-Q1-E1-A8

Method BLASTX NCBI GI g1703200 BLAST score 136 E value 3.0e-10 Match length 76 % identity 54

NCBI Description PROTEIN KINASE AFC2 >gi 601789 (U16177) protein kinase [Arabidopsis thaliana] >gi\_642130\_dbj\_BAA08214\_ (D45353)



protein kinase [Arabidopsis thaliana]
>gi\_4220516\_emb\_CAA22989\_ (AL035356) protein kinase (AFC2)
[Arabidopsis thaliana]

 Seq. No.
 36007

 Seq. ID
 LIB3051-013-Q1-E1-C5

 Method
 BLASTX

 NCBI GI
 g4539453

 BLAST score
 289

 E value
 6.0e-26

Match length 90 % identity 58

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 36008

Seq. ID LIB3051-013-Q1-E1-C9

Method BLASTX
NCBI GI g2352492
BLAST score 320
E value 1.0e-29
Match length 124
% identity 51

NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis

thaliana] >gi\_2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

Seq. No. 36009

Seq. ID LIB3051-013-Q1-E1-D7

Method BLASTX
NCBI GI g3355474
BLAST score 201
E value 8.0e-16
Match length 101
% identity 43

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 36010

Seq. ID LIB3051-013-Q1-E1-F10

Method BLASTX
NCBI GI g3152577
BLAST score 175
E value 9.0e-13
Match length 96
% identity 44

NCBI Description (AC002986) Contains similarity to Kinesin-like protein C

gb D21138 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 36011

Seq. ID LIB3051-013-Q1-E1-G12

Method BLASTX
NCBI GI g2317901
BLAST score 279
E value 8.0e-25
Match length 121
% identity 54

NCBI Description (U89959) Similar to vesicle transport protein, PIR

Accession Number A55931 [Arabidopsis thaliana]

% identity

NCBI Description

44



```
36012
Seq. No.
                  LIB3051-013-Q1-E1-G6
Seq. ID
                  BLASTX
Method
                  g2501231
NCBI GI
                  188
BLAST score
                  3.0e-14
E value
                  68
Match length
                  60
% identity
                  HYPOTHETICAL 38.1 KD PROTEIN >gi_99505_pir__S24930
NCBI Description
                  hypothetical protein - pink corydalis
                  >gi 18258_emb_CAA45139_ (X63595) protein of unknown
                  function [Corydalis sempervirens] >gi_444333_prf__1906382A
                  pCSC71 protein [Corydalis sempervirens]
                  36013
Seq. No.
                  LIB3051-013-Q1-E1-H10
Seq. ID
                  BLASTX
Method
                  g729880
NCBI GI
                  254
BLAST score
                  6.0e-22
E value
                  77
Match length
                  60
% identity
                  CASEIN KINASE II BETA CHAIN (CK II) >gi_1076299_pir__S47967
NCBI Description
                  casein kinase II (EC 2.7.1.-) beta chain CKB1 - Arabidopsis
                  thaliana >gi_468264 (L22563) casein kinase II beta subunit
                  CKB1 [Arabidopsis thaliana]
                   36014
Seq. No.
                  LIB3051-014-Q1-E1-A6
Seq. ID
                  BLASTN
Method
                   g3821780
NCBI GI
                   36
BLAST score
                   1.0e-10
E value
                   38
Match length
                   44
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   36015
Seq. No.
                   LIB3051-014-Q1-E1-A7
Seq. ID
                   BLASTN
Method
                   q18723
NCBI GI
BLAST score
                   155
                   9.0e-82
E value
                   167
Match length
                   98
 % identity
                   Glycine max mRNA for pyrroline-5-carboxylate reductase
NCBI Description
                   36016
 Seq. No.
Seq. ID
                   LIB3051-014-Q1-E1-A8
                   BLASTX
 Method
 NCBI GI
                   q3790581
                   262
 BLAST score
                   8.0e-23
 E value
 Match length
                   110
```

5482

(AF079179) RING-H2 finger protein RHBla [Arabidopsis

NCBI Description



## thaliana]

```
36017
Seq. No.
                   LIB3051-014-Q1-E1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1077378
                   316
BLAST score
                   3.0e-29
E value
                   123
Match length
                   12
% identity
                   probable membrane protein YLR222c - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >gi_609371 (U19027) Ylr222cp [Saccharomyces
                   cerevisiae]
                   36018
Seq. No.
                   LIB3051-014-Q1-E1-E3
Seq. ID
Method
                   BLASTX
                   g4538981
NCBI GI
                   188
BLAST score
                   3.0e-14
E value
                   122
Match length
                   42
% identity
NCBI Description (AL049487) putative protein [Arabidopsis thaliana]
                   36019
Seq. No.
                   LIB3051-014-Q1-E1-G10
Seq. ID
                   BLASTN
Method
                   g210811
NCBI GI
                   56
BLAST score
                   8.0e-23
E value
                   107
Match length
                   90
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   36020
Seq. No.
                   LIB3051-014-Q1-E1-G5
Seq. ID
                   BLASTX
Method
                   g3875417
NCBI GI
                   163
BLAST score
                   3.0e-11
E value
Match length
                   94
 % identity
                   (Z83223) cDNA EST EMBL:D35113 comes from this gene; cDNA
NCBI Description
                   EST yk230c6.5 comes from this gene [Caenorhabditis elegans]
                   36021
 Seq. No.
 Seq. ID
                   LIB3051-014-Q1-E1-H1
                   BLASTN
Method
                   q472849
NCBI GI
                   264
BLAST score
 E value
                   1.0e-147
                    357
 Match length
                    93
 % identity
```

homolog mRNA, complete cds

Glycine max Essex desiccation protectant protein Lea14



```
Seq. No.
                  LIB3051-014-Q1-E1-H11
Seq. ID
                  BLASTN
Method
                  g169980
NCBI GI
                  334
BLAST score
                  0.0e+00
E value
                  366
Match length
                  98
% identity
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
NCBI Description
                  36023
Seq. No.
                  LIB3051-015-Q1-E1-A12
Seq. ID
                  BLASTX
Method
                   q3036812
NCBI GI
                   311
BLAST score
                   9.0e-29
E value
                   104
Match length
                   58
% identity
                  (AL022373) ATM-like protein [Arabidopsis thaliana]
NCBI Description
                   36024
Seq. No.
                   LIB3051-015-Q1-E1-A4
Seq. ID
                   BLASTN
Method
                   g2270989
NCBI GI
                   38
BLAST score
                   5.0e-12
E value
                   74
Match length
                   88
% identity
NCBI Description Glycine max dehydrin (GmPM12) mRNA, complete cds
                   36025
Seq. No.
Seq. ID
                   LIB3051-015-Q1-E1-D11
                   BLASTX
Method
                   g531829
NCBI GI
                   161
BLAST score
                   5.0e-11
E value
                   79
Match length
                   44
% identity
                   (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
                   36026
Seq. No.
                   LIB3051-015-Q1-E1-D2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g18743
                   69
BLAST score
                   1.0e-30
E value
Match length
                   245
                   82
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
                   36027
Seq. No.
                   LIB3051-015-Q1-E1-E5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3886025
BLAST score
                   154
```

4.0e-10

E value



Match length % identity 38 (AF106576) similar to the nucleolar protein NOF1/NOP2 NCBI Description family [Caenorhabditis elegans] 36028 Seq. No. Seq. ID LIB3051-015-Q1-E1-E7 Method BLASTX NCBI GI g2245020 ₹ 350 BLAST score E value 4.0e-33 Match length 84 % identity 71 (Z97341) growth regulator homolog [Arabidopsis thaliana] NCBI Description 36029 Seq. No. Seq. ID LIB3051-015-Q1-E1-F11 Method BLASTX NCBI GI g3341685 BLAST score 150 E value 2.0e-13 Match length 61 69 % identity (AC003672) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 36030 LIB3051-015-Q1-E1-F9 Seq. ID Method BLASTX NCBI GI q1561774 BLAST score 350 E value 7.0e-43 Match length 121 % identity 83 (U67426) malate dehydrogenase [Vitis vinifera] NCBI Description 36031 Seq. No. LIB3051-015-Q1-E1-H7 Seq. ID Method BLASTN NCBI GI g488576 BLAST score 137 5.0e-71 E value Match length 241 89 % identity NCBI Description Medicago sativa Regen S clone pH3c131 histone H3.2 mRNA, complete cds 36032 Seq. No. Seq. ID LIB3051-016-Q1-E1-A10 Method BLASTX NCBI GI g3142303 BLAST score 332 134

E value 5.0e-31 Match length 133

% identity 44 (AC002411) Strong similarity to MRP-like ABC transporter NCBI Description

gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb L49379 from Rattus norvegicus.



## [Arabidopsis thaliana]

```
36033
Seq. No.
                  LIB3051-016-Q1-E1-B5
Seq. ID
                  BLASTX
Method
                  g2801442
NCBI GI
BLAST score
                  364
                  9.0e-35
E value
                  120
Match length
                  60
% identity
                  (AF028338) ubiquitin-conjugating enzyme 15 [Arabidopsis
NCBI Description
                  thaliana]
                   36034
Seq. No.
                  LIB3051-016-Q1-E1-C1
Seq. ID
                  BLASTX
Method
                  g2129820
NCBI GI
                   646
BLAST score
                   9.0e-68
E value
                   129
Match length
                   85
% identity
                  chitinase (EC 3.2.1.14) class II - peanut
NCBI Description
                   >gi_1237025_emb_CAA57773_ (X82329) chitinase (class II)
                   [Arachis hypogaea]
                   36035
Seq. No.
                   LIB3051-016-Q1-E1-D9
Seq. ID
                   BLASTN
Method
                   g927504
NCBI GI
                   74
BLAST score
                   2.0e-33
E value
Match length
                   130
                   89
% identity
                   P.sativum mRNA for fructose-1, 6-biphosphate aldolase
NCBI Description
                   (clone aldcyt2)
                   36036
Seq. No.
                   LIB3051-016-Q1-E1-E6
Seq. ID
                   BLASTX
Method
                   g2507421
NCBI GI
BLAST score
                   180
                   2.0e-13
E value
                   55
Match length
                   65
% identity
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277
NCBI Description
                   (U81042) translation initiation factor [Arabidopsis
                   thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680)
                   translation initiation factor [Arabidopsis thaliana]
                   36037
 Seq. No.
 Seq. ID
                   LIB3051-016-Q1-E1-F9
Method
                   BLASTX
                   q4538964
NCBI GI
                   401
 BLAST score
                   4.0e-39
 E value
Match length
                   108
```

69

% identity



```
NCBI Description (AL049488) NAM/NAP like protein [Arabidopsis thaliana]
                  36038
Seq. No.
                  LIB3051-016-Q1-E1-H6
Seq. ID
                  BLASTN
Method
                  g2062691
NCBI GI
                  33
BLAST score
                  5.0e-09
E value
                  33
Match length
                  100
% identity
                  Human sodium phosphate transporter (NPT4) mRNA, complete
NCBI Description
                  36039
Seq. No.
                  LIB3051-017-Q1-E1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g475603
BLAST score
                  60
                  1.0e-25
E value
                  116
Match length
% identity
NCBI Description Glycine max Century 84 beta-1,3-glucanase mRNA, partial cds
Seq. No.
                   36040
                  LIB3051-017-Q1-E1-B11
Seq. ID
                  BLASTX
Method
                   q99992
NCBI GI
                   146
BLAST score
E value
                   3.0e-09
                   98
Match length
                   39
% identity
                  protein disulfide-isomerase (EC 5.3.4.1) precursor -
NCBI Description
                   alfalfa (clone B2) >gi_166418 (M82973) putative
                   endomembrane protein; putative [Medicago sativa]
                   36041
Seq. No.
                   LIB3051-017-Q1-E1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3021266
                   173
BLAST score
                   1.0e-12
E value
                   90
Match length
% identity
                   44
                   (AL022347) serine/threonine kinase - like protein
NCBI Description
                   [Arabidopsis thaliana] >gi_3292840_emb_CAA19830_ (AL031018)
                   serine/threonine kinase - like protein [Arabidopsis
                   thaliana]
                   36042
Seq. No.
                   LIB3051-017-Q1-E1-D3
Seq. ID
                   BLASTX
Method
                   g4467147
NCBI GI
BLAST score
                   280
                   5.0e-25
E value
                   128
Match length
                   46
% identity
```

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. ID

NCBI GI

Method



```
36043
Seq. No.
Seq. ID
                  LIB3051-017-Q1-E1-E2
Method
                  BLASTX
NCBI GI
                  g441457
                  297
BLAST score
                  3.0e-27
E value
                  69
Match length
                  81
% identity
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
                  36044
Seq. No.
Seq. ID
                  LIB3051-017-Q1-E1-F11
                  BLASTX
Method
                  g2245099
NCBI GI
                  364
BLAST score
                  9.0e-35
E value
                  138
Match length
                  54
% identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  36045
Seq. No.
                  LIB3051-017-Q1-E1-G7
Seq. ID
                  BLASTX
Method
                   g1177405
NCBI GI
                  136
BLAST score
                   6.0e-18
E value
                   115
Match length
                   46
% identity
                  (X89855) citrate binding protein [Hevea brasiliensis]
NCBI Description
                   36046
Seq. No.
Seq. ID
                  LIB3051-017-Q1-E1-H12
                   BLASTX
Method
NCBI GI
                   q4322421
                   238
BLAST score
                   5.0e-20
E value
                   133
Match length
                   41
% identity
                   (AF085230) cadmium resistance factor 1 [Arabidopsis
NCBI Description
                   thaliana]
                   36047
Seq. No.
                   LIB3051-018-Q1-E1-A1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2780193
                   58
BLAST score
                   7.0e-24
E value
                   154
Match length
% identity
                   Lupinus albus mRNA for adenine nucleotide translocator
NCBI Description
                   36048
Seq. No.
```

5488

LIB3051-018-Q1-E1-A3

BLASTX

g2655098

NCBI Description

```
BLAST score
                  2.0e-12
E value
Match length
                  72
                  53
% identity
                  (AF023472) peptide transporter [Hordeum vulgare]
NCBI Description
                  36049
Seq. No.
Seq. ID
                  LIB3051-018-Q1-E1-D1
                  BLASTX
Method
NCBI GI
                  q3075397
                  313
BLAST score
                  8.0e-29
E value
                  120
Match length
                  55
% identity
                  (AC004484) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  36050
Seq. ID
                  LIB3051-018-Q1-E1-D2
                  BLASTN
Method
                  g2370311
NCBI GI
BLAST score
                  148
                  1.0e-77
E value
                  321
Match length
                  86
% identity
NCBI Description Medicago sativa mRNA for DnaJ-like protein
                   36051
Seq. No.
Seq. ID
                  LIB3051-018-Q1-E1-E7
                  BLASTX
Method
                   g3912927
NCBI GI
                   141
BLAST score
E value
                   1.0e-08
Match length
                   115
                   33
% identity
NCBI Description (AF001308) hypothetical protein [Arabidopsis thaliana]
                   36052
Seq. No.
Seq. ID
                   LIB3051-018-Q1-E1-E9
                   BLASTN
Method
                   g18743
NCBI GI
                   68
BLAST score
E value
                   8.0e-30
                   188
Match length
                   85
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
                   36053
Seq. No.
Seq. ID
                   LIB3051-018-Q1-E1-F6
                   BLASTX
Method
NCBI GI
                   g3023305
BLAST score
                   142
                   9.0e-09
E value
                   98
Match length
% identity
                   41
```

alternative oxidase [Glycine max]

ALTERNATIVE OXIDASE 3 PRECURSOR >gi\_1946338 (U87907)



```
36054
Seq. No.
                  LIB3051-018-Q1-E1-H3
Seq. ID
Method
                  BLASTX
                  q4467095
NCBI GI
BLAST score
                  166
                  5.0e-13
E value
                  93
Match length
                  51
% identity
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                  36055
Seq. No.
                  LIB3051-018-Q1-E1-H6
Seq. ID
                  BLASTX
Method
                  q416731
NCBI GI
BLAST score
                  236
                  9.0e-20
E value
                  115
Match length
                  40
% identity
                  POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi_82655_pir__JQ1107
NCBI Description
                  18.3K protein precursor, pollen - maize
                  >gi_255569_bbs_113677 (S44171) pollen specific protein [Zea
                  mays=corn, Peptide, 170 aa] [Zea mays]
                  >qi 1588669 prf 2209273A Zm13 [Zea mays]
                  36056
Seq. No.
                  LIB3051-019-Q1-E1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3763918
                  172
BLAST score
                  1.0e-12
E value
Match length
                   63
% identity
                   57
                   (AC004450) putative isopropylmalate dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                   36057
Seq. No.
Seq. ID
                   LIB3051-019-Q1-E1-A8
                   BLASTN
Method
NCBI GI
                   g479059
                   184
BLAST score
E value
                   4.0e-99
                   368
Match length
% identity
                   G.max (Fiskeby V) mRNA for cysteine endopeptidase
NCBI Description
                   36058
Seq. No.
Seq. ID
                   LIB3051-019-Q1-E1-B11
                   BLASTX
Method
                   q4539423
NCBI GI
                   288
BLAST score
                   2.0e-27
E value
Match length
                   80
% identity
                   (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 36059



```
LIB3051-019-Q1-E1-B4
Seq. ID
                  BLASTX
Method
                  g2088651
NCBI GI
                  289
BLAST score
                  6.0e-26
E value
Match length
                  110
                  52
% identity
                   (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   36060
Seq. No.
                  LIB3051-019-Q1-E1-C3
Seq. ID
                  BLASTX
Method
                   q3643249
NCBI GI
                   296
BLAST score
                   7.0e-27
E value
Match length
                   123
% identity
                   49
                   (AF090143) thaumatin-like protein precursor Mdtl1 [Malus
NCBI Description
                   domestica]
Seq. No.
                   36061
                   LIB3051-019-Q1-E1-D4
Seq. ID
                   BLASTX
Method
                   g2829926
NCBI GI
                   151
BLAST score
                   9.0e-10
E value
Match length
                   53
                   62
% identity
                   (AC002291) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   36062
Seq. No.
                   LIB3051-019-Q1-E1-E6
Seq. ID
                   BLASTX
Method
                   g2244989
NCBI GI
                   165
BLAST score
                   2.0e-11
E value
                   79
Match length
% identity
                   52
                   (Z97340) strong similarity to naringenin 3-dioxygenase
NCBI Description
                   [Arabidopsis thaliana]
                   36063
Seq. No.
                   LIB3051-019-Q1-E1-F10
Seq. ID
                   BLASTX
Method
                   g2245032
NCBI GI
                   211
BLAST score
                   8.0e-17
E value
                   99
Match length
                   44
 % identity
                   (Z97342) gibberellin oxidase homolog [Arabidopsis thaliana]
NCBI Description
                   36064
 Seq. No.
                   LIB3051-019-Q1-E1-F3
 Seq. ID
                   BLASTX
Method
```

g2459412

418

NCBI GI BLAST score



```
4.0e-41
E value
                  141
Match length
                  56
% identity
                  (AC002332) putative G9a protein [Arabidopsis thaliana]
NCBI Description
                  36065
Seq. No.
                  LIB3051-019-Q1-E1-F5
Seq. ID
                  BLASTX
Method
                  q1351856
NCBI GI
                  205
BLAST score
                  4.0e-17
E value
                  76
Match length
                   62
% identity
                  ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
NCBI Description
                   (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase
                   [Cucurbita sp.]
                   36066
Seq. No.
                   LIB3051-019-Q1-K1-A8
Seq. ID
                  BLASTN
Method
                   g479059
NCBI GI
BLAST score
                   109
                   1.0e-54
E value
                   175
Match length
                   95
% identity
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
Seq. No.
                   36067
                   LIB3051-019-Q1-K1-D5
Seq. ID
                   BLASTN
Method
                   g2920665
NCBI GI
                   38
BLAST score
                   1.0e-12
E value
                   94
Match length
                   85
% identity
                   Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                   (GSTa) mRNA, complete cds
                   36068
Seq. No.
                   LIB3051-019-Q1-K1-E11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3461828
                   141
BLAST score
                   1.0e-08
E value
                   63
Match length
                   43
% identity
NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]
                   36069
Seq. No.
                   LIB3051-020-Q1-E1-A4
Seq. ID
                   BLASTN
Method
                   g2252639
NCBI GI
BLAST score
                   52
                   3.0e-20
E value
                   128
Match length
                   85
 % identity
```



## [Arabidopsis thaliana]

```
36070
Seq. No.
                  LIB3051-020-Q1-E1-B11
Seq. ID
                  BLASTX
Method
                  g2689720
NCBI GI
BLAST score
                  144
                  2.0e-09
E value
                  76
Match length
                  37
% identity
                  (AF037168) DnaJ homologue [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  36071
                  LIB3051-020-Q1-E1-D4
Seq. ID
                  BLASTX
Method
                   g4335731
NCBI GI
                   357
BLAST score
                   6.0e-34
E value
                   142
Match length
                   49
% identity
                  (AC006248) putative polyprotein [Arabidopsis thaliana]
NCBI Description
                   36072
Seq. No.
                   LIB3051-020-Q1-E1-D6
Seq. ID
                   BLASTX
Method
                   g2499555
NCBI GI
                   336
BLAST score
E value
                   7.0e-33
Match length
                   139
                   58
% identity
                   PHYTOCHROME TYPE A >gi_1848273 (U84970) phytochrome type A
NCBI Description
                   [Lathyrus sativus]
Seq. No.
                   36073
                   LIB3051-020-Q1-E1-E9
Seq. ID
                   BLASTX
Method
                   g1076331
NCBI GI
                   292
BLAST score
                   1.0e-26
E value
                   77
Match length
                   73
 % identity
                   histidine transport protein - Arabidopsis thaliana
NCBI Description
                   >gi_510238_emb_CAA54634_ (X77503) oligopeptide transporter
                   1-1 [Arabidopsis thaliana] >gi_744157_prf__2014244A His
                   transporter [Arabidopsis thaliana]
                   36074
 Seq. No.
                   LIB3051-020-Q1-E1-F3
 Seq. ID
                   BLASTN
 Method
                   g791097
 NCBI GI
                   126
 BLAST score
                   2.0e-64
 E value
                   323
 Match length
                   89
 % identity
 NCBI Description P.vulgaris plsB mRNA
```

36075

Seq. No.

NCBI GI

E value

BLAST score



```
LIB3051-022-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244827
BLAST score
                  158
E value
                  3.0e-11
Match length
                  57
% identity
                  32
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  36076
Seq. No.
Seq. ID
                  LIB3051-022-Q1-K1-G1
Method
                  BLASTN
NCBI GI
                  q516853
BLAST score
                  91
                  7.0e-44
E value
Match length
                  131
% identity
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
Seq. No.
                  36077
Seq. ID
                  LIB3051-023-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  q3953478
                  495
BLAST score
                  3.0e-50
E value
                  129
Match length
% identity
                  76
NCBI Description (AC002328) F2202.23 [Arabidopsis thaliana]
Seq. No.
                  36078
Seq. ID
                  LIB3051-023-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  q3123230
BLAST score
                  267
E value
                  2.0e-23
Match length
                  138
% identity
                  38
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT
NCBI Description
                  (EIF-3 BETA) (EIF3 P116) (EIF3 P110) >gi 2558668 (U78525)
                  eukaryotic translation initiation factor [Homo sapiens]
                  36079
Seq. No.
                 LIB3051-023-Q1-K1-B5
Seq. ID
                  BLASTX
Method
                  g1911166
NCBI GI
BLAST score
                  492
                  7.0e-50
E value
Match length
                  126
% identity
NCBI Description (X94400) soluble-starch-synthase [Solanum tuberosum]
Seq. No.
                  36080
Seq. ID
                  LIB3051-023-Q1-K1-C1
Method
                  BLASTX
```

g3075391

7.0e-43



```
Match length
                  71
% identity
                  (AC004484) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  36081
Seq. ID
                  LIB3051-023-Q1-K1-C2
                  BLASTX
Method
                  g2117303
NCBI GI
                  144
BLAST score
                  4.0e-09
E value
                  51
Match length
                  59
% identity
                  (Z95620) n-acetylglucosaminyl-phosphatidylinositol
NCBI Description
                  [Schizosaccharomyces pombe]
Seq. No.
                  36082
                  LIB3051-023-Q1-K1-C3
Seq. ID
                  BLASTN
Method
                  g1305548
NCBI GI
                  57
BLAST score
                  1.0e-23
E value
Match length
                  89
% identity
                  91
NCBI Description Glycine max asparagine synthetase mRNA, complete cds
                  36083
Seq. No.
                  LIB3051-023-Q1-K1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g18743
                  99
BLAST score
                  2.0e-48
E value
Match length
                  273
                  85
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
                   36084
Seq. No.
Seq. ID
                  LIB3051-023-Q1-K1-E1
Method
                  BLASTX
                   g134194
NCBI GI
BLAST score
                   273
E value
                   2.0e-24
Match length
                   86
                   63
% identity
                   STRESS-INDUCED PROTEIN SAM22 >gi 99918 pir S20518
NCBI Description
                   hypothetical protein - soybean >gi 18744_emb CAA42646_
                   (X60043) ORF [Glycine max]
                   36085
Seq. No.
                   LIB3051-023-Q1-K1-F9
Seq. ID
                   BLASTN
Method
NCBI GI
                   q18764
BLAST score
                   80
```

4.0e-37 E value Match length 288 % identity

NCBI Description G.max tefS1 gene for elongation factor EF-1a

NCBI GI

BLAST score



```
Seq. No.
                  LIB3051-023-Q1-K1-G11
Seq. ID
                  BLASTX
Method
                  g1197461
NCBI GI
                   406
BLAST score
                   2.0e-43
E value
                   93
Match length
                   92
% identity
                  (X78819) casein kinase I [Arabidopsis thaliana]
NCBI Description
                   36087
Seq. No.
                   LIB3051-023-Q1-K1-G2
Seq. ID
                   BLASTX
Method
                   q3603353
NCBI GI
BLAST score
                   187
                   4.0e-14
E value
                   108
Match length
                   41
% identity
                   (AF074843) peroxisomal targeting signal type 1 receptor
NCBI Description
                   [Arabidopsis thaliana]
                   36088
Seq. No.
Seq. ID
                   LIB3051-024-Q1-K1-C2
                   BLASTN
Method
                   g18743
NCBI GI
                   153
BLAST score
                   7.0e-81
E value
                   205
Match length
                   95
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
                   36089
Seq. No.
Seq. ID
                   LIB3051-024-Q1-K1-D3
Method
                   BLASTX
                   g3450842
NCBI GI
BLAST score
                   199
                   5.0e-16
E value
                   59
Match length
% identity
                   (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   36090
                   LIB3051-024-Q1-K1-E6
Seq. ID
                   BLASTN
Method
                   q456713
NCBI GI
BLAST score
                   294
                   1.0e-164
E value
                   381
Match length
                   28
% identity
                   Glycine max gene for ubiquitin, complete cds
NCBI Description
                   36091
Seq. No.
Seq. ID
                   LIB3051-024-Q1-K1-H10
Method
                   BLASTX
```

g4415936

NCBI Description



```
3.0e-10
E value
Match length
                   41
                   63
% identity
                  (AC006418) unknown protein [Arabidopsis thaliana]
NCBI Description
                   36092
Seq. No.
                  LIB3051-025-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3122264
BLAST score
                   290
                   4.0e-26
E value
                   123
Match length
                   43
% identity
                   PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA
NCBI Description
                   SUBUNIT (EIF-3 ALPHA) (EIF3 P150) >gi_2281117 (U49332)
                   150-kD protein [Dictyostelium discoideum]
                   36093
Seq. No.
                   LIB3051-025-Q1-K1-A6
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4102858
                   35
BLAST score
                   2.0e-10
E value
                   55
Match length
                   91
% identity
                   Populus tremuloides cytoplasmic superoxide dismutase 1
NCBI Description
                   (SODcyt1) mRNA, complete cds
                   36094
Seq. No.
                   LIB3051-025-Q1-K1-B1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1561774
                   449
BLAST score
                   1.0e-44
E value
                   134
Match length
                   78
% identity
NCBI Description (U67426) malate dehydrogenase [Vitis vinifera]
                   36095
Seq. No.
Seq. ID
                   LIB3051-025-Q1-K1-B5
                   BLASTN
Method
NCBI GI
                   g3821780
BLAST score
                   36
E value
                   1.0e-10
Match length
                   39
                   62
% identity
                   Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   36096
Seq. No.
                   LIB3051-025-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4376650
BLAST score
                   141
                   1.0e-08
E value
Match length
                   49
% identity
                   55
```

(AE001621) GcpE Protein [Chlamydia pneumoniae]



```
36097
Seq. No.
                  LIB3051-025-Q1-K1-F8
Seq. ID
                  BLASTN
Method
                  g1752733
NCBI GI
                  80
BLAST score
                   5.0e-37
E value
                   320
Match length
                   82
% identity
                  Glycine max mRNA for beta-glucan-elicitor receptor,
NCBI Description
                   complete cds
                   36098
Seq. No.
                   LIB3051-026-Q1-K1-A11
Seq. ID
                   BLASTN
Method
                   g456713
NCBI GI
                   149
BLAST score
                   2.0e-78
E value
                   251
Match length
                   34
% identity
NCBI Description Glycine max gene for ubiquitin, complete cds
Seq. No.
                   36099
                   LIB3051-026-Q1-K1-B4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g18521
                   207
BLAST score
E value
                   1.0e-113
                   381
Match length
                   57
% identity
                   Soybean 5S rDNA gene for 5S rRNA
NCBI Description
Seq. No.
                   36100
                   LIB3051-026-Q1-K1-C3
Seq. ID
Method
                   BLASTN
                   g18743
NCBI GI
                   76
BLAST score
                   1.0e-34
E value
                   348
Match length
                   81
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
Seq. No.
                   36101
                   LIB3051-026-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   g3879531
NCBI GI
                   154
BLAST score
E value
                   3.0e-10
                   104
Match length
                   33
% identity
```

NCBI Description

on (Z49130) cDNA EST EMBL:M75904 comes from this gene; cDNA EST EMBL:Z14422 comes from this gene; cDNA EST EMBL:Z14423 comes from this gene; cDNA EST EMBL:D76244 comes from this

gene; cDNA EST EMBL:D73235 comes from this gene; cDN

Seq. No. 36102

Seq. ID LIB3051-026-Q1-K1-D1



```
Method
                  BLASTX
NCBI GI
                  g1788928
                  155
BLAST score
E value
                  2.0e-14
Match length
                  109
% identity
                  44
NCBI Description
                  (AE000344) quinolinate synthetase, B protein [Escherichia
                  36103
Seq. No.
Seq. ID
                  LIB3051-026-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  q2828294
BLAST score
                  383
E value
                  5.0e-37
Match length
                  107
% identity
                  77
NCBI Description
                  (AL021687) putatative protein [Arabidopsis thaliana]
Seq. No.
                  36104
Seq. ID
                  LIB3051-026-Q1-K1-E11
Method
                  BLASTN
                  g2654121
NCBI GI
BLAST score
                  54
                  2.0e-21
E value
Match length
                  118
% identity
                  86
                  Arabidopsis thaliana ribosomal protein L23a (AtrpL23a)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  36105
Seq. ID
                  LIB3051-026-Q1-K1-H7
                  BLASTN
Method
NCBI GI
                  q2661014
BLAST score
                  96
E value
                  8.0e-47
Match length
                  212
% identity
                  86
NCBI Description
                  Glycine max catalase (cat1) mRNA, complete cds
                  36106
Seq. No.
Seq. ID
                  LIB3051-027-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g2829910
BLAST score
                  462
E value
                  3.0e-46
Match length
                  141
% identity
                  16
NCBI Description
                  (AC002291) Unknown protein, contains regulator of
                  chromosome condensation motifs [Arabidopsis thaliana]
Seq. No.
                  36107
Seq. ID
                  LIB3051-027-Q1-K1-A8
```

Method BLASTX
NCBI GI 93551247
BLAST score 338
E value 1.0e-31

```
Match length
% identity
                  99
                  (AB012703) 181 [Daucus carota]
NCBI Description
                  36108
Seq. No.
Seq. ID
                  LIB3051-027-Q1-K1-B5
Method
                  BLASTX
                  g4544404
NCBI GI
BLAST score
                  336
                  2.0e-31
E value
                  106
Match length
% identity
                  67
                  (AC007047) unknown protein [Arabidopsis thaliana]
NCBI Description
                  36109
Seq. No.
Seq. ID
                  LIB3051-027-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g2245071
BLAST score
                  194
E value
                  8.0e-15
Match length
                  78
% identity
                  55
                  (Z97342) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  36110
                  LIB3051-028-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914019
BLAST score
                  142
E value
                  7.0e-13
Match length
                  55
                  75
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi 2305014
                   (AF004317) S-adenosyl-L-methionine synthetase homolog [Musa
                  acuminata]
Seq. No.
                  36111
Seq. ID
                  LIB3051-028-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  g1514643
BLAST score
                  318
E value
                   9.0e-30
Match length
                  81
% identity
                   67
NCBI Description
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
```

Seq. No. 36112

Seq. ID LIB3051-028-Q1-K1-C11

Method BLASTN
NCBI GI g303900
BLAST score 310
E value 1.0e-174
Match length 382
% identity 33

NCBI Description Soybean gene for ubiquitin, complete cds

```
Seq. No.
                  LIB3051-028-Q1-K1-C9
Seq. ID
                  BLASTX
Method
                  g544015
NCBI GI
                  171
BLAST score
                  2.0e-12
E value
Match length
                  80
% identity
                  ENDOCHITINASE PRECURSOR >gi_2118033_pir__S59947 chitinase
NCBI Description
                   (EC 3.2.1.14) Al precursor - garden pea
                  >gi_20687_emb_CAA45359_ (X63899) chitinase [Pisum sativum]
Seq. No.
                  LIB3051-028-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                  q1168410
NCBI GI
                   184
BLAST score
E value
                   4.0e-14
                   70
Match length
                   59
% identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 2
NCBI Description
                   >gi_2118267_pir__S58167 fructose-bisphosphate aldolase (EC
                   4.1.2.13) - garden pea >gi 927505_emb_CAA61947 (X89829)
                   fructose-1,6-bisphosphate aldolase [Pisum sativum]
Seq. No.
                   36115
                   LIB3051-028-Q1-K1-E2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4490313
                   236
BLAST score
                   1.0e-23
E value
                   122
Match length
                   57
% identity
                   (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   36116
                   LIB3051-028-Q1-K1-E8
Seq. ID
Method
                   BLASTX
                   q2465923
NCBI GI
                   198
BLAST score
                   3.0e-15
E value
                   97
Match length
                   44
 % identity
                   (AF024648) receptor-like serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
                   36117
 Seq. No.
                   LIB3051-028-Q1-K1-G12
 Seq. ID
                   BLASTX
Method
                   g2160161
 NCBI GI
                   163
 BLAST score
                   3.0e-11
E value
                   117
Match length
 % identity
                   (AC000132) F21M12.7 gene product [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   36118
```

```
LIB3051-028-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                  g3953470
NCBI GI
                  243
BLAST score
                  2.0e-20
E value
                  77
Match length
                  65
% identity
NCBI Description (AC002328) F20N2.15 [Arabidopsis thaliana]
                   36119
Seq. No.
                  LIB3051-028-Q1-K1-G4
Seq. ID
                  BLASTN
Method
                  q18644
NCBI GI
                   39
BLAST score
                   4.0e-13
E value
                   67
Match length
                   90
% identity
NCBI Description Soybean mRNA for HMG-1 like protein
                   36120
Seq. No.
                   LIB3051-028-Q1-K1-H1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1675195
                   49
BLAST score
                   9.0e-19
E value
                   185
Match length
                   82
% identity
                   Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
NCBI Description
                   complete cds
                   36121
Seq. No.
                   LIB3051-028-Q1-K1-H9
Seq. ID
Method
                   BLASTX
                   g1504008
NCBI GI
                   246
BLAST score
                   7.0e-21
E value
                   124
Match length
                   42
 % identity
                   (D86967) Containing ATP/GTP-binding site motif A(P-loop):
 NCBI Description
                   Similar to C.elegans protein(P1:CEC47E128); Similar to Mouse
                   alpha-mannosidase(P1:B54407) [Homo sapiens]
                   36122
 Seq. No.
                   LIB3051-029-Q1-K1-A5
 Seq. ID
                   BLASTX
 Method
                   g3242783
 NCBI GI
 BLAST score
                   155
                   3.0e-10
 E value
                   38
 Match length
                   74
 % identity
                   (AF055354) respiratory burst oxidase protein B [Arabidopsis
 NCBI Description
                   thaliana]
                    36123
 Seq. No.
                   LIB3051-029-Q1-K1-C10
 Seq. ID
                    BLASTX
 Method
```

5502

q1730560

NCBI GI

E value

Match length

3.0e-27

```
BLAST score
E value
                  8.0e-41
Match length
                  117
                  66
% identity
                 ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
NCBI Description
                  H) >gi_510932_emb_CAA84494_ (Z35117) alpha 1,4-glucan
                  phosphorylase type H [Vicia faba]
Seq. No.
                  36124
                  LIB3051-029-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2244973
BLAST score
                  197
E value
                  2.0e-15
Match length
                  79
% identity
                  57
NCBI Description (Z97340) similarity to extensin class 1 protein
                  [Arabidopsis thaliana]
Seq. No.
                  36125
Seq. ID
                  LIB3051-029-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g4567314
BLAST score
                  166
E value
                  1.0e-11
Match length
                  36
                  86
% identity
NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  36126
Seq. ID
                  LIB3051-029-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g3421104
BLAST score
                  352
                  2.0e-33
E value
Match length
                  83
% identity
                  81
NCBI Description
                  (AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis
                  thaliana]
                  36127
Seq. No.
Seq. ID
                  LIB3051-029-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g4200044
BLAST score
                  217
E value
                  1.0e-17
Match length
                  63
% identity
                  60
NCBI Description (AB022732) cytochrome P450 [Glycyrrhiza echinata]
Seq. No.
                  36128
Seq. ID
                  LIB3051-030-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  q3915022
BLAST score
                  299
```

% identity 53
NCBI Description SUCROSE-PHOSPHATE SYNTHASE 2

(UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 2) >gi 2190350 emb CAA72491 (Y11795) sucrose-phosphate

synthase [Craterostigma plantagineum]

Seq. No. 36129

Seq. ID LIB3051-030-Q1-K1-A7

Method BLASTX
NCBI GI g2529663
BLAST score 526
E value 7.0e-54
Match length 119
% identity 78

NCBI Description (AC002535) putative lysophospholipase [Arabidopsis

thaliana] >gi\_3738277 (AC005309) putative lysophospholipase

[Arabidopsis thaliana]

Seq. No. 36130

Seq. ID LIB3051-030-Q1-K1-B10

Method BLASTX
NCBI GI g2341035
BLAST score 174
E value 9.0e-13
Match length 62
% identity 52

NCBI Description (AC000104) Match to Arabidopsis photolysase (PHH1) gene

(gb X99061) and cryptochrome 2 apoprotein (CRY2)

(gb\_U43397). ESTs gb\_W43661 and gb\_Z25638 come from this

gene. [Arabidopsis thaliana]

Seq. No. 36131

Seq. ID LIB3051-030-Q1-K1-B5

Method BLASTN
NCBI GI g3928141
BLAST score 124
E value 3.0e-63
Match length 324
% identity 85

NCBI Description Cicer arietinum mRNA for protein phosphatase

Seq. No. 36132

Seq. ID LIB3051-030-Q1-K1-C12

Method BLASTX
NCBI GI g417060
BLAST score 157
E value 2.0e-10
Match length 84
% identity 45

NCBI Description GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA

LIGASE) (GS) >gi\_170637 (M94765) glutamine synthetase [Vigna aconitifolia] >gi\_1094850\_prf\_\_2106409A Gln

synthetase [Vigna aconitifolia]

Seq. No. 36133

Seq. ID LIB3051-030-Q1-K1-E4

Method BLASTX

Seq. ID Method

NCBI GI

```
NCBI GI
                   g3047117
                  490
BLAST score
E value
                  1.0e-49
                  94
Match length
                  97
% identity
                  (AF058919) similar to ATP-dependent RNA helicases
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  36134
                  LIB3051-030-Q1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2642237
BLAST score
                   74
E value
                  2.0e-33
                  221
Match length
% identity
                  Glycine max endoplasmic reticulum HSC70-cognate binding
NCBI Description
                  protein precursor (BIP) mRNA, complete cds
Seq. No.
                   36135
                  LIB3051-030-Q1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1208536
BLAST score
                  178
                  1.0e-95
E value
                  198
Match length
                   97
% identity
                  Glycine max guanine nucleotide regulatory protein (rab2)
NCBI Description
                  mRNA, complete cds
Seq. No.
                   36136
                  LIB3051-031-Q1-K1-A10
Seq. ID
                   BLASTX
Method
NCBI GI
                  q2598589
BLAST score
                   190
E value
                   2.0e-14
Match length
                  100
% identity
                   45
                  (Y15367) MtN19 [Medicago truncatula]
NCBI Description
Seq. No.
                   36137
                  LIB3051-031-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2393910
BLAST score
                   239
E value
                   3.0e-20
Match length
                  121
                   41
% identity
NCBI Description
                  (AF008308) arginine regulatory protein [Pseudomonas
                   aeruginosa] >gi_2654608 (AF011922) ArgR regulatory protein
                   [Pseudomonas aeruginosa] >gi_2668600 (AF012537) ArgR
                   [Pseudomonas aeruginosa]
Seq. No.
                   36138
```

LIB3051-031-Q1-K1-A5

BLASTX

g4204304

E value

Match length

2.0e-32

```
BLAST score
                  2.0e-17
E value
Match length
                  71
% identity
                  58
NCBI Description
                  (AC003027) 1cl prt seq No definition line found
                  [Arabidopsis thaliana]
                  36139
Seq. No.
                  LIB3051-031-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3915737
BLAST score
                  386
E value
                  2.0e-37
Match length
                  97
% identity
                  49
                  IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (KAP
NCBI Description
                  ALPHA) >gi_3228370 (AF017252) importin alpha [Lycopersicon
                  esculentum]
Seq. No.
                  36140
Seq. ID
                  LIB3051-031-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  g1449179
BLAST score
                  255
E value
                  4.0e-22
                  83
Match length
                  61
% identity
                  (D86506) N-ethylmaleimide sensitive fusion protein
NCBI Description
                  [Nicotiana tabacum]
Seq. No.
                  36141
Seq. ID
                  LIB3051-031-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  q3402699
BLAST score
                  257
E value
                  3.0e-24
Match length
                  80
                  70
% identity
NCBI Description (AC004261) unknown protein [Arabidopsis thaliana]
                  36142
Seq. No.
                  LIB3051-031-Q1-K1-D2
Seq. ID
Method
                  BLASTX
                  g285741
NCBI GI
BLAST score
                  153
E value
                  5.0e-10
                  80
Match length
% identity
                  42
NCBI Description (D14550) EDGP precursor [Daucus carota]
Seq. No.
                  36143
Seq. ID
                  LIB3051-031-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g4510376
BLAST score
                  208
```

```
% identity
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
                  36144
Seq. No.
                  LIB3051-031-Q1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4262224
                  165
BLAST score
                   1.0e-11
E value
                   79
Match length
                   57
% identity
                   (AC006200) putative amino acid or GABA permease
NCBI Description
                   [Arabidopsis thaliana]
                   36145
Seq. No.
                   LIB3051-031-Q1-K1-F12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1513298
                   292
BLAST score
                   2.0e-26
E value
                   116
Match length
                   47
% identity
NCBI Description (U66526) AbcA [Dictyostelium discoideum]
                   36146
Seq. No.
                   LIB3051-031-Q1-K1-F6
Seq. ID
                   BLASTX
Method
                   q2462822
NCBI GI
BLAST score
                   424
E value
                   7.0e-42
                   125
Match length
                   64
% identity
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   36147
Seq. No.
                   LIB3051-031-Q1-K1-G5
 Seq. ID
                   BLASTX
Method
                   q3355486
NCBI GI
BLAST score
                   125
                   6.0e-11
E value
                   60
Match length
                   58
 % identity
                   (AC004218) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   36148
 Seq. No.
                   LIB3051-031-Q1-K1-H6
 Seq. ID
                   BLASTN
 Method
                    g3821780
 NCBI GI
 BLAST score
                    36
                    9.0e-11
 E value
                    37
 Match length
                    61
 % identity
 NCBI Description Xenopus laevis cDNA clone 27A6-1
                    36149
 Seq. No.
                    LIB3051-032-Q1-K1-A1
 Seq. ID
                    BLASTX
 Method
```

NCBI GI

BLAST score

```
NCBI GI
                   g2924515
BLAST score
                   205
                   3.0e-16
E value
Match length
                   52
% identity
                   81
NCBI Description
                   (AL022023) putative protein [Arabidopsis thaliana]
                   36150
Seq. No.
Seq. ID
                   LIB3051-032-Q1-K1-C1
Method
                   BLASTX
NCBI GI
                   q4038037
BLAST score
                   176
                   6.0e-17
E value
                   85
Match length
% identity
                  (AC005936) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   36151
Seq. ID
                   LIB3051-032-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   g3402699
                   432
BLAST score
                   9.0e-43
E value
                   123
Match length
                   69
% identity
NCBI Description
                  (AC004261) unknown protein [Arabidopsis thaliana]
Seq. No.
                   36152
                   LIB3051-032-Q1-K1-D6
Seq. ID
Method
                   BLASTX
                   g3800878
NCBI GI
BLAST score
                   150
                   1.0e-09
E value
Match length
                   62
% identity
                   50
                   (AF096281) threonine dehydratase/deaminase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   36153
                   LIB3051-032-Q1-K1-D9
Seq. ID
Method
                   BLASTX
                   g1502430
NCBI GI
BLAST score
                   295
                   9.0e-27
E value
Match length
                   95
                   59
% identity
NCBI Description
                   (U62331) phosphate transporter [Arabidopsis thaliana]
                   >gi_2564661 (AF022872) phosphate transporter [Arabidopsis
                   thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770)
                   phosphate transporter, AtPT2 [Arabidopsis thaliana]
Seq. No.
                   36154
Seq. ID
                   LIB3051-032-Q1-K1-E3
Method
                   BLASTX
```

g2194131

```
E value
Match length
                  132
% identity
NCBI Description (AC002062) Similar to Synechocystis antiviral protein
                  (gb D90917). [Arabidopsis thaliana]
                  36155
Seq. No.
                  LIB3051-032-Q1-K1-F3
Seq. ID
Method
                  BLASTN
                  g3873174
NCBI GI
BLAST score
                  71
                  1.0e-31
E value
Match length
                  239
% identity
                  82
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14N23,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  36156
                  LIB3051-032-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006876
BLAST score
                  157
E value
                  2.0e-10
Match length
                  89
% identity
                  53
NCBI Description (Z99707) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  36157
Seq. ID
                  LIB3051-032-Q1-K1-H5
                  BLASTX
Method
NCBI GI
                  g3193292
BLAST score
                  335
                  8.0e-36
E value
                  107
Match length
                  78
% identity
NCBI Description
                 (AF069298) similar to ATPases associated with various
                  cellular activites (Pfam: AAA.hmm, score: 230.91)
                  [Arabidopsis thaliana]
```

Seq. No. 36158

Seq. ID LIB3051-032-Q1-K1-H9

Method BLASTN
NCBI GI g2765090
BLAST score 37
E value 2.0e-11
Match length 65
% identity 89

NCBI Description Glycine max mRNA for cytochrome P450-like protein, clone

CP6

Seq. No. 36159

Seq. ID LIB3051-033-Q1-K1-C10

Method BLASTX
NCBI GI g2664214
BLAST score 254
E value 6.0e-22
Match length 120

```
NCBI Description
                 (AJ222646) G2484-1 [Arabidopsis thaliana]
```

LIB3051-034-Q1-K1-D10 Seq. ID Method BLASTX NCBI GI g2739387 155 BLAST score E value 3.0e-10 Match length 129 % identity 40

36160

NCBI Description (AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No. 36161 Seq. ID LIB3051-034-Q1-K1-F4 Method BLASTX NCBI GI g3980413 BLAST score 205

E value 4.0e-16 Match length 141 % identity 40

% identity

Seq. No.

NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No. 36162

Seq. ID LIB3051-034-Q1-K1-H1

Method BLASTX g3776567 NCBI GI 144 BLAST score 6.0e-09 E value Match length 45 % identity 62

(AC005388) Strong similarity to F21B7.33 gi 2809264 from A. NCBI Description

thaliana BAC gb AC002560. EST gb N65119 comes from this

gene. [Arabidopsis thaliana]

Seq. No. 36163

LIB3051-034-Q1-K1-H2 Seq. ID

Method BLASTN NCBI GI g170007 BLAST score 354 0.0e + 00E value 357 Match length % identity 100

NCBI Description Soybean 18 kD late embryogenesis abundant (Lea) protein

mRNA, complete cds

Seq. No. 36164

Seq. ID LIB3051-035-Q1-K1-C3

Method BLASTX NCBI GI q3874155 BLAST score 252 E value 1.0e-21 Match length 93 51 % identity

(Z73103) Similarity to Yeast ATP-dependent RNA helicase NCBI Description

(SW:SUV3 YEAST); cDNA EST EMBL:T01340 comes from this gene;

cDNA EST yk244e10.3 comes from this gene; cDNA EST

```
yk213b9.3 comes from this gene; cDNA EST yk244e10.5 comes
Seq. No.
                  36165
                  LIB3051-035-Q1-K1-C5
Seq. ID
                 BLASTN
```

Method NCBI GI g4097568 BLAST score 125 6.0e-64 E value Match length 165 % identity 94

NCBI Description Glycine max farnesylated protein GMFP4 mRNA, partial cds

Seq. No. Seq. ID LIB3051-035-Q1-K1-D1 Method BLASTN NCBI GI g451192 BLAST score 139 3.0e-72 E value Match length 329 % identity 86

NCBI Description Triticum aestivum (wali7) mRNA, 3' end, partial cds

36167 Seq. No. LIB3051-035-Q1-K1-E3 Seq. ID BLASTX Method NCBI GI g3935138

36166

BLAST score 171 4.0e-12 E value Match length 74 % identity 41

NCBI Description (AC005106) T25N20.2 [Arabidopsis thaliana]

Seq. No. 36168

LIB3051-035-Q1-K1-E8 Seq. ID

Method BLASTX NCBI GI g3097321 BLAST score 223 E value 3.0e-18 Match length 86 52 % identity

NCBI Description (AB013289) Bd 30K [Glycine max]

36169 Seq. No.

Seq. ID LIB3051-035-Q1-K1-F2

Method BLASTX NCBI GI g2342679 BLAST score 169 E value 3.0e-12 Match length 44 70 % identity

NCBI Description (AC000106) Similar to Vicia sativa ENBP1 (gb X95995).

[Arabidopsis thaliana]

Seq. No. 36170

Seq. ID LIB3051-035-Q1-K1-F6

Method BLASTX

```
q3047117
NCBI GI
                  654
BLAST score
                  1.0e-68
E value
                  149
Match length
                  83
% identity
                   (AF058919) similar to ATP-dependent RNA helicases
NCBI Description
                   [Arabidopsis thaliana]
                  36171
Seq. No.
                  LIB3051-035-Q1-K1-H10
Seq. ID
                  BLASTX
Method
                  g3176709
NCBI GI
                   157
BLAST score
                   2.0e-10
E value
                   144
Match length
                   30
% identity
                   (AC002392) putative anthranilate
NCBI Description
                   N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis
                   thaliana]
                   36172
Seq. No.
                   LIB3051-036-Q1-K1-B11
Seq. ID
                   BLASTN
Method
                   q170053
NCBI GI
                   166
BLAST score
                   2.0e-88
E value
                   190
Match length
                   97
% identity
                  Soybean ribosomal protein S11 mRNA, 3' end
NCBI Description
                   36173
Seq. No.
Seq. ID
                   LIB3051-036-Q1-K1-C11
                   BLASTX
Method
                   q464367
NCBI GI
                   157
BLAST score
                   4.0e-11
E value
                   53
Match length
                   64
% identity
                   POLYGALACTURONASE INHIBITOR PRECURSOR
NCBI Description
                   (POLYGALACTURONASE-INHIBITING PROTEIN)
                   >gi 543660_pir__JQ2262 Polygalacturonase inhibitor
                   precursor - Pyrus communis >gi_169684 (L09264)
                   polygalacturonase inhibitor [Pyrus communis]
Seq. No.
                   36174
Seq. ID
                   LIB3051-036-Q1-K1-C6
Method
                   BLASTX
                   q542175
NCBI GI
                   174
BLAST score
                   9.0e-19
E value
                   112
Match length
% identity
                   47
                   endoxyloglucan transferase - wheat >gi_469511_dbj_BAA03924_
NCBI Description
                   (D16457) endo-xyloglucan transferase [Triticum aestivum]
Seq. No.
                   36175
                   LIB3051-036-Q1-K1-D11
Seq. ID
```

```
BLASTX
Method
                  q1657617
NCBI GI
                   284
BLAST score
                   1.0e-25
E value
                   80
Match length
% identity
                   68
                   (U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236)
NCBI Description
                   putative nuclear DNA-binding protein G2p [Arabidopsis
                   thaliana]
Seq. No.
                   36176
                   LIB3051-036-Q1-K1-E3
Seq. ID
Method
                   BLASTX
                   g2462925
NCBI GI
BLAST score
                   232
                   3.0e-19
E value
                   112
Match length
% identity
                   53
                   (AJ000053) GTP cyclohydrolase II /
NCBI Description
                   3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis
                   thaliana]
Seq. No.
                   36177
                   LIB3051-036-Q1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4262224
BLAST score
                   151
E value
                   1.0e-12
Match length
                   142
                   35
% identity
                   (AC006200) putative amino acid or GABA permease
NCBI Description
                   [Arabidopsis thaliana]
                   36178
Seq. No.
                   LIB3051-036-Q1-K1-H4
Seq. ID
                   BLASTX
Method
                   g3738325
NCBI GI
                   149
BLAST score
                   6.0e-10
E value
                   34
Match length
                   82
% identity
                   (AC005170) putative CaMB-channel protein [Arabidopsis
NCBI Description
                   thaliana]
                   36179
Seq. No.
                   LIB3051-037-Q1-K1-B11
Seq. ID
                   BLASTX
Method
                   q1107526
NCBI GI
                   170
BLAST score
                   4.0e-12
E value
                   90
Match length
                   47
 % identity
                   (X87931) SIEP1L protein [Beta vulgaris]
 NCBI Description
                   36180
 Seq. No.
 Seq. ID
                   LIB3051-037-Q1-K1-B3
                   BLASTX
 Method
```

```
g2828280
NCBI GI
                   555
BLAST score
E value
                   3.0e-57
                   119
Match length
                   87
% identity
                   (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi 2832633_emb_CAA16762_ (AL021711) putative protein
                   [Arabidopsis thaliana]
                   36181
Seq. No.
Seq. ID
                   LIB3051-037-Q1-K1-F11
                   BLASTX
Method
                   g3789942
NCBI GI
                   122
BLAST score
                   5.0e-09
E value
                   98
Match length
% identity
                   11
                   (AF093505) polyubiquitin [Saccharum hybrid cultivar
NCBI Description
                   H32-8560]
                   36182
Seq. No.
                   LIB3051-037-Q1-K1-F12
Seq. ID
                   {\tt BLASTX}
Method
                   g2160161
NCBI GI
                   221
BLAST score
                   5.0e-18
E value
                   129
Match length
                   5
% identity
                  (AC000132) F21M12.7 gene product [Arabidopsis thaliana]
NCBI Description
                   36183
Seq. No.
Seq. ID
                   LIB3051-037-Q1-K1-F6
                   BLASTX
Method
                   q2191129
NCBI GI
                   259
BLAST score
                   1.0e-22
E value
Match length
                   77
                   65
% identity
                   (AF007269) similar to SPF1 DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   36184
Seq. No.
Seq. ID
                   LIB3051-037-Q1-K1-F7
Method
                   BLASTX
                   q2765093
NCBI GI
                   265
BLAST score
E value
                   3.0e-23
                   70
Match length
% identity
                   (Y10983) putative cytochrome P450 [Glycine max]
NCBI Description
Seq. No.
                   36185
                   LIB3051-037-Q1-K1-G2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4432811
BLAST score
                   45
E value
                   4.0e-16
```

```
Match length
% identity
                  87
NCBI Description Arabidopsis thaliana chromosome II BAC F16D14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  36186
Seq. No.
Seq. ID
                  LIB3051-037-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  q3738325
BLAST score
                  169
E value
                  5.0e-12
Match length
                  92
% identity
                  43
                  (AC005170) putative CaMB-channel protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  36187
Seq. ID
                  LIB3051-038-Q1-K1-A11
Method
                  BLASTX
                  g4220522
NCBI GI
BLAST score
                  188
                  2.0e-14
E value
                  70
Match length
                  46
% identity
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                  36188
Seq. No.
Seq. ID
                  LIB3051-038-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  q497896
BLAST score
                  429
                  2.0e-42
E value
Match length
                  125
% identity
NCBI Description (D12921) transcription factor HBP-1b(c1) [Triticum
                  aestivum]
Seq. No.
                  36189
Seq. ID
                  LIB3051-038-Q1-K1-B10
Method
                  BLASTN
NCBI GI
                  g1834452
                  66
BLAST score
                  1.0e-28
E value
Match length
                  146
                  97
% identity
NCBI Description G.max mRNA for alpha subunit of G protein
Seq. No.
                  36190
Seq. ID
                  LIB3051-038-Q1-K1-C9
```

25

Method BLASTX
NCBI GI g4033446
BLAST score 297
E value 6.0e-27
Match length 129
% identity 45

NCBI Description AGGLUTININ II PRECURSOR (CLAII) (LECCLAII)

>gi\_2147661\_pir\_\_S72502 mannose/glucose-binding lectin

% identity

49

CLAII precursor - Cladrastis lutea >gi\_1141759 (U21959) lectin precursor [Cladrastis lutea]

```
Seq. No.
                   36191
                   LIB3051-038-Q1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3098571
BLAST score
                   327
                   2.0e-30
E value
Match length
                   125
% identity
                   55
NCBI Description (AF049028) BURP domain containing protein [Brassica napus]
Seq. No.
                   36192
Seq. ID
                   LIB3051-038-Q1-K1-E6
Method
                   BLASTX
NCBI GI
                   g133940
                   353
BLAST score
                   1.0e-33
E value
Match length
                   107
                   73
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S3A (S1A) >gi 70851 pir R3XL3A
                   ribosomal protein S3a - African clawed frog >gi_65091_emb_CAA40592 (X57322) ribosomal protein S1a
                   [Xenopus laevis]
Seq. No.
                   36193
                   LIB3051-039-Q1-K1-A1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q310569
BLAST score
                   120
E value
                   6.0e-61
Match length
                   326
                   86
% identity
NCBI Description
                   Glycine max seed maturation protein (GmPM3) mRNA, complete
Seq. No.
                   36194
Seq. ID
                   LIB3051-039-Q1-K1-B2
Method
                   BLASTX
NCBI GI
                   q2129668
BLAST score
                   180
E value
                   1.0e-13
Match length
                   82
% identity
                   55
                   phosphoglycerate kinase - Arabidopsis thaliana (fragment)
NCBI Description
                   >gi 1022803 (U37700) phosphoglycerate kinase [Arabidopsis
                   thaliana]
Seq. No.
                   36195
Seq. ID
                   LIB3051-039-Q1-K1-D12
Method
                   BLASTX
NCBI GI
                   g231610
BLAST score
                   213
E value
                   4.0e-17
Match length
                   88
```

% identity

```
NCBI Description
                  ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
                  >gi 67880 pir PWNTG H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, chloroplast - common
                  tobacco >gi 19785 emb_CAA45152_ (X63606) ATP synthase
                  (gamma subunit) [Nicotiana tabacum]
                  36196
Seq. No.
                  LIB3051-039-Q1-K1-D9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q18764
BLAST score
                  216
E value
                  1.0e-118
Match length
                  376
                  90
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
Seq. No.
                  36197
                  LIB3051-039-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                  g2129652
NCBI GI
BLAST score
                  159
E value
                  9.0e-11
Match length
                  133
                  35
% identity
NCBI Description myosin heavy chain homolog - Arabidopsis thaliana
                  (fragment) >gi 699495 (U19616) myosin heavy chain homolog
                  [Arabidopsis thaliana]
Seq. No.
                  36198
Seq. ID
                  LIB3051-039-Q1-K1-E7
Method
                  BLASTX
                  g3402709
NCBI GI
BLAST score
                  230
E value
                  5.0e~19
Match length
                  128
                  1.5
% identity
NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  36199
                  LIB3051-039-Q1-K1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g758249
BLAST score
                  230
E value
                  1.0e-126
Match length
                  362
                  91
% identity
NCBI Description P.vulgaris mRNA for plasma membrane H+ ATPase
                  36200
Seq. No.
Seq. ID
                  LIB3051-039-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2651305
BLAST score
                  224
                  2.0e-18
E value
Match length
                  111
```

NCBI Description (AC002336) hypothetical protein [Arabidopsis thaliana]



```
Seq. No.
                    36201
Seq. ID
                    LIB3051-040-Q1-K1-A1
Method
                    BLASTX
NCBI GI
                    g2130105
BLAST score
                    217
E value
                    2.0e-17
Match length
                    67
% identity
                    66
                    histone H2A type 2 (clone wcH2A-4) - wheat
NCBI Description
                    >gi_536892_dbj_BAA07278 (D38089) protein H2A [Triticum
aestivum] >gi_536896_dbj_BAA07280 (D38091) protein H2A
                    [Triticum aestivum]
Seq. No.
                    36202
Seq. ID
                    LIB3051-040-Q1-K1-A2
Method
                    BLASTN
NCBI GI
                    g166857
BLAST score
                    53
                    7.0e-21
E value
Match length
                    153
% identity
                    84
NCBI Description Arabidopsis thaliana cytoplasmic ribosomal protein mRNA,
                    complete cds
                    36203
Seq. No.
Seq. ID
                    LIB3051-040-Q1-K1-D4
Method
                    BLASTN
NCBI GI
                    q2654093
BLAST score
                    228
E value
                    1.0e-125
Match length
                    319
                    97
% identity
NCBI Description Glycine max aspartate aminotransferase glyoxysomal isozyme
                    AAT1 precursor and aspartate aminotransferase cytosolic
                    isozyme AAT2 (AAT) mRNA, complete cds
Seq. No.
                    36204
Seq. ID
                    LIB3051-040-Q1-K1-D5
Method
                    BLASTX
NCBI GI
                    a135535
BLAST score
                    521
E value
                    4.0e-53
Match length
                    119
% identity
                    87
                    T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
NCBI Description
                    (CCT-ALPHA) >gi 322602 pir JN0448 t-complex polypeptide
                    Tcp-1 - Arabidopsis thaliana >gi 217871 dbj BAA01955 (D11351) t-complex polypeptide 1 homologue [Arabidopsis
                    thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT
                    alpha/TCP-1 [Arabidopsis thaliana]
Seq. No.
                    36205
```

Seq. ID LIB3051-040-Q1-K1-E2

Method BLASTN NCBI GI g1204128

BLAST score 80

```
0e-37
E value
                  236
Match length
                  84
% identity
NCBI Description M.sativa MMK2 mRNA for protein kinase
                  36206
Seq. No.
                  LIB3051-040-Q1-K1-H10
Seq. ID
                  BLASTN
Method
                  g18764
NCBI GI
                  261
BLAST score
                  1.0e-145
E value
                  333
Match length
                  95
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-la
                  36207
Seq. No.
                  LIB3051-040-Q1-K1-H7
Seq. ID
                  BLASTX
Method
                   g3219797
NCBI GI
                   289
BLAST score
                   6.0e-26
E value
Match length
                   141
% identity
                   45
                   PROTEIN GT197 >gi_2135426_pir__154209 hypothetical protein
NCBI Description
                   - human (fragment) >gi_1008840 (L38932) partial ORF;
                   putative [Homo sapiens]
                   36208
Seq. No.
                   LIB3051-040-Q1-K1-H8
Seq. ID
                   BLASTX
Method
                   g4115363
NCBI GI
                   143
BLAST score
                   2.0e-12
E value
                   140
Match length
% identity
                   (AC005957) putative disease resistance protein [Arabidopsis
NCBI Description
                   thaliana]
                   36209
Seq. No.
                   LIB3051-040-Q1-K1-H9
Seq. ID
                   BLASTX
Method
                   g3850576
 NCBI GI
                   670
 BLAST score
                   1.0e-70
 E value
                   140
Match length
                   89
 % identity
                   (AC005278) Strong similarity to gb_U04968 nucleotide
 NCBI Description
                   excision repair protein (ERCC2) from Cricetulus grisseus.
                    [Arabidopsis thaliana]
                    36210
 Seq. No.
 Seq. ID
                   LIB3051-041-Q1-K1-A4
                   BLASTX
 Method
```

5519

q2618702

295 1.0e-26

81

NCBI GI BLAST score

E value

Match length

% identity NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

36211 Seq. No. Seq. ID

LIB3051-041-Q1-K1-D1

Method NCBI GI BLASTX g1173027

156 BLAST score

2.0e-10 E value

82 Match length 48 % identity

60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal NCBI Description

protein L31 [Nicotiana glutinosa]

36212 Seq. No.

Seq. ID

LIB3051-041-Q1-K1-D12

BLASTX Method g417103 NCBI GI 270 BLAST score 6.0e-47 E value 115 Match length % identity 89

HISTONE H3.2, MINOR >gi 282871 pir S24346 histone NCBI Description

H3.3-like protein - Arabidopsis thaliana

>gi 16324 emb CAA42957 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_404825 emb\_CAA42958\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 488563 (U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460) histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2

[Medicago sativa]  $>gi_4885\overline{7}7$  (U09465) histone H3.2

[Medicago sativa] >gi 510911 emb CAA56153 (X79714) histone H3 [Lolium temulentum] >gi 14351 $\overline{5}$ 7 emb CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]

>gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi 3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana  $tab\overline{a}cum$ ] >gi 3885890 (AF093633) histone H3 [Oryza sativa] >gi 4038469 gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone

H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1 (AL035708) Histon H3 [Arabidopsis thaliana]

36213 Seq. No.

Seq. ID LIB3051-041-Q1-K1-E3

BLASTN Method q169980 NCBI GI 369 BLAST score 0.0e + 00E value 436 Match length 99 % identity

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

36214 Seq. No.

Seq. ID LIB3051-041-Q1-K1-E6

BLASTX Method NCBI GI q2244816 204 BLAST score

NCBI Description

```
e-16
E value
                  60
Match length
                  75
% identity
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  36215
Seq. No.
Seq. ID
                  LIB3051-041-Q1-K1-F1
                  BLASTN
Method
                  q473216
NCBI GI
                  94
BLAST score
                  2.0e-45
E value
                  302
Match length
                  83
% identity
NCBI Description P.sativum (little marvel) HSC71.0 mRNA
                  36216
Seq. No.
                  LIB3051-042-Q1-K1-C4
Seq. ID
                  BLASTX
Method
                  g1177405
NCBI GI
                  197
BLAST score
                   4.0e-15
E value
Match length
                   65
% identity
                   58
                  (X89855) citrate binding protein [Hevea brasiliensis]
NCBI Description
                   36217
Seq. No.
                   LIB3051-042-Q1-K1-C8
Seq. ID
                   BLASTX
Method
                   g1084334
NCBI GI
                   417
BLAST score
                   3.0e-41
E value
Match length
                   91
                   88
% identity
                   calcium-dependent protein kinase (EC 2.7.1.-) 1 -
NCBI Description
                   Arabidopsis thaliana >gi_604880_dbj_BAA04829_ (D21805)
                   calcium-dependent protein kinase [Arabidopsis thaliana]
                   36218
Seq. No.
                   LIB3051-042-Q1-K1-F10
Seq. ID
                   BLASTN
Method
NCBI GI
                   q170046
BLAST score
                   118
                   1.0e-59
E value
                   284
Match length
% identity
                   Glycine max protein kinase (PK6) mRNA, complete cds
NCBI Description
                   36219
Seq. No.
Seq. ID
                   LIB3051-042-Q1-K1-F5
                   BLASTN
Method
                   q510545
NCBI GI
BLAST score
                   58
                   7.0e-24
E value
                   94
Match length
                   90
 % identity
                  P.sativum mRNA for starch branching enzyme I
```

Method

BLASTN

```
Seq. No.
                  LIB3051-042-Q1-K1-G9
Seq. ID
                  BLASTN
Method
                  q170025
NCBI GI
                   40
BLAST score
                   4.0e-13
E value
                  132
Match length
                  89
% identity
                  Soybean malate synthase (MS) mRNA, 3' end
NCBI Description
                   36221
Seq. No.
                  LIB3051-043-Q1-K1-B9
Seq. ID
                   BLASTX
Method
                   g134646
NCBI GI
                   203
BLAST score
                   5.0e-16
E value
                   47
Match length
                   70
% identity
                   SUPEROXIDE DISMUTASE, CHLOROPLAST PRECURSOR (FE) >gi_169955
NCBI Description
                   (M64267) Fe-superoxide dismutase [Glycine max]
                   >gi_228415_prf__1803527A Fe superoxide dismutase [Glycine
                   max]
                   36222
Seq. No.
Seq. ID
                   LIB3051-043-Q1-K1-D11
                   BLASTX
Method
                   q4106061
NCBI GI
                   143
BLAST score
                   6.0e-09
E value
                   40
Match length
                   68
% identity
                   (AF053318) CCR4-associated factor 1 [Homo sapiens]
NCBI Description
                   36223
Seq. No.
Seq. ID
                   LIB3051-043-Q1-K1-E4
                   BLASTX
Method
                   g3135493
NCBI GI
                   302
BLAST score
                   4.0e-31
E value
                   133
Match length
% identity
                   (AF060248) unknown [Arabidopsis thaliana]
NCBI Description
                   36224
Seq. No.
                   LIB3051-043-Q1-K1-E7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3790188
BLAST score
                   156
                   2.0e-10
E value
Match length
                   67
                   57
 % identity
                   (Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana
NCBI Description
                   tabacum]
 Seq. No.
                    36225
                   LIB3051-043-Q1-K1-F3
 Seq. ID
```

BLAST score

319

```
q3821780
NCBI GI
                  37
BLAST score
                  2.0e-11
E value
                  37
Match length
                  100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  36226
Seq. No.
Seq. ID
                  LIB3051-044-Q1-K1-C3
                  BLASTX
Method
                  q544015
NCBI GI
                  325
BLAST score
                  3.0e-30
E value
                  68
Match length
                  81
% identity
                  ENDOCHITINASE PRECURSOR >gi_2118033_pir__S59947 chitinase
NCBI Description
                  (EC 3.2.1.14) Al precursor — garden pea
                  >gi_20687_emb_CAA45359_ (X63899) chitinase [Pisum sativum]
                  36227
Seq. No.
                  LIB3051-044-Q1-K1-C7
Seq. ID
                  BLASTN
Method
                  g3241927
NCBI GI
                  42
BLAST score
                  3.0e-14
E value
                  90
Match length
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTE17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  36228
                  LIB3051-044-Q1-K1-D10
Seq. ID
                  BLASTN
Method
                  q3821780
NCBI GI
BLAST score
                   36
E value
                   8.0e-11
Match length
                   37
                   61
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
Seq. No.
                   36229
                   LIB3051-044-Q1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3834302
BLAST score
                   172
                   3.0e-12
E value
Match length
                   38
                   89
% identity
                   (AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase
NCBI Description
                   from Oryza sativa. ESTs gb_F14272 and gb_F14273 come from
                   this gene. [Arabidopsis thaliana]
                   36230
Seq. No.
                   LIB3051-044-Q1-K1-D9
Seq. ID
                   BLASTX
Method
                   g2529686
NCBI GI
```

```
E value
Match length
                  104
% identity
                  53
                 (AC002535) putative G-beta-repeat containing protein, 5'
NCBI Description
                  partial [Arabidopsis thaliana]
                  36231
Seq. No.
Seq. ID
                  LIB3051-045-Q1-K1-B12
                  BLASTX
Method
                  g2655098
NCBI GI
BLAST score
                  141
                  9.0e-09
E value
                  79
Match length
                  41
% identity
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]
Seq. No.
                  36232
Seq. ID
                  LIB3051-045-Q1-K1-F7
                  BLASTN
Method
NCBI GI
                  g2827313
BLAST score
                  50
E value
                  4.0e-19
                  90
Match length
                  89
% identity
NCBI Description Oryza sativa casein kinase mRNA, partial cds
Seq. No.
                  36233
                  LIB3051-045-Q1-K1-H7
Seq. ID
Method
                  BLASTX
                  g3522938
NCBI GI
BLAST score
                  252
E value
                  1.0e-21
Match length
                  110
% identity
                  52
NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]
                  36234
Seq. No.
Seq. ID
                  LIB3051-046-Q1-K1-A7
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  37
E value
                  2.0e-11
Match length
                  37
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  36235
Seq. ID
                  LIB3051-046-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g2911067
BLAST score
                  407
E value
                  7.0e-40
Match length
                  85
% identity
NCBI Description
                  (AL021960) UV-damaged DNA-binding protein-like
```

[Arabidopsis thaliana]

```
Seq. No.
Seq. ID
                  LIB3051-046-Q1-K1-F9
Method
                  BLASTN
                  q3821780
NCBI GI
BLAST score
                  36
                  9.0e-11
E value
Match length
                  36
                  100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  36237
Seq. No.
                  LIB3051-046-Q1-K1-G3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1675195
BLAST score
                  114
                   3.0e-57
E value
                   240
Match length
                   87
% identity
                  Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
NCBI Description
                   complete cds
                   36238
Seq. No.
Seq. ID
                   LIB3051-047-Q1-K1-A9
                   BLASTX
Method
NCBI GI
                   g1174745
                   143
BLAST score
                   6.0e-09
E value
Match length
                   63
                   49
% identity
                   TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                   >gi 1363523 pir S53761 triose-phosphate isomerase (EC
                   5.3.1.1) precursor, chloroplast - rye
                   >gi_609262_emb_CAA83533_ (Z32521) triosephosphate isomerase
                   [Secale cereale] >gi_1095494_prf__2109226B triosephosphate
                   isomerase [Secale cereale]
                   36239
Seq. No.
                   LIB3051-047-Q1-K1-E7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2347188
BLAST score
                   511
                   6.0e-52
E value
Match length
                   149
                   69
% identity
                   (AC002338) laccase isolog [Arabidopsis thaliana]
NCBI Description
                   >qi 3150401 (AC004165) putative laccase [Arabidopsis
                   thaliana]
                   36240
Seq. No.
                   LIB3051-047-Q1-K1-H2
Seq. ID
Method
                   BLASTN
                   g169930
NCBI GI
                   43
BLAST score
                   3.0e-15
E value
                   115
Match length
                   84
 % identity
NCBI Description Glycine max calcium dependent protein kinase mRNA
```



```
Seq. No.
                  36241
                  LIB3051-047-Q1-K1-H7
Seq. ID
Method
                  BLASTX
                  g3953482
NCBI GI
                  143
BLAST score
                  6.0e-09
E value
                  120
Match length
                  35
% identity
                  (AC002328) F2202.27 [Arabidopsis thaliana]
NCBI Description
                  36242
Seq. No.
                  LIB3051-048-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351271
BLAST score
                  179
                  4.0e-13
E value
Match length
                  76
                   54
% identity
                  TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                  >gi 1084309 pir S52032 triose-phosphate isomerase (EC
                   5.3.1.1) precursor, chloroplast - spinach >gi_806312
                   (L36387) triosephosphate isomerase, chloroplast isozyme
                   [Spinacia oleracea]
                   36243
Seq. No.
                   LIB3051-048-Q1-K1-H2
Seq. ID
                   BLASTX
Method
                   g322577
NCBI GI
BLAST score
                   417
                   6.0e-41
E value
Match length
                   112
                   71
% identity
                  Raf protein kinase homolog CTR1 - Arabidopsis thaliana
NCBI Description
                   36244
Seq. No.
                   LIB3051-049-Q1-K1-C2
Seq. ID
Method
                   BLASTX
                   g3421123
NCBI GI
BLAST score
                   286
                   8.0e-26
E value
Match length
                   82
                   72
% identity
                  (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis
NCBI Description
                   thaliana]
                   36245
Seq. No.
                   LIB3051-049-Q1-K1-E5
Seq. ID
                   BLASTN
Method
                   g18737
NCBI GI
BLAST score
                   327
                   0.0e+00
E value
Match length
                   371
                   12
% identity
NCBI Description Glycine max RPRP3 gene for repetitive proline-rich protein
```

36246

Seq. No.

% identity

54

```
B3051-049-Q1-K1-G12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3879813
                  156
BLAST score
                  2.0e-10
E value
Match length
                  63
                  52
% identity
                  (Z66524) Similarity at the 3' end with the Yeast pre-mRNA
NCBI Description
                  splicing factor PRP9 (PIR Acc. No. S12320); cDNA EST
                  EMBL: C08800 comes from this gene; cDNA EST EMBL: C07438
                  comes from this gene; cDNA EST yk494b4.3 comes from this
                  gene
                  36247
Seq. No.
                  LIB3051-049-Q1-K1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2506276
BLAST score
                  152
                  5.0e-10
E value
Match length
                  78
% identity
                  45
                  RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60
NCBI Description
                  KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)
                  >gi 2129561 pir S71235 chaperonin-60 alpha chain -
                  Arabidopsis thaliana >gi 1223910 (U49357) chaperonin-60
                  alpha subunit [Arabidopsis thaliana]
                  >gi 4510416 gb AAD21502.1 (AC006929) putative rubisco
                  binding protein alpha subunit [Arabidopsis thaliana]
Seq. No.
                  36248
Seq. ID
                  LIB3051-050-Q1-K1-E10
Method
                  BLASTN
                  q510514
NCBI GI
                  142
BLAST score
                   5.0e-74
E value
Match length
                  285
                   88
% identity
NCBI Description
                  G.max KTi-S mRNA
Seq. No.
                   36249
Seq. ID
                  LIB3051-050-Q1-K1-F4
Method
                   BLASTX
NCBI GI
                   g3522943
BLAST score
                   152
E value
                   4.0e-10
Match length
                   103
% identity
                   39
                  (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
NCBI Description
                   36250
Seq. No.
                   LIB3051-050-Q1-K1-G9
Seq. ID
Method
                   BLASTX
                   g4467148
NCBI GI
BLAST score
                   189
                   9.0e-18
E value
Match length
                   105
```

```
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
Seq. No. 36251
```

 Seq. ID
 LIB3051-051-Q1-K1-C12

 Method
 BLASTX

 NCBI GI
 g3395441

NCBI GI g3395441 BLAST score 167 E value 8.0e-12 Match length 49 % identity 63

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 36252

Seq. ID LIB3051-051-Q1-K1-D11

Method BLASTX
NCBI GI g1345570
BLAST score 188
E value 3.0e-14
Match length 72
% identity 61

NCBI Description (X80009) starch branching enzyme I [Pisum sativum]

Seq. No. 36253

Seq. ID LIB3051-053-Q1-K2-A12

Method BLASTX
NCBI GI g1085621
BLAST score 154
E value 2.0e-10
Match length 75
% identity 52

NCBI Description alcohol dehydrogenase (EC 1.1.1.1) 1CN - Phaseolus acutifolius >qi 452767 emb CAA80692 (Z23171) alcohol

dehydrogenase-1CN [Phaseolus acutifolius]

Seq. No. 36254

Seq. ID LIB3051-053-Q1-K2-C9

Method BLASTX 92055374
BLAST score 208
E value 7.0e-17
Match length 80
% identity 62

NCBI Description (U29095) serine-threonine protein kinase [Triticum

aestivum]

Seq. No. 36255

Seq. ID LIB3051-053-Q1-K2-D5

Method BLASTX
NCBI GI g116324
BLAST score 219
E value 8.0e-18
Match length 87
% identity 49

NCBI Description ENDOCHITINASE PR4 PRECURSOR >gi 100000 pir\_\_S16579

chitinase (EC 3.2.1.14) precursor - kidney bean

Seq. No. 36256

% identity

82

```
LTB3051-053-Q1-K2-E10
Seq. ID
Method
                  BLASTN
                  g18743
NCBI GI
BLAST score
                  320
E value
                  1.0e-180
                  400
Match length
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
                  36257
Seq. No.
Seq. ID
                  LIB3051-053-Q1-K2-E5
Method
                  BLASTX
NCBI GI
                  q1350988
BLAST score
                  199
                  1.0e-15
E value
Match length
                  88
% identity
                  56
NCBI Description 40S RIBOSOMAL PROTEIN S3B (S1B) >gi 2119058 pir_ I51635
                  ribosomal protein S1 - African clawed frog
                  >gi 587600 emb CAA84291 (Z34530) ribosomal protein S1
                  [Xenopus laevis] >gi 587602 emb CAA84290 (Z34529)
                  ribosomal protein [Xenopus laevis]
                  36258
Seq. No.
Seq. ID
                  LIB3051-053-Q1-K2-E8
Method
                  BLASTX
NCBI GI
                  q477819
BLAST score
                  145
                  4.0e-09
E value
Match length
                  86
% identity
                  41
NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) beta
                  chain precursor - potato >gi 410634 bbs 136741 cytochrome c
                  reductase-processing peptidase subunit II, MPP subunit II,
                  P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,
                  530 aa]
Seq. No.
                  36259
Seq. ID
                  LIB3051-053-Q1-K2-F10
Method
                  BLASTX
NCBI GI
                  q3806098
BLAST score
                  353
E value
                  1.0e-33
Match length
                  123
% identity
NCBI Description (AF079100) arginine-tRNA-protein transferase 1; Atelp
                  [Arabidopsis thaliana]
Seq. No.
                  36260
Seq. ID
                  LIB3051-053-Q1-K2-F5
                  BLASTN
Method
NCBI GI
                  g169980
BLAST score
                  75
E value
                  3.0e-34
Match length
                  275
```

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds



```
36261
Seq. No.
                  LIB3051-053-Q1-K2-F7
Seq. ID
                  BLASTX
Method
                  g4388726
NCBI GI
                  266
BLAST score
                   3.0e-23
E value
                  122
Match length
                   48
% identity
                   (AC006413) putative 12-oxophytodienoate-10,11-reductase
NCBI Description
                   [Arabidopsis thaliana]
                   36262
Seq. No.
                   LIB3051-053-Q1-K2-G7
Seq. ID
                   BLASTX
Method
                   g4056432
NCBI GI
BLAST score
                   184
                   2.0e-29
E value
                   125
Match length
                   56
% identity
                   (AC005990) Similar to gi 2245014 glucosyltransferase
NCBI Description
                   homolog from Arabidopsis thaliana chromosome 4 contig
                   gb Z97341. ESTs gb_T20778 and gb_AA586281 come from this
                   gene. [Arabidopsis Thaliana]
                   36263
Seq. No.
                   LIB3051-054-Q1-K1-E11
Seq. ID
                   BLASTN
Method
                   g2267594
NCBI GI
                   46
BLAST score
                   9.0e-17
E value
                   168
Match length
% identity
                   82
NCBI Description Oryza sativa plastocyanin precursor, mRNA, complete cds
                   36264
Seq. No.
                   LIB3051-054-Q1-K1-G11
Seq. ID
                   BLASTN
Method
                   g607751
NCBI GI
                   49
BLAST score
                   1.0e-18
E value
                   61
Match length
 % identity
                   Urochloa panicoides phosphoenolpyruvate carboxykinase
NCBI Description
                   (PCK1) mRNA, complete cds
                   36265
 Seq. No.
                   LIB3051-054-Q1-K2-D7
Seq. ID
                   BLASTN
Method
                   q1326162
NCBI GI
                   96
 BLAST score
```

BLAST score 96
E value 1.0e-46
Match length 184
% identity 88

NCBI Description Phaseolus vulgaris stress related protein PvSRP mRNA,

complete cds

BLAST score

91

```
Seq. No.
                  LIB3051-055-Q1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1778822
BLAST score
                   306
                  1.0e-172
E value
                  310
Match length
                  100
% identity
                  Glycine max early light-induced protein (ELIP) mRNA,
NCBI Description
                  complete cds
                   36267
Seq. No.
                  LIB3051-056-Q1-K1-D12
Seq. ID
Method
                  BLASTN
NCBI GI
                   g22524
BLAST score
                   70
                   2.0e-31
E value
Match length
                   126
                   75
% identity
                  Zea mays mRNA encoding a zein (clone ZG31A)
NCBI Description
Seq. No.
                   36268
                   LIB3051-056-Q1-K1-F12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22544
                   60
BLAST score
                   3.0e-25
E value
                   104
Match length
% identity
                   89
                  Maize mRNA (clone A30) for zein (a plant storage protein)
NCBI Description
Seq. No.
                   36269
                   LIB3051-056-Q1-K1-G10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q168665
BLAST score
                   82
                   9.0e-39
E value
Match length
                   126
% identity
                   92
                  Maize 16-kDa zein-2 mRNA, complete cds
NCBI Description
Seq. No.
                   36270
                   LIB3051-057-Q1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1449179
BLAST score
                   230
                   4.0e-19
E value
                   66
Match length
                   65
% identity
                   (D86506) N-ethylmaleimide sensitive fusion protein
NCBI Description
                   [Nicotiana tabacum]
                   36271
Seq. No.
                   LIB3051-057-Q1-K1-E11
Seq. ID
                   BLASTN
Method
                   g343344
NCBI GI
```

```
E value
                  174
Match length
                  89
% identity
                  Soybean chloroplast 16S rRNA (3' end), 18S rRNA (5' end),
NCBI Description
                  Ile-tRNA, and Ala-tRNA genes
                  36272
Seq. No.
                  LIB3051-058-Q1-K1-C3
Seq. ID
                  BLASTN
Method
                  g2738999
NCBI GI
                  108
BLAST score
                  1.0e-53
E value
                  220
Match length
                  87
% identity
                  Glycine max cytochrome P450 monooxygenase CYP71D10p
NCBI Description
                  (CYP71D10) mRNA, complete cds
                  36273
Seq. No.
Seq. ID
                  LIB3051-058-Q1-K1-D4
                  BLASTN
Method
                  g2052028
NCBI GI
                  40
BLAST score
                  1.0e-13
E value
                  48
Match length
                  96
% identity
NCBI Description G.max mRNA for glutathione transferase
                  36274
Seq. No.
                  LIB3051-058-Q1-K1-G7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2661020
                   50
BLAST score
                  2.0e-19
E value
                  122
Match length
                   85
% identity
NCBI Description Glycine max catalase (cat4) mRNA, complete cds
                   36275
Seq. No.
Seq. ID
                  LIB3051-058-Q1-K1-H1
                   BLASTX
Method
NCBI GI
                   g99902
                   162
BLAST score
                   1.0e-11
E value
                   52
Match length
% identity
                   67
                  translation elongation factor eEF-1 alpha chain (gene
NCBI Description
                   tefS1) - soybean
                   36276
Seq. No.
                   LIB3051-058-Q1-K1-H3
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2661020
BLAST score
                   94
                   1.0e-45
E value
Match length
                   102
                   98
% identity
NCBI Description Glycine max catalase (cat4) mRNA, complete cds
```



```
36277
Seq. No.
Seq. ID
                  LIB3051-058-Q1-K2-A6
Method
                  BLASTX
                  g3128228
NCBI GI
                  585
BLAST score
E value
                  1.0e-60
                  130
Match length
                  86
% identity
                  (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                  thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                  L18A [Arabidopsis thaliana]
                  36278
Seq. No.
Seq. ID
                  LIB3051-058-Q1-K2-B12
Method
                  BLASTN
                  q650
NCBI GI
                  199
BLAST score
                  1.0e-108
E value
                  301
Match length
                  98
% identity
                  Bovine mRNA for preprolactin, 3' end
NCBI Description
                  >gi_163624_gb_M36874_BOVPROB2 Cattle prolactin mRNA, 3' end
                  36279
Seq. No.
Seq. ID
                  LIB3051-058-Q1-K2-B9
                  BLASTN
Method
                  g2911586
NCBI GI
BLAST score
                  67
                  3.0e-29
E value
                  281
Match length
                  87
% identity
NCBI Description Homo sapiens mRNA for putative methyltransferase
                  36280
Seq. No.
Seq. ID
                  LIB3051-058-Q1-K2-C10
                  BLASTX
Method
                   g2911026
NCBI GI
BLAST score
                   347
E value
                   7.0e-33
                   124
Match length
                   57
% identity
                  (AL021958) fadE9 [Mycobacterium tuberculosis]
NCBI Description
                   36281
Seq. No.
Seq. ID
                   LIB3051-058-Q1-K2-C11
                   BLASTN
Method
                   q2258466
NCBI GI
                   198
BLAST score
                   1.0e-107
E value
                   278
Match length
                   93
% identity
                  Sus scrofa succinyl-CoA synthetase alpha subunit (SCS)
NCBI Description
```

Seq. No. 36282

Seq. ID LIB3051-058-Q1-K2-C12

alternatively spliced mRNA, complete cds

BLAST score

E value

328 0.0e+00

```
Method
                  g1825645
NCBI GI
BLAST score
                  303
                  1.0e-27
E value
                  67
Match length
                  81
% identity
                  (U88173) weak similarity to Arabidopsis thaliana
NCBI Description
                  ubiquitin-like protein 8 [Caenorhabditis elegans]
                  36283
Seq. No.
                  LIB3051-058-Q1-K2-D11
Seq. ID
                  BLASTN
Method
                  q1710289
NCBI GI
BLAST score
                  100
                   5.0e-49
E value
                   320
Match length
                   83
% identity
                  Human clone 23882 mRNA, complete cds
NCBI Description
                  >gi_3005692_gb_AF054984_AF054984 Homo sapiens clone 23709
                  mRNA sequence
                   36284
Seq. No.
                  LIB3051-058-Q1-K2-D12
Seq. ID
                  BLASTN
Method
                   g1036792
NCBI GI
BLAST score
                   68
                   7.0e-30
E value
                   138
Match length
                   68
% identity
                  Bos taurus ornithine decarboxylase (ODC) gene, complete cds
NCBI Description
                   36285
Seq. No.
                   LIB3051-058-Q1-K2-D4
Seq. ID
                   BLASTX
Method
                   q4432807
NCBI GI
BLAST score
                   301
                   2.0e-27
E value
                   124
Match length
% identity
                   (AC006570) putative polyprotein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   36286
Seq. ID
                   LIB3051-058-Q1-K2-E10
                   BLASTN
Method
NCBI GI
                   g1205
BLAST score
                   335
                   0.0e + 00
E value
Match length
                   375
                   97
% identity
                   Sheep mRNA for (Na+ and K+) ATPase catalytic subunit alpha
NCBI Description
                   36287
Seq. No.
                   LIB3051-058-Q1-K2-E11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g35219
```

```
Match length
                  95
% identity
NCBI Description Human mRNA for p68 protein
                  36288
Seq. No.
                  LIB3051-058-Q1-K2-E12
Seq. ID
                  BLASTN
Method
                  g189596
NCBI GI
                  248
BLAST score
                  1.0e-137
E value
                  320
Match length
% identity
                  95
                  Homo sapiens pancreatic tumor-related protein mRNA, partial
NCBI Description
                  36289
Seq. No.
                  LIB3051-058-Q1-K2-F12
Seq. ID
Method
                  BLASTN
                  g162710
NCBI GI
                  383
BLAST score
                  0.0e+00
E value
Match length
                  389
% identity
                  99
NCBI Description Bovine F-1-ATPase beta-subunit mRNA, complete cds
                  36290
Seq. No.
                  LIB3051-058-Q1-K2-G11
Seq. ID
Method
                  BLASTN
                  g4156137
NCBI GI
                   43
BLAST score
                   6.0e-15
E value
                   99
Match length
% identity
                   86
                  Homo sapiens clone NH0569I24, complete sequence [Homo
NCBI Description
                   sapiens]
                   36291
Seq. No.
                   LIB3051-058-Q1-K2-G12
Seq. ID
                   BLASTN
Method
                   g292923
```

Seq. ID LIB3051-058Method BLASTN
NCBI GI g292923
BLAST score 141
E value 2.0e-73
Match length 369

NCBI Description Human lysyl oxidase (LOX) gene, exon 7

 Seq. No.
 36292

 Seq. ID
 LIB3051-058-Q1-K2-G9

 Method
 BLASTN

85

NCBI GI g163611 BLAST score 167 E value 3.0e-89 Match length 171 % identity 99

% identity

NCBI Description Bovine prolactin gene, exon 5

Seq. No. 36293

BLAST score

E value

32 9.0e-09

```
LIB3051-058-Q1-K2-H10
Seq. ID
                  BLASTN
Method
                  g432358
NCBI GI
                  274
BLAST score
                  1.0e-153
E value
                  386
Match length
                  93
% identity
NCBI Description Human mRNA for ribosomal protein, complete cds
                  36294
Seq. No.
                  LIB3051-058-Q1-K2-H11
Seq. ID
                  BLASTN
Method
                  q529414
NCBI GI
                  196
BLAST score
                   1.0e-106
E value
                  296
Match length
                   92
% identity
NCBI Description Bovine ADP/ATP translocase T1 mRNA, complete cds
                   36295
Seq. No.
Seq. ID
                  LIB3051-058-Q1-K2-H9
                  BLASTN
Method
                   g1160468
NCBI GI
                   187
BLAST score
                   1.0e-101
E value
Match length
                   396
                   91
% identity
                  Human DNA sequence from cosmid cU177E8, between markers
NCBI Description
                   DXS366 and DXS87 on chromosome X
                   36296
Seq. No.
                   LIB3051-060-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   a2315668
NCBI GI
                   170
BLAST score
                   4.0e-12
E value
                   120
Match length
                   37
% identity
                  (AF016671) similar to alpha/gamma adaptins [Caenorhabditis
NCBI Description
                   elegans]
                   36297
Seq. No.
Seq. ID
                   LIB3051-060-Q1-K1-C2
                   BLASTX
Method
                   q4027897
NCBI GI
BLAST score
                   592
E value
                   2.0e-61
Match length
                   145
% identity
                  (AF049353) alpha-expansin precursor [Nicotiana tabacum]
NCBI Description
Seq. No.
                   36298
                   LIB3051-060-Q1-K1-D3
Seq. ID
                   BLASTN
Method
NCBI GI
                   g210811
```

```
Match length
                   97
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                   36299
Seq. No.
                  LIB3051-060-Q1-K1-D4
Seq. ID
                  BLASTN
Method
                  g169980
NCBI GI
                  150
BLAST score
                   8.0e-79
E value
                   294
Match length
```

% identity 88 NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. ID LIB3051-060-Q1-K1-D5
Method BLASTN
NCBI GI g169980
BLAST score 113
E value 9.0e-57
Match length 268
% identity 87

Seq. No.

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No. 36301

Seq. ID LIB3051-060-Q1-K1-E4

36300

Method BLASTX
NCBI GI g3068809
BLAST score 141
E value 1.0e-08
Match length 64
% identity 48

NCBI Description (AF059295) Skpl homolog [Arabidopsis thaliana]

Seq. No. 36302

Seq. ID LIB3051-060-Q1-K1-E5

Method BLASTX
NCBI GI g3719211
BLAST score 130
E value 2.0e-11
Match length 102
% identity 51

NCBI Description (U97021) UIP2 [Arabidopsis thaliana]

Seq. No. 36303

Seq. ID LIB3051-060-Q1-K1-F3

Method BLASTX
NCBI GI g1420871
BLAST score 136
E value 4.0e-13
Match length 115
% identity 51

NCBI Description (X98890) inorganic phosphate transporter 1 [Solanum

tuberosum]

Seq. No. 36304

```
LIB3051-060-Q1-K1-G9
Seq. ID
                   BLASTN
Method
NCBI GI
                   g733453
                   69
BLAST score
                   1.0e-30
E value
                   201
Match length
                   84
 % identity
                   Zea mays chlorophyll a/b-binding apoprotein CP26 (Lhcb5-1)
NCBI Description
                   mRNA, complete cds
di.
                   36305
 Seq. No.
                   LIB3051-061-Q1-K1-A7
 Seq. ID
                   BLASTN
 Method
                    q531832
 NCBI GI
 BLAST score
                    58
                    6.0e-24
 E value
                    174
 Match length
                    83
 % identity
                   Cloning vector pSport2, complete sequence
 NCBI Description
 Seq. No.
                    36306
                   LIB3051-061-Q1-K1-C6
 Seq. ID
                    BLASTX
 Method
                    q4263521
 NCBI GI
                    440
 BLAST score
                    1.0e-43
 E value
                    121
 Match length
                    20
 % identity
                   (AC004044) putative WD-repeat protein [Arabidopsis
 NCBI Description
                    thaliana]
                    36307
 Seq. No.
 Seq. ID
                    LIB3051-061-Q1-K1-E10
 Method
                    BLASTX
                    q3914468
 NCBI GI
 BLAST score
                    191
                    1.0e-14
 E value
                    92
 Match length
                    48
 % identity
                    26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
 NCBI Description
                    >gi_478411_pir__JQ2257 nuclear antigen 21D7 - carrot
                    >gi_217911_dbj_BAA02696_ (D13434) 21D7 antigen [Daucus
                    carota]
                    36308
 Seq. No.
                    LIB3051-061-Q1-K1-H9
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g22075
 BLAST score
                    108
                    1.0e-53
 E value
 Match length
                    247
                    91
 % identity
 NCBI Description Vigna unguiculata cDNA for stored cotyledon mRNA
                    36309
 Seq. No.
                    LIB3051-062-Q1-K1-B4
 Seq. ID
                    BLASTX
 Method
```

```
d3096935
NCBI GI
BLAST score
                  148
E value
                  3.0e-15
Match length
                  105
% identity
                  57
                  (AL023094) putative protein [Arabidopsis thaliana]
NCBI Description
                  36310
Seq. No.
Seq. ID
                  LIB3051-062-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  g3913008
BLAST score
                  210
                   2.0e-17
E value
Match length
                   51
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                   >gi_3021338_emb_CAA06308_ (AJ005041) cytosolic
                   fructose-1,6-bisphosphate aldolase [Cicer arietinum]
Seq. No.
                   36311
Seq. ID
                   LIB3051-062-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   g2465925
                   151
BLAST score
                   8.0e-10
E value
                   68
Match length
                   44
% identity
                   (AF024649) receptor-like serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   36312
                   LIB3051-062-Q1-K1-F4
Seq. ID
Method
                   BLASTX
                   q3395428
NCBI GI
                   193
BLAST score
E value
                   1.0e-14
                   120
Match length
                   44
% identity
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   36313
                   LIB3051-062-Q1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1707015
BLAST score
                   181
                   2.0e-13
E value
Match length
                   63
                   57
% identity
                   (U78721) protein phosphatase 2C isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   36314
                   LIB3051-062-Q1-K1-G5
Seq. ID
Method
                   BLASTN
                   g4097570
NCBI GI
                   53
BLAST score
                   5.0e-21
E value
```

```
Match length
                  92
% identity
                  Glycine max farnesylated protein GMFP5 mRNA, partial cds
NCBI Description
                  36315
Seq. No.
Seq. ID
                  LIB3051-063-Q1-K1-B11
                  BLASTN
Method
                  q18644
NCBI GI
BLAST score
                  361
                  0.0e + 00
E value
                  369
Match length
                   99
% identity
                  Soybean mRNA for HMG-1 like protein
NCBI Description
                  36316
Seq. No.
                  LIB3051-063-Q1-K1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2894599
                   343
BLAST score
E value
                   2.0e-32
                   88
Match length
                   67
% identity
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   36317
Seq. No.
                   LIB3051-063-Q1-K1-C5
Seq. ID
                   BLASTN
Method
NCBI GI
                   q18729
                   43
BLAST score
                   5.0e-15
E value
Match length
                   211
                   81
% identity
                  Soybean (Glycine max) 18S ribosomal RNA
NCBI Description
Seq. No.
                   36318
                   LIB3051-063-Q1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2982311
BLAST score
                   262
E value
                   8.0e-23
Match length
                   93
                   55
% identity
                   (AF051240) probable ubiquitin-conjugating enzyme E2 [Picea
NCBI Description
                   mariana]
Sea. No.
                   36319
                   LIB3051-063-Q1-K1-H7
Seq. ID
Method
                   BLASTX
                   g2191171
NCBI GI
                   277
BLAST score
                   2.0e-29
E value
                   103
Match length
                   59
% identity
                   (AF007270) similar to A. thaliana DI19 mRNA (NID:g469110)
NCBI Description
                   [Arabidopsis thaliana]
```

5540

36320

Seq. No.

```
LIB3051-064-Q1-K1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4455172
                  163
BLAST score
                  3.0e-11
E value
Match length
                  51
% identity
                   61
                  (AL035521) putative protein [Arabidopsis thaliana]
NCBI Description
                  36321
Seq. No.
                  LIB3051-064-Q1-K1-B8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2407789
                  38
BLAST score
                   4.0e-12
E value
                   42
Match length
                   98
% identity
NCBI Description Glycine max grr1 (grr1) mRNA, complete cds
                   36322
Seq. No.
                  LIB3051-064-Q1-K1-D11
Seq. ID
Method
                  BLASTX
                   g3176072
NCBI GI
                   202
BLAST score
                   5.0e-16
E value
                   57
Match length
                   65
% identity
                  (AJ002485) protein phosphatase 1, catalytic beta subunit
NCBI Description
                   [Medicago sativa]
Seq. No.
                   36323
                   LIB3051-064-Q1-K1-F10
Seq. ID
                   BLASTN
Method
                   q18764
NCBI GI
                   75
BLAST score
E value
                   3.0e - 34
                   215
Match length
                   84
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
                   36324
Seq. No.
                   LIB3051-064-Q1-K1-F8
Seq. ID
Method
                   BLASTN
                   q758249
NCBI GI
BLAST score
                   83
                   9.0e-39
E value
Match length
                   338
% identity
                   82
NCBI Description P.vulgaris mRNA for plasma membrane H+ ATPase
                   36325
Seq. No.
Seq. ID
                   LIB3051-064-Q1-K1-H10
                   BLASTN
Method
NCBI GI
                   g169980
BLAST score
                   160
                   9.0e-85
E value
Match length
                   304
```

```
% identity
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                  36326
Seq. No.
                  LIB3051-065-Q1-K1-A4
Seq. ID
Method
                  BLASTX
                  q461736
NCBI GI
                   261
BLAST score
                   1.0e-22
E value
                   95
Match length
                   57
% identity
                  MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR
NCBI Description
                   >qi 478786 pir S29316 chaperonin 60 - cucurbit
                   >gi_12546_emb_CAA50218_ (X70868) chaperonin 60 [Cucurbita
                   sp. ]
                   36327
Seq. No.
Seq. ID
                   LIB3051-065-Q1-K1-G7
                   BLASTX
Method
                   g3063465
NCBI GI
BLAST score
                   191
                   2.0e-14
E value
                   41
Match length
                   93
% identity
                  (AC003981) F22013.27 [Arabidopsis thaliana]
NCBI Description
                   36328
Seq. No.
                   LIB3051-066-Q1-K1-B9
Seq. ID
                   BLASTN
Method
                   q1370165
NCBI GI
BLAST score
                   315
                   1.0e-177
E value
                   399
Match length
                   95
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB1C
                   36329
Seq. No.
                   LIB3051-066-Q1-K1-F12
Seq. ID
                   BLASTX
Method
                   q2832700
NCBI GI
BLAST score
                   384
                   4.0e-37
E value
Match length
                   112
                   70
% identity
                  (AL021713) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   36330
                   LIB3051-066-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   g3043415
NCBI GI
BLAST score
                   152
E value
                   4.0e-10
Match length
                   77
                   49
% identity
                   (Y17053) At-hsc70-3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   36331
```

```
Seq. ID
                     В́3051-066-Q1-К1-н6
Method
                  BLASTN
NCBI GI
                  g1732555
                  95
BLAST score
                  5.0e-46
E value
                  235
Match length
                  85
% identity
                  Glycine max desiccation protective protein LEA5 (Lea5)
NCBI Description
                  mRNA, complete cds
                  36332
Seq. No.
                  LIB3051-067-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244904
BLAST score
                  133
                  2.0e-09
E value
                  91
Match length
% identity
                   46
NCBI Description
                   (Z97339) similar to hypothetical protein C02F5.7 - Caenorha
                   [Arabidopsis thaliana]
Seq. No.
                   36333
                  LIB3051-067-Q1-K1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                   g22075
BLAST score
                   108
                   1.0e-53
E value
Match length
                   176
% identity
                   90
NCBI Description
                  Vigna unguiculata cDNA for stored cotyledon mRNA
Seq. No.
                   36334
                  LIB3051-067-Q1-K1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                   g414976
BLAST score
                   84
                   2.0e-39
E value
                   230
Match length
                   76
% identity
NCBI Description
                  Glycine max Shi-shi 51 kDa seed maturation protein
                   (pGmPM10) mRNA, complete cds
                   36335
Seq. No.
                  LIB3051-067-Q1-K1-E4
Seq. ID
Method
                  BLASTN
                   g2920665
NCBI GI
BLAST score
                   74
E value
                   2.0e-33
Match length
                   166
                   87
% identity
NCBI Description
                  Glycine max 2,4-D inducible glutathione S-transferase
                   (GSTa) mRNA, complete cds
Seq. No.
                   36336
Seq. ID
                  LIB3051-068-Q1-K1-D12
Method
                  BLASTN
NCBI GI
                   g3378649
```

138

BLAST score 138
E value 1.0e-71
Match length 318
% identity 86

NCBI Description M.sativa mRNA translated from abscisic activated gene

Seq. No. 36337

Seq. ID LIB3051-068-Q1-K1-E8

Method BLASTN
NCBI GI g169958
BLAST score 66
E value 9.0e-29
Match length 214
% identity 83

NCBI Description Glycine max G-box binding factor (GBF2A) mRNA, 3' end

Seq. No. 36338

Seq. ID LIB3051-069-Q1-K1-B7

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 48
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 36339

Seq. ID LIB3051-069-Q1-K1-C7

Method BLASTN
NCBI GI 9456713
BLAST score 144
E value 2.0e-75
Match length 270
% identity 32

NCBI Description Glycine max gene for ubiquitin, complete cds

Seq. No. 36340

Seq. ID LIB3051-069-Q1-K1-D12

Method BLASTX
NCBI GI g461753
BLAST score 309
E value 3.0e-28
Match length 126
% identity 42

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

PRECURSOR >gi 419773 pir S31164 ATP-dependent ClpB

proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi\_169128 (L09547) nuclear encoded precursor

to chloroplast protein [Pisum sativum]

Seq. No. 36341

Seq. ID LIB3051-069-Q1-K1-G2

Method BLASTX
NCBI GI g4325324
BLAST score 227
E value 9.0e-19
Match length 125

Seq. ID

```
% identity
                  (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis
NCBI Description
                  thaliana]
                  36342
Seq. No.
                  LIB3051-069-Q1-K1-G9
Seq. ID
                  BLASTX
Method
                  g433970
NCBI GI
                  145
BLAST score
                  8.0e-21
E value
                  132
Match length
% identity
                  11
                 (Z28649) polyubiquitin [Acetabularia cliftonii]
NCBI Description
                  36343
Seq. No.
                  LIB3051-069-Q1-K1-H8
Seq. ID
Method
                  BLASTX
                  g1220180
NCBI GI
                  150
BLAST score
                  1.0e-09
E value
                  54
Match length
% identity
                  54
                  (Z69996) dormancy related protein [Trollius ledebourii]
NCBI Description
                  36344
Seq. No.
                  LIB3051-070-Q1-K1-B11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2815245
                  58
BLAST score
                  7.0e-24
E value
                  242
Match length
                  81
% identity
                  C.arietinum mRNA for class I type 2 metallothionein (clone:
NCBI Description
                  CanMT-2)
                   36345
Seq. No.
Seq. ID
                  LIB3051-070-Q1-K1-B9
Method
                  BLASTX
                   g3075397
NCBI GI
                   179
BLAST score
                   3.0e-13
E value
Match length
                   95
% identity
                   44
                  (AC004484) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   36346
Seq. No.
Seq. ID
                   LIB3051-070-Q1-K1-E4
Method
                   BLASTX
NCBI GI
                   q2760323
                   287
BLAST score
                   1.0e-25
E value
Match length
                   54
% identity
                  (AC002130) F1N21.8 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   36347
```

5545

LIB3051-070-Q1-K1-F5

```
Method
                  g4263722
NCBI GI
BLAST score
                   200
                   1.0e-15
E value
                   101
Match length
                   42
% identity
                  (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   36348
Seq. ID
                  LIB3051-071-Q1-K1-A11
                  BLASTN
Method
                   q4097879
NCBI GI
                   102
BLAST score
                   4.0e-50
E value
                   365
Match length
                   84
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   36349
Seq. No.
Seq. ID
                   LIB3051-071-Q1-K1-A3
Method
                   BLASTN
                   g170007
NCBI GI
                   273
BLAST score
                   1.0e-152
E value
                   385
Match length
                   93
% identity
                   Soybean 18 kD late embryogenesis abundant (Lea) protein
NCBI Description
                   mRNA, complete cds
                   36350
Seq. No.
                   LIB3051-071-Q1-K1-B3
Seq. ID
                   BLASTX
Method
NCBI GI
                   a81812
                   194
BLAST score
                   6.0e-15
E value
                   119
Match length
                   39
% identity
                   seed maturation protein - soybean >gi_18750_emb_CAA45126_
NCBI Description
                   (X63565) soybean seed maturation polypeptides [Glycine max]
                   >gi 169963 (M97285) maturation protein [Glycine max]
                   >gi_1079650 (U38246) late embryogenesis abundant protein
                   [Glycine soja] >gi_445632_prf__1909377A maturation protein
                   GmPM9 [Glycine max]
Seq. No.
                   36351
                   LIB3051-071-Q1-K1-B4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1518358
BLAST score
                   66
```

E value 1.0e-28 Match length 304 % identity 83

M.soulangeana mitochondrial gene for NADH dehydrogenase NCBI Description

subunit3 and ribosomal protein S12

Seq. No. 36352

NCBI GI

```
LIB3051-071-Q1-K1-B5
Seq. ID
                  BLASTX
Method
                  g421954
NCBI GI
                  230
BLAST score
                  2.0e-27
E value
                  153
Match length
                  42
% identity
                  hypothetical protein 3 - potato transposon Tst1
NCBI Description
                  >gi 21433 emb CAA36615 (X52387) ORF3 [Solanum tuberosum]
                  36353
Seq. No.
                  LIB3051-071-Q1-K1-D3
Seq. ID
                  BLASTX
Method
                  q1841870
NCBI GI
                  201
BLAST score
                  1.0e-15
E value
Match length
                  66
                  59
% identity
                  (U87222) elongation factor 1-beta [Pimpinella brachycarpa]
NCBI Description
                  36354
Seq. No.
                  LIB3051-071-Q1-K1-D9
Seq. ID
Method
                  BLASTN
                  g2055229
NCBI GI
BLAST score
                  94
                  2.0e-45
E value
                  246
Match length
                  85
% identity
NCBI Description Soybean mRNA for SRC2, complete cds
                  36355
Seq. No.
Seq. ID
                  LIB3051-071-Q1-K1-F5
                  BLASTX
Method
NCBI GI
                   g4204288
BLAST score
                   314
                   5.0e-29
E value
Match length
                  105
                   52
% identity
                  (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   36356
Seq. ID
                  LIB3051-071-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                   q2499613
                   199
BLAST score
                   1.0e-15
E value
Match length
                   103
                   44
% identity
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG MMK2
NCBI Description
                   >gi 1204129 emb CAA57719 (X82268) protein kinase [Medicago
                   sativa]
Seq. No.
                   36357
Seq. ID
                   LIB3051-072-Q1-K1-B5
Method
                   BLASTX
```

g2738248

```
BLAST score
                  8.0e-16
E value
                  66
Match length
                  65
% identity
                  (U97200) cobalamin-independent methionine synthase
NCBI Description
                  [Arabidopsis thaliana]
                  36358
Seq. No.
                  LIB3051-072-Q1-K1-E2
Seq. ID
Method
                  BLASTX
                  q4538923
NCBI GI
BLAST score
                  159
                  7.0e-11
E value
Match length
                   65
                   48
% identity
                   (AL049483) predicted protein destination factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   36359
                  LIB3051-072-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4538923
BLAST score
                   240
                   2.0e-20
E value
                   68
Match length
                   68
% identity
                   (AL049483) predicted protein destination factor
NCBI Description
                   [Arabidopsis thaliana]
                   36360
Seq. No.
                   LIB3051-072-Q1-K1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q464986
                   199
BLAST score
                   1.0e-15
E value
                   63
Match length
                   62
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                   >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
                   6.3.2.19) UBC9 - Arabidopsis thaliana
                   >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639)
                   ubiquitin conjugating enzyme [Arabidopsis thaliana]
                   >qi 600391 emb CAA51201 (X72626) ubiquitin conjugating
                   enzyme E2 [Arabidopsis thaliana]
                   >qi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein
                   ligase UBC9 [Arabidopsis thaliana]
                   36361
Seq. No.
Seq. ID
                   LIB3051-072-Q1-K1-H9
                   BLASTX
Method
                   g4455208
NCBI GI
                   140
BLAST score
                   5.0e-09
E value
Match length
                   57
```

51

% identity

```
(AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                  36362
Seq. No.
Seq. ID
                  LIB3051-073-Q1-K1-A6
                  BLASTN
Method
                  g3821780
NCBI GI
                  33
BLAST score
                  3.0e-09
E value
                  38
Match length
% identity
                  45
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  36363
Seq. No.
                  LIB3051-073-Q1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4160280
                  164
BLAST score
                  2.0e-11
E value
                  53
Match length
                  60
% identity
                  (AJ006224) purple acid phosphatase [Ipomoea batatas]
NCBI Description
Seq. No.
                  36364
                  LIB3051-073-Q1-K1-F11
Seq. ID
                  BLASTX
Method
                  q464985
NCBI GI
                   250
BLAST score
                  2.0e-21
E value
                  86
Match length
                   59
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A)
                   >gi 398699 emb CAA78713 (Z14989) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana]
                   36365
Seq. No.
Seq. ID
                   LIB3051-074-Q1-K1-B6
                   BLASTX
Method
                   g1168410
NCBI GI
BLAST score
                   155
                   7.0e-11
E value
Match length
                   48
                   69
% identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 2
NCBI Description
                   >gi_2118267_pir S58167 fructose-bisphosphate aldolase (EC
                   4.1.2.13) - garden pea >gi 927505 emb_CAA61947_ (X89829)
                   fructose-1,6-bisphosphate aldolase [Pisum sativum]
                   36366
Seq. No.
Seq. ID
                   LIB3051-074-Q1-K1-C1
Method
                   BLASTX
NCBI GI
                   g3063708
BLAST score
                   471
                   3.0e-47
E value
Match length
                   134
% identity
                   67
                   (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
```

BLAST score

E value

36 1.0e-10

```
36367
Seq. No.
                  LIB3051-074-Q1-K1-C5
Seq. ID
                  BLASTX
Method
                  g2921317
NCBI GI
                  145
BLAST score
                  2.0e-09
E value
                  66
Match length
                  50
% identity
NCBI Description (AF034108) beta-1,3-glucanase 3 [Glycine max]
                  36368
Seq. No.
                  LIB3051-074-Q1-K1-G9
Seq. ID
                  BLASTX
Method
                  g2598589
NCBI GI
                  197
BLAST score
                  1.0e-15
E value
                   76
Match length
                   50
% identity
NCBI Description (Y15367) MtN19 [Medicago truncatula]
Seq. No.
                   36369
                   LIB3051-075-Q1-K1-B12
Seq. ID
                   BLASTN
Method
                   q3821780
NCBI GI
                   36
BLAST score
                   6.0e-11
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   36370
Seq. No.
                   LIB3051-075-Q1-K1-D4
Seq. ID
                   BLASTN
Method
                   g3821780
NCBI GI
                   36
BLAST score
                   1.0e-10
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   36371
Seq. No.
                   LIB3051-075-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   g1177405
NCBI GI
                   145
BLAST score
                   2.0e-09
E value
                   70
Match length
                   41
 % identity
                  (X89855) citrate binding protein [Hevea brasiliensis]
NCBI Description
                   36372
 Seq. No.
                   LIB3051-075-Q1-K1-F7
 Seq. ID
                   BLASTN
Method
                   g3821780
 NCBI GI
```

200

```
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  36373
Seq. No.
                  LIB3051-077-Q1-K1-B6
Seq. ID
                  BLASTX
Method
                  g2708744
NCBI GI
                  306
BLAST score
                  5.0e-28
E value
                  130
Match length
% identity
                   46
                   (AC003952) putative Bop-like zinc finger protein
NCBI Description
                   [Arabidopsis thaliana]
                   36374
Seq. No.
                  LIB3051-077-Q1-K1-E5
Seq. ID
                  BLASTX
Method
                   g3135265
NCBI GI
                   125
BLAST score
                   5.0e-15
E value
Match length
                   80
% identity
                   57
                   (AC003058) unknown protein [Arabidopsis thaliana]
NCBI Description
                   36375
Seq. No.
                   LIB3051-077-Q1-K1-H12
Seq. ID
Method
                   BLASTX
                   g2708741
NCBI GI
                   307
BLAST score
                   5.0e-28
E value
                   128
Match length
% identity
                   53
                  (AC003952) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   36376
Seq. No.
                   LIB3051-078-Q1-K1-A12
Seq. ID
                   BLASTN
Method
                   g2052028
NCBI GI
                   123
BLAST score
                   8.0e-63
E value
                   219
Match length
                   89
 % identity
                   G.max mRNA for glutathione transferase
 NCBI Description
                   36377
 Seq. No.
                   LIB3051-078-Q1-K1-B3
 Seq. ID
                   BLASTX
 Method
                   q2435519
NCBI GI
```

Method BLASTX
NCBI GI g2435519
BLAST score 214
E value 2.0e-17
Match length 88
% identity 52

NCBI Description (AF024504) similar to mouse MEM3 (GB:U47024 and S.

cerevisiae vacuolar sorting protein 35 (SW; P34110)

[Arabidopsis thaliana]

```
Seq. No.
                  LIB3051-078-Q1-K1-C2
Seq. ID
                  BLASTN
Method
                  g1498171
NCBI GI
                  133
BLAST score
                  5.0e-69
E value
                  165
Match length
                  95
% identity
NCBI Description Glycine max mRNA for uricase (Nod-35), complete cds
                  36379
Seq. No.
                  LIB3051-078-Q1-K1-E6
Seq. ID
                  BLASTX
Method
                  g1707640
NCBI GI
                   301
BLAST score
                   2.0e-27
E value
                   90
Match length
                   63
% identity
                  (X98355) transcription factor GAMyb [Oryza sativa]
NCBI Description
                   36380
Seq. No.
                   LIB3051-078-Q1-K1-E9
Seq. ID
                  BLASTX
Method
                   g1542941
NCBI GI
                   226
BLAST score
                   9.0e-19
E value
                   57
Match length
                   81
% identity
                  (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
NCBI Description
                   36381
Seq. No.
                   LIB3051-078-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   g159967
NCBI GI
                   158
BLAST score
                   8.0e-11
E value
                   80
Match length
                   46
% identity
                   (M36919) histone H3 [Paracentrotus lividus]
NCBI Description
                   36382
Seq. No.
Seq. ID
                   LIB3051-078-Q1-K1-G11
                   BLASTX
Method
                   g2147484
NCBI GI
                   414
BLAST score
                   9.0e-41
E value
Match length
                   115
                   64
% identity
                   homeotic protein - Phalaenopsis sp >gi 1173622 (U34743)
NCBI Description
                   homeobox protein [Phalaenopsis sp. 'hybrid SM9108']
Seq. No.
                   36383
                   LIB3051-079-Q1-K1-D5
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3510343
BLAST score
                   46
                   1.0e-16
E value
```

% identity

NCBI Description

pSport2]

```
Match length
                  84
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
                  36384
Seq. No.
                  LIB3051-079-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  g4378659
NCBI GI
                  150
BLAST score
                  7.0e-10
E value
                  32
Match length
                  88
% identity
                   (AF107726) cyclic nucleotide gated channel [Arabidopsis
NCBI Description
                  thaliana]
                   36385
Seq. No.
                  LIB3051-079-Q1-K1-H10
Seq. ID
                  BLASTN
Method
                   g479059
NCBI GI
BLAST score
                   373
                   0.0e + 00
E value
                   381
Match length
                   99
% identity
                  G.max (Fiskeby V) mRNA for cysteine endopeptidase
NCBI Description
                   36386
Seq. No.
                   LIB3051-079-Q1-K1-H11
Seq. ID
                   BLASTN
Method
                   g479059
NCBI GI
                   170
BLAST score
E value
                   7.0e-91
                   210
Match length
                   95
% identity
                   G.max (Fiskeby V) mRNA for cysteine endopeptidase
NCBI Description
                   36387
Seq. No.
Seq. ID
                   LIB3051-080-Q1-K1-G6
                   BLASTN
Method
                   g2270993
NCBI GI
BLAST score
                   43
                   2.0e-15
E value
                   91
Match length
                   87
% identity
                   Glycine max Ca+2-binding EF hand protein (GmPM13) mRNA,
NCBI Description
                   complete cds
                   36388
Seq. No.
                   LIB3051-081-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   g825756
NCBI GI
BLAST score
                   161
                   5.0e-11
E value
                   75
Match length
```

(U12391) beta-galactosidase alpha peptide [Cloning vector



```
36389
Seq. No.
Seq. ID
                  LIB3051-081-Q1-K1-G1
                  BLASTX
Method
                  g2887288
NCBI GI
                  281
BLAST score
                  5.0e-25
E value
                  109
Match length
                  47
% identity
                  (AJ001810) mRNA cleavage factor I 25 kDa subunit [Homo
NCBI Description
                  sapiens]
                  36390
Seq. No.
                  LIB3051-081-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                   g1514643
NCBI GI
                   220
BLAST score
                   7.0e-18
E value
                   136
Match length
                   39
% identity
NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
                   36391
Seq. No.
                   LIB3051-082-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   g282994
NCBI GI
                   163
BLAST score
                   2.0e-24
E value
                   86
Match length
                   76
% identity
                   Sip1 protein - barley >gi_167100 (M77475) seed imbibition
NCBI Description
                   protein [Hordeum vulgare]
                   36392
Seq. No.
Seq. ID
                   LIB3051-083-Q1-K1-B4
                   BLASTX
Method
                   g3776581
NCBI GI
                   141
BLAST score
                   1.0e-08
E value
                   75
Match length
% identity
                   (AC005388) Similar to Beta integral membrane protein
NCBI Description
                   homolog gb_U43629 from A. thaliana. [Arabidopsis thaliana]
                   36393
Seq. No.
                   LIB3051-083-Q1-K1-D4
Seq. ID
                   BLASTN
Method
                   q1161251
NCBI GI
                   327
BLAST score
                   0.0e + 00
E value
                   335
Match length
                   99
 % identity
                   Glycine max nucleosome assembly protein 1 (SNAP-1) mRNA,
NCBI Description
                   complete cds
```

Seq. No. 36394

Seq. ID LIB3051-084-Q1-K1-B11

```
Method
                  q4512653
NCBI GI
BLAST score
                   506
                   2.0e-51
E value
                   126
Match length
                   79
% identity
                  (AC007048) unknown protein [Arabidopsis thaliana]
NCBI Description
                   36395
Seq. No.
Seq. ID
                  LIB3051-084-Q1-K1-D12
                   BLASTN
Method
                   g18743
NCBI GI
                   42
BLAST score
E value
                   1.0e-14
Match length
                   122
                   84
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
                   36396
Seq. No.
Seq. ID
                   LIB3051-084-Q1-K1-H7
Method
                   BLASTX
                   g3033386
NCBI GI
                   163
BLAST score
                   4.0e-11
E value
                   87
Match length
                   44
% identity
                   (ACO04238) RING3-like protein [Arabidopsis thaliana]
NCBI Description
                   36397
Seq. No.
Seq. ID
                   LIB3051-085-Q1-K1-B11
Method
                   BLASTX
                   q3421123
NCBI GI
                   408
BLAST score
                   6.0e-40
E value
                   113
Match length
% identity
                   (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   36398
Seq. ID
                   LIB3051-085-Q1-K1-D9
                   BLASTX
Method
NCBI GI
                   g3688193
BLAST score
                   206
                   3.0e-16
E value
Match length
                   93
 % identity
                   51
                   (AJ010091) MAP3K alpha 1 protein kinase [Brassica napus]
NCBI Description
                   36399
 Seq. No.
                   LIB3051-085-Q1-K1-E5
 Seq. ID
                   BLASTX
Method
                   g4218535
NCBI GI
 BLAST score
                   183
                   9.0e-14
 E value
                   70
 Match length
                   54
 % identity
```

## (AJ010829) GRAB1 protein [Triticum sp.] NCBI Description 36400 Seq. No. LIB3051-085-Q1-K1-H11 Seq. ID BLASTX Method q2507421 NCBI GI 183 BLAST score 1.0e-14E value 72 Match length 64 % identity PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi\_1800277 NCBI Description (U81042) translation initiation factor [Arabidopsis thaliana] >gi 4490709 emb CAB38843.1 (AL035680) translation initiation factor [Arabidopsis thaliana] 36401 Seq. No. LIB3051-085-Q1-K1-H4 Seq. ID BLASTX Method g2982303 NCBI GI 220 BLAST score 4.0e-18 E value 76 Match length % identity 62 (AF051236) hypothetical protein [Picea mariana] NCBI Description 36402 Seq. No. LIB3051-086-Q1-K1-A3 Seq. ID BLASTX Method g2970051 NCBI GI 287 BLAST score 7.0e-26 E value 107 Match length % identity 59 (AB012110) ARG10 [Vigna radiata] NCBI Description 36403 Seq. No. LIB3051-086-Q1-K1-C10 Seq. ID BLASTX Method g1168529 NCBI GI 231 BLAST score 4.0e-25 E value 107 Match length 58 % identity SERINE/THREONINE-PROTEIN KINASE ASK1 >gi\_541890\_pir\_ NCBI Description probable serine/threonine-specific protein kinase (EC 2.7.1.-) (clone ASK1) - Arabidopsis thaliana >gi\_166882 (M91548) serine/threonine kinase [Arabidopsis thaliana] >gi\_1931648 (U95973) Ser/Thr kinase [Arabidopsis thaliana] 36404 Seq. No. LIB3051-086-Q1-K1-E11 Seq. ID BLASTN Method q18764 NCBI GI 124 BLAST score 2.0e-63 E value

228

89

Match length

% identity

```
NCBI Description G.max tefS1 gene for elongation factor EF-la
                  36405
Seq. No.
                  LIB3051-086-Q1-K1-E3
Seq. ID
                  BLASTN
Method
                  g18743
NCBI GI
                  70
BLAST score
                  5.0e-31
E value
                  166
Match length
                  86
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
                  36406
Seq. No.
                  LIB3051-086-Q1-K1-H12
Seq. ID
                  BLASTX
Method
                  g464981
NCBI GI
BLAST score
                   158
                   7.0e-11
E value
                   76
Match length
                   49
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762)
                   ubiquitin carrier protein [Lycopersicon esculentum]
                   36407
Seq. No.
                   LIB3051-087-Q1-K1-B2
Seq. ID
                   BLASTX
Method
                   g2275216
NCBI GI
                   162
BLAST score
                   1.0e-11
E value
                   47
Match length
                   62
% identity
                   (AC002337) cytochrome c oxidase Vc subunit isolog
NCBI Description
                   [Arabidopsis thaliana]
                   36408
 Seq. No.
                   LIB3051-087-Q1-K1-C10
 Seq. ID
                   BLASTX
 Method
                   q1708152
 NCBI GI
                   177
 BLAST score
                   8.0e-13
 E value
                   114
 Match length
                   35
 % identity
                   PROBABLE ATP-DEPENDENT RNA HELICASE DBP5 (HELICASE CA5/6)
 NCBI Description
                   >gi_2133053_pir__S66920 probable RNA helicase CA5/6 - yeast
                   (Saccharomyces cerevisiae) >gi_1353268 (U28135) Dbp5p
```

Seq. No. 36409

Seq. ID LIB3051-087-Q1-K1-E9

Method BLASTX
NCBI GI g2342682
BLAST score 169
E value 2.0e-12
Match length 56
% identity 57

[Saccharomyces cerevisiae] >gi\_1420175\_emb\_CAA99237\_(Z74954) ORF YOR046c [Saccharomyces cerevisiae]

NCBI Description

```
protein kinase (gb_X95577). [Arabidopsis thaliana]
                  36410
Seq. No.
                  LIB3051-087-Q1-K1-F3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g18743
                  114
BLAST score
E value
                  3.0e-57
                  382
Match length
                  83
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
                  36411
Seq. No.
                  LIB3051-087-Q1-K1-F8
Seq. ID
                  BLASTX
Method
                  g4049532
NCBI GI
BLAST score
                   197
                   4.0e-15
E value
                   73
Match length
% identity
NCBI Description (AL031764) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                   36412
                   LIB3051-087-Q1-K1-G6
Seq. ID
                   BLASTN
Method
                   q473987
NCBI GI
                   36
BLAST score
                   5.0e-11
E value
                   92
Match length
% identity
NCBI Description Rice mRNA, partial homologous to histone H3 gene
Seq. No.
                   36413
                   LIB3051-087-Q1-K1-H4
Seq. ID
Method
                   BLASTX
                   q4559353
NCBI GI
                   319
BLAST score
                   2.0e-29
E value
                   140
Match length
                   50
% identity
                   (AC006585) putative extragenic suppressor protein
NCBI Description
                   [Arabidopsis thaliana]
                   36414
Seq. No.
                   LIB3051-087-Q1-K1-H9
Seq. ID
                   BLASTX
Method
                   g3319354
NCBI GI
                   272
BLAST score
                   8.0e-37
E value
                   111
Match length
                   78
 % identity
                   (AF077407) contains similarity to sugar transporters (Pfam:
NCBI Description
                   sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
                   36415
 Seq. No.
                   LIB3051-088-Q1-K1-B3
 Seq. ID
```

(AC000106) Contains similarity to Rattus AMP-activated

```
BLASTX
Method
                  g3641252
NCBI GI
                  185
BLAST score
                  9.0e-14
E value
                  87
Match length
% identity
                  17
                   (AF053127) leucine-rich receptor-like protein kinase [Malus
NCBI Description
                  domestica]
                   36416
Seq. No.
                  LIB3051-088-Q1-K1-C7
Seq. ID
Method
                  BLASTX
                  q134194
NCBI GI
                  159
BLAST score
                   4.0e-11
E value
Match length
                   51
                   63
% identity
                  STRESS-INDUCED PROTEIN SAM22 >gi 99918 pir S20518
NCBI Description
                   hypothetical protein - soybean >gi_18744_emb_CAA42646_
                   (X60043) ORF [Glycine max]
Seq. No.
                   36417
                   LIB3051-088-Q1-K1-H10
Seq. ID
Method
                   BLASTX
                   g1549222
NCBI GI
                   233
BLAST score
                   3.0e-41
E value
Match length
                   89
                   96
% identity
                   (D87821) NtSarl protein [Nicotiana tabacum]
NCBI Description
                   36418
Seq. No.
                   LIB3051-090-Q1-K1-A12
Seq. ID
                   BLASTN
Method
                   g3171875
NCBI GI
                   169
BLAST score
                   3.0e-90
E value
                   266
Match length
                   98
% identity
                   Homo sapiens DNA sequence from PAC 127D3 on chromosome
NCBI Description
                   1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing
                   Monooxygenase 2 and Flavin-containing Monooxygenase 3
                   (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.1
                   36419
Seq. No.
                   LIB3051-090-Q1-K1-C12
Seq. ID
                   BLASTN
Method
                   g339567
NCBI GI
BLAST score
                   363
                   0.0e + 00
E value
                   383
Match length
                   99
 % identity
                   Human transforming growth factor-beta induced gene product
NCBI Description
                   (BIGH3) mRNA, complete cds.
                   >qi 4507466 ref NM 000358.1 TGFBI_ Homo sapiens
```

transforming growth factor, beta-induced, 68kD (TGFBI) mRNA

>gi\_996468 gb\_I14045\_I14045 Sequence 1 from patent US



```
36420
Seq. No.
                  LIB3051-090-Q1-K1-D12
Seq. ID
Method
                  BLASTN
                  g4557017
NCBI GI
                  391
BLAST score
                  0.0e+00
E value
                  411
Match length
                  99
% identity
                  Homo sapiens chitinase 3-like 1 (cartilage glycoprotein-39)
NCBI Description
                   (CHI3L1) mRNA
Seq. No.
                  LIB3051-090-Q1-K1-E7
Seq. ID
                  BLASTN
Method
                   q510514
NCBI GI
                   116
BLAST score
                   2.0e-58
E value
                   403
Match length
% identity
NCBI Description G.max KTi-S mRNA
                   36422
Seq. No.
                   LIB3051-090-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   q3080371
NCBI GI
                   94
BLAST score
                   1.0e-08
E value
                   84
Match length
                   45
% identity
                   (AL022580) putative pectinacetylesterase protein
NCBI Description
                   [Arabidopsis thaliana]
                   36423
Seq. No.
                   LIB3051-090-Q1-K1-F4
Seq. ID
Method
                   BLASTX
                   g4006893
NCBI GI
                   423
BLAST score
                   1.0e-41
E value
                   136
Match length
                   78
% identity
                   (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
NCBI Description
                   36424
 Seq. No.
                   LIB3051-090-Q1-K1-G12
 Seq. ID
                   BLASTN
Method
                   g452937
 NCBI GI
                   279
 BLAST score
                   1.0e-156
 E value
                   303
 Match length
                   98
 % identity
                   complement factor B [human, liver, mRNA, 2447 nt]
 NCBI Description
                   36425
 Seq. No.
                   LIB3051-090-Q1-K1-H1
 Seq. ID
```

BLASTX

g4455155

Method

NCBI GI

```
BLAST score
                  6.0e-21
E value
                  93
Match length
% identity
                   58
                   (AL022023) EF-1 alpha - like protein (fragment)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   36426
                   LIB3051-090-Q1-K1-H2
Seq. ID
Method
                   BLASTX
                   q1906826
NCBI GI
BLAST score
                   160
                   5.0e-11
E value
                   87
Match length
                   52
% identity
NCBI Description (Y11827) heat shock protein [Arabidopsis thaliana]
                   36427
Seq. No.
                   LIB3051-090-Q1-K1-H7
Seq. ID
Method
                   BLASTN
                   g170009
NCBI GI
                   149
BLAST score
E value
                   3.0e-78
Match length
                   245
% identity
                   Soybean late embryogenesis abundant (LEA) protein mRNA,
NCBI Description
                   complete cds
Seq. No.
                   36428
                   LIB3051-091-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   g4102839
NCBI GI
BLAST score
                   161
                   1.0e-11
E value
                   96
Match length
% identity
                   45
                   (AF016713) LeOPT1 [Lycopersicon esculentum]
NCBI Description
                   36429
Seq. No.
                   LIB3051-091-Q1-K1-A5
Seq. ID
                   BLASTN
Method
                   g1778373
NCBI GI
                   55
BLAST score
                   4.0e-22
 E value
                   103
Match length
                   89
 % identity
                   Pisum sativum glycine-rich RNA-binding protein PsGRBP mRNA,
 NCBI Description
                   complete cds
                    36430
 Seq. No.
                   LIB3051-091-Q1-K1-B5
 Seq. ID
                   BLASTX
 Method
                    g4580467
 NCBI GI
                    360
 BLAST score
                    3.0e-34
 E value
                    131
 Match length
                    59
 % identity
```

```
(AC006081) putative protein phosphatase; similar to protein
NCBI Description
                   phosphatase 2C from Mesembryanthemum [Arabidopsis thaliana]
                   36431
Seq. No.
                   LIB3051-091-Q1-K1-C1
Seq. ID
                   BLASTX
Method
                   g2959358
NCBI GI
                   189
BLAST score
                   2.0e-14
E value
                   76
Match length
 % identity
                   (X96758) clathrin coat assembly protein AP17 [Zea mays]
NCBI Description
                   36432
 Seq. No.
                   LIB3051-091-Q1-K1-D6
 Seq. ID
                   BLASTX
 Method
                   g2632527
 NCBI GI
 BLAST score
                   120
                   7.0e-15
 E value
                   82
 Match length
 % identity
                    (Z99105) similar to hypothetical proteins [Bacillus
 NCBI Description
                    subtilis] >gi_3599664_dbj_BAA33139_ (AB006424) ybgG
                    [Bacillus subtilis]
                    36433
 Seq. No.
                    LIB3051-091-Q1-K1-E12
 Seq. ID
                    BLASTX
 Method
                    g3927830
 NCBI GI
                    187
 BLAST score
                    1.0e-14
 E value
                    63
 Match length
 % identity
                    (AC005727) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    36434
 Seq. No.
                    LIB3051-091-Q1-K1-F7
 Seq. ID
                    BLASTN
 Method
                    q762878
 NCBI GI
                    61
 BLAST score
                    1.0e-25
 E value
                    136
 Match length
                    87
 % identity
                    Psophocarpus tetragonolobus mRNA for chitinase, complete
 NCBI Description
                    cds
                    36435
 Seq. No.
                    LIB3051-091-Q1-K1-H7
 Seq. ID
                    BLASTX
 Method
                    g2661840
 NCBI GI
                    271
 BLAST score
                    7.0e-24
 E value
                    109
 Match length
                    53
  % identity
                    (Y15430) adenosine kinase [Physcomitrella patens]
  NCBI Description
                    36436
  Seq. No.
```

```
LIB3051-091-Q1-K1-H9
Seq. ID
                  BLASTX
Method
                  g2924777
NCBI GI
                  190
BLAST score
                  3.0e-14
E value
                  147
Match length
% identity
                  (AC002334) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  36437
Seq. No.
                  LIB3051-092-Q1-K1-B6
Seq. ID
                  BLASTX
Method
                  g2130051
NCBI GI
                  227
BLAST score
                  6.0e-19
E value
                  89
Match length
                  54
% identity
                  xylose isomerase (EC 5.3.1.5) - barley
NCBI Description
                  >gi_1296807_emb_CAA64544 (X95256) xylose isomerase
                   [Hordeum vulgare] >gi_1588664_prf__2209268A xylose
                   isomerase [Hordeum vulgare]
                   36438
Seq. No.
                  LIB3051-092-Q1-K1-C4
Seq. ID
                  BLASTN
Method
                   g4519672
NCBI GI
                   63
BLAST score
                   7.0e-27
E value
                   131
Match length
                   87
% identity
NCBI Description Nicotiana tabacum WREBP-2 mRNA, complete cds
                   36439
Seq. No.
                   LIB3051-092-Q1-K1-D1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1707021
BLAST score
                   265
                   3.0e-23
E value
                   113
Match length
% identity
                   (U78721) Ubiquitin-conjugating enzyme, E2-16kD isolog
NCBI Description
                   [Arabidopsis thaliana]
                   36440
Seq. No.
                   LIB3051-092-Q1-K1-G2
Seq. ID
Method
                   BLASTX
                   g1848212
NCBI GI
                   151
BLAST score
                   4.0e-10
E value
                   70
Match length
                   24
 % identity
                   (Y11209) protein disulfide-isomerase precursor [Nicotiana
NCBI Description
                   tabacum]
 Seq. No.
                   36441
 Seq. ID
                   LIB3051-092-Q1-K1-H8
```

Seq. ID

Method NCBI GI

```
Method
NCBI GI
                  q2580499
                  185
BLAST score
                   9.0e-14
E value
                  111
Match length
                   42
% identity
                  (U67186) NADPH: ferrihemoprotein oxidoreductase
NCBI Description
                   [Eschscholzia californica]
                   36442
Seq. No.
                  LIB3051-093-Q1-K1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                   q2338731
                   345
BLAST score
                   0.0e+00
E value
                   365
Match length
% identity
                   Homo sapiens phosphatidylinositol synthase (PIS) mRNA,
NCBI Description
                   complete cds
                   36443
Seq. No.
                   LIB3051-093-Q1-K1-C10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q23896
BLAST score
                   347
                   0.0e + 00
E value
                   379
Match length
                   99
% identity
                   Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5)
NCBI Description
                   >gi_4505466_ref_NM_002526.1 NT5 Homo sapiens 5'
                   nucleotidase (CD73) (NT5) mRNA
Seq. No.
                   LIB3051-093-Q1-K1-C3
Seq. ID
Method
                   BLASTX
                   g2665890
NCBI GI
                   194
BLAST score
                   7.0e-15
E value
                   70
Match length
                   57
% identity
                   (AF035944) calcium-dependent protein kinase [Fragaria x
NCBI Description
                   ananassa]
                   36445
Seq. No.
                   LIB3051-093-Q1-K1-F12
Seq. ID
                   BLASTN
Method
                   g303900
NCBI GI
                   311
BLAST score
                   1.0e-175
E value
                   389
Match length
                   29
 % identity
                   Soybean gene for ubiquitin, complete cds
 NCBI Description
                   36446
 Seq. No.
```

5564

LIB3051-093-Q1-K1-H7

BLASTX

q3738316

```
BLAST score
                  3.0e-21
E value
                  73
Match length
                   64
% identity
                   (AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
                   36447
Seq. No.
                   LIB3051-094-Q1-K1-A1
Seq. ID
                   BLASTN
Method
                   q3821780
NCBI GI
                   32
BLAST score
                   1.0e-08
E value
                   72
Match length
                   41
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   36448
Seq. No.
                   LIB3051-094-Q1-K1-B12
Seq. ID
                   BLASTX
Method
                   g2244876
NCBI GI
BLAST score
                   184
E value
                   4.0e-15
Match length
                   105
                   45
% identity
                   (Z97338) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   36449
Seq. No.
                   LIB3051-094-Q1-K1-F12
Seq. ID
Method
                   BLASTX
                   g3355478
NCBI GI
                   195
BLAST score
                   6.0e-15
E value
                   106
Match length
                   42
% identity
                   (AC004218) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   36450
Seq. No.
                   LIB3051-094-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   g1109697
NCBI GI
                   218
BLAST score
                   1.0e-17
E value
                   73
Match length
                   53
 % identity
                   (X83380) gibberellin 20-oxidase [Arabidopsis thaliana]
NCBI Description
                   36451
 Seq. No.
                   LIB3051-094-Q1-K1-H8
 Seq. ID
                   BLASTN
Method
NCBI GI
                   q456713
 BLAST score
                   164
                   3.0e-87
 E value
                   252
Match length
                   29
 % identity
                   Glycine max gene for ubiquitin, complete cds
 NCBI Description
```

36452

Seq. No.

```
LIB3051-095-Q1-K1-A11
Seq. ID
                  BLASTN
Method
                  g1794171
NCBI GI
                   41
BLAST score
                   7.0e-14
E value
                  109
Match length
                   85
% identity
NCBI Description Glycine max lipoxygenase-3 mRNA, complete cds
                   36453
Seq. No.
                  LIB3051-095-Q1-K1-C8
Seq. ID
                   BLASTX
Method
                   q4090259
NCBI GI
                   223
BLAST score
                   1.0e-18
E value
                   76
Match length
                   53
% identity
                   (AJ131733) ubiquitin-conjugating enzyme E2 [Pseudotsuga
NCBI Description
                   menziesii]
                   36454
Seq. No.
                   LIB3051-095-Q1-K1-D3
Seq. ID
                   BLASTX
Method
                   g2829927
NCBI GI
                   196
BLAST score
                   4.0e-15
E value
                   121
Match length
                   43
% identity
                   (AC002291) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   36455
Seq. No.
                   LIB3051-095-Q1-K1-D7
Seq. ID
                   BLASTX
Method
                   g4006829
NCBI GI
                   213
BLAST score
                   3.0e-35
E value
                   93
Match length
                   86
% identity
                   (AC005970) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   36456
Seq. No.
                   LIB3051-095-Q1-K1-F6
Seq. ID
                   BLASTN
Method
NCBI GI
                   q170065
                   290
BLAST score
                   1.0e-162
E value
                   346
Match length
                   12
% identity
                   Soybean (G.max) proline-rich cell wall protein (SbPRP2)
NCBI Description
                   gene, complete cds
                   36457
Seq. No.
Seq. ID
                   LIB3051-095-Q1-K1-H1
                   BLASTN
Method
                   g170065
NCBI GI
BLAST score
                   194
                   1.0e-105
E value
```

```
Match length
                  19
% identity
                  Soybean (G.max) proline-rich cell wall protein (SbPRP2)
NCBI Description
                  gene, complete cds
                  36458
Seq. No.
                  LIB3051-096-Q1-K1-B12
Seq. ID
                  BLASTX
Method
                  g3548802
NCBI GI
                  610
BLAST score
                  1.0e-63
E value
                  147
Match length
                  75
% identity
                   (AC005313) axi 1-like protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein
                   [Nicotiana tabacum] [Arabidopsis thaliana]
                   36459
Seq. No.
                   LIB3051-096-Q1-K1-C1
Seq. ID
                   BLASTX
Method
                   g4567286
NCBI GI
BLAST score
                   312
                   1.0e-28
E value
                   89
Match length
% identity
                   (AC006841) putative coatomer alpha subunit [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   36460
                   LIB3051-096-Q1-K1-E1
Seq. ID
                   BLASTX
Method
                   g3482974
NCBI GI
                   187
BLAST score
                   3.0e-17
E value
                   136
Match length
                   46
% identity
                   (AL031369) ATP-dependent Clp proteinase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   36461
Seq. No.
                   LIB3051-096-Q1-K1-F1
Seq. ID
                   BLASTX
Method
                   g4567286
NCBI GI
                   486
BLAST score
                   5.0e-49
E value
                   100
Match length
 % identity
                   (AC006841) putative coatomer alpha subunit [Arabidopsis
 NCBI Description
                   thaliana]
                   36462
 Seq. No.
Seq. ID
                   LIB3051-096-Q1-K1-F5
                   BLASTX
 Method
                   q4567286
 NCBI GI
 BLAST score
                   168
                    9.0e-12
 E value
                    92
 Match length
```

```
% identity
NCBI Description
                   (AC006841) putative coatomer alpha subunit [Arabidopsis
                  thaliana]
Seq. No.
                  36463
Seq. ID
                  LIB3051-096-Q1-K1-G3
Method
                  BLASTX
                  g4538947
NCBI GI
BLAST score
                  458
E value
                  9.0e-46
                  117
Match length
% identity
                  38
                   (AL049483) putative mitochondrial carrier protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  36464
Seq. ID
                  LIB3051-096-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g3021348
BLAST score
                  183
                  3.0e-17
E value
                  89
Match length
                  64
% identity
                  (AJ004961) ribosomal protein L18 [Cicer arietinum]
NCBI Description
Seq. No.
                  36465
                  LIB3051-097-Q1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1399379
BLAST score
                  95
E value
                  5.0e-46
Match length
                  211
% identity
                  94
                  Glycine max S-adenosyl-L-methionine:delta24-sterol-C-
NCBI Description
                  methyltransferase mRNA, complete cds
Seq. No.
                  36466
                  LIB3051-097-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3641868
BLAST score
                  156
                  5.0e-11
E value
Match length
                  51
% identity
                  61
NCBI Description
                  (AJ011012) hypothetical protein [Cicer arietinum]
```

Seq. No. 36467

Seq. ID LIB3051-097-Q1-K1-F11

Method BLASTN
NCBI GI g2920665
BLAST score 47
E value 7.0e-18
Match length 115
% identity 88

NCBI Description Glycine max 2,4-D inducible glutathione S-transferase

(GSTa) mRNA, complete cds

```
Seq. No.
                  LIB3051-097-Q1-K1-H11
Seq. ID
                  BLASTX
Method
                  g3834316
NCBI GI
                  159
BLAST score
                  1.0e-10
E value
                  53
Match length
                  49
% identity
                  (AC005679) Similar to gb X16648 pathogenesis related
NCBI Description
                  protein from Hordeum vulgare. EST gb_Z18206 comes from
                  this gene. [Arabidopsis thaliana]
                  36469
Seq. No.
                  LIB3051-098-Q1-K1-E1
Seq. ID
                  BLASTX
Method
                  g3643607
NCBI GI
                  233
BLAST score
                   6.0e-20
E value
                  74
Match length
                   42
% identity
                   (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   36470
                   LIB3051-098-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                   q1171978
NCBI GI
                   186
BLAST score
                   4.0e-15
E value
                   74
Match length
                   65
% identity
                  POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
NCBI Description
                   (PABP 2) >gi 304109 (L19418) poly(A)-binding protein
                   [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)
                   poly(A)-binding protein [Arabidopsis thaliana]
                   36471
Seq. No.
                   LIB3051-099-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   g1750376
NCBI GI
                   211
BLAST score
                   3.0e-17
E value
                   75
Match length
                   61
% identity
                   (U80808) ubiquitin activating enzyme [Arabidopsis thaliana]
NCBI Description
                   >gi 3150409 (AC004165) ubiquitin activating enzyme (UBA1)
                   [Arabidopsis thaliana]
                   36472
Seq. No.
                   LIB3051-099-Q1-K1-E10
Seq. ID
                   BLASTN
Method
                   g3334666
NCBI GI
BLAST score
                   116
                   2.0e-58
E value
                   260
Match length
```

G.max mRNA for putative cytochrome P450, clone CP7

87

% identity

NCBI Description

```
Seq. No.
                  LIB3051-100-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  g1632831
NCBI GI
BLAST score
                  204
                  2.0e-16
E value
                  63
Match length
                  68
% identity
NCBI Description (Z49698) orf [Ricinus communis]
                  36474
Seq. No.
                  LIB3051-100-Q1-K1-C11
Seq. ID
Method
                  BLASTN
                  q2055227
NCBI GI
                   203
BLAST score
                   1.0e-110
E value
                   243
Match length
% identity
                   95
NCBI Description Glycine max mRNA for SRC1, complete cds
                   36475
Seq. No.
                   LIB3051-100-Q1-K1-E11
Seq. ID
Method
                   BLASTN
NCBI GI
                   q516853
BLAST score
                   117
                   4.0e-59
E value
                   202
Match length
                   32
% identity
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
                   36476
Seq. No.
                   LIB3051-100-Q1-K1-E5
Seq. ID
Method
                   BLASTN
                   q4115336
NCBI GI
BLAST score
                   133
                   1.0e-68
E value
                   341
Match length
                   21
 % identity
NCBI Description Pisum sativum (Alaska) ubiquitin (PUB3) gene, complete cds
                   36477
Seq. No.
                   LIB3051-100-Q1-K1-H11
 Seq. ID
                   BLASTX
 Method
                   g3426131
 NCBI GI
                   299
 BLAST score
                   4.0e-27
 E value
                   99
 Match length
                   56
 % identity
                    (AL031307) yeast anti-silencing protein homolog
 NCBI Description
                    [Schizosaccharomyces pombe]
                   36478
 Seq. No.
                   LIB3051-100-Q1-K1-H3
 Seq. ID
                   BLASTX
 Method
                   g3044218
 NCBI GI
```

208

1.0e-16

BLAST score

E value

```
Match length 97
% identity 45
NCBI Description (AF057144) signal peptidase [Arabidopsis thaliana]
Seq. No. 36479
Seq. ID LIB3051-101-Q1-K1-B10
```

Method BLASTN
NCBI GI g1575726
BLAST score 76
E value 1.0e-34
Match length 84
% identity 98

% identity 98
NCBI Description Glycine max 14-3-3 related protein SGF14B mRNA, partial cds

 Seq. No.
 36480

 Seq. ID
 LIB3051-101-Q1-K1-E12

 Method
 BLASTX

 NCBI GI
 g2760843

NCBI GI g2760843 BLAST score 151 E value 1.0e-17 Match length 122 % identity 45

NCBI Description (AC003105) unknown protein [Arabidopsis thaliana]

Seq. No. 36481

Seq. ID LIB3051-101-Q1-K1-G3

Method BLASTX
NCBI GI g1076660
BLAST score 207
E value 6.0e-20
Match length 94
% identity 62

NCBI Description D13F(MYBST1) protein - potato >gi\_786426\_bbs\_159122

(S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes,

leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No. 36482

Seq. ID LIB3051-101-Q1-K1-G4

Method BLASTX
NCBI GI g3451068
BLAST score 145
E value 4.0e-09
Match length 86
% identity 58

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 36483

Seq. ID LIB3051-101-Q1-K1-G8

Method BLASTX
NCBI GI g3335355
BLAST score 210
E value 7.0e-17
Match length 95
% identity 14

NCBI Description (AC004512) Match to polyubiquitin DNA gb L05401 from A.

thaliana. Contains insertion of mitochondrial NADH



dehydrogenase gb\_X82618 and gb\_X98301. May be a pseudogene with an expressed insert. EST gb\_AA586248 comes from this region. [Arabi

```
36484
Seq. No.
                  LIB3051-101-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3036806
BLAST score
                  137
E value
                  1.0e-08
Match length
                  66
% identity
                  47
NCBI Description
                  (AL022373) glycine-rich protein [Arabidopsis thaliana]
                  36485
Seq. No.
                  LIB3051-101-Q1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2465527
BLAST score
                  199
E value
                  1.0e-15
Match length
                  103
% identity
                  42
                  (AF000354) phosphate transporter [Medicago truncatula]
NCBI Description
Seq. No.
                  36486
Seq. ID
                  LIB3051-102-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g113497
BLAST score
                  250
E value
                  2.0e-21
Match length
                  85
% identity
                  59
                  ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE)
NCBI Description
                   (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE)
                  >qi 99880 pir S07472 alpha-galactosidase (EC 3.2.1.22)
                  precursor - guar >gi 18292 emb CAA32772 (X14619)
                  alpha-galactosidase preproprotein [Cyamopsis tetragonoloba]
                  36487
Seq. No.
Seq. ID
                  LIB3051-102-Q1-K1-B5
Method
                  BLASTN
NCBI GI
                  q182063
BLAST score
                  381
                  0.0e+00
E value
                  433
Match length
                  93
% identity
NCBI Description Homo sapiens elastin (ELN) mRNA, 3' end
Seq. No.
                  36488
Seq. ID
                  LIB3051-102-Q1-K1-B6
                  BLASTN
Method
                  q2388688
NCBI GI
BLAST score
                   73
E value
                   7.0e-33
Match length
                  133
% identity
                  90
```

NCBI Description Glycine max GH1 protein (GH1) mRNA, partial cds



```
36489
Seq. No.
                  LIB3051-102-Q1-K1-D3
Seq. ID
                  BLASTN
Method
                  g18743
NCBI GI
                  54
BLAST score
                  6.0e-22
E value
                  122
Match length
                  86
% identity
                 G.max mRNA from stress-induced gene (SAM22)
NCBI Description
                  36490
Seq. No.
                  LIB3051-102-Q1-K1-E2
Seq. ID
                  BLASTN
Method
                  g310566
NCBI GI
                  124
BLAST score
                  3.0e-63
E value
                  297
Match length
                  95
% identity
                  Soybean glutamate 1-semialdehyde aminotransferase mRNA,
NCBI Description
                  complete cds
Seq. No.
                   36491
                  LIB3051-102-Q1-K1-F3
Seq. ID
Method
                  BLASTX
                   g322571
NCBI GI
                   155
BLAST score
                   3.0e-10
E value
                   49
Match length
                   49
% identity
                   proteinase inhibitor II - Arabidopsis thaliana
NCBI Description
                   >gi_16427_emb_CAA48892_ (X69139) protease inhibitor II
                   [Arabidopsis thaliana] >gi 4038041 (AC005936) proteinase
                   inhibitor II [Arabidopsis Thaliana]
                   36492
Seq. No.
                   LIB3051-103-Q1-K1-B11
Seq. ID
                   BLASTX
Method
                   g2914706
NCBI GI
                   258
BLAST score
                   3.0e-22
E value
                   64
Match length
% identity
                   (AC003974) putative homeobox protein [Arabidopsis thaliana]
NCBI Description
                   36493
Seq. No.
Seq. ID
                   LIB3051-103-Q1-K1-C7
                   BLASTN
Method
                   g603189
NCBI GI
                   47
BLAST score
                   3.0e-17
E value
Match length
                   95
 % identity
                   Zea mays translation initiation factor eIF-4A mRNA,
NCBI Description
                   complete cds
```

5573

36494

Seq. No.

BLAST score

E value

190

5.0e-15

```
Seq. ID
                   LIB3051-103-Q1-K1-F11
Method
                   BLASTN
NCBI GI
                   g2921327
BLAST score
                   89
                   2.0e-42
E value
Match length
                   305
                   83
% identity
                   Glycine max beta-1,3-glucanase 10 (SGlu10) gene, partial
NCBI Description
                   sequence
                   36495
Seq. No.
Seq. ID
                   LIB3051-103-Q1-K1-F9
Method
                   BLASTX
NCBI GI
                   g3860247
BLAST score
                   262
                   8.0e-23
E value
                   88
Match length
% identity
                   59
NCBI Description
                  (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                   36496
Seq. ID
                   LIB3051-104-Q1-K1-C11
Method
                   BLASTN
NCBI GI
                   g2055227
BLAST score
                   45
E value
                   3.0e-16
Match length
                   141
                   83
% identity
NCBI Description
                  Glycine max mRNA for SRC1, complete cds
Seq. No.
                   36497
Seq. ID
                   LIB3051-104-Q1-K1-D9
Method
                   BLASTX
NCBI GI
                   q1177405
BLAST score
                   156
E value
                   2.0e-10
Match length
                   79
% identity
                   38
NCBI Description
                  (X89855) citrate binding protein [Hevea brasiliensis]
Seq. No.
                   36498
Seq. ID
                  LIB3051-104-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g4539301
BLAST score
                   187
E value
                   5.0e-14
Match length
                   43
% identity
                  77
NCBI Description
                   (AL049480) putative mitochondrial protein [Arabidopsis
                  thaliana]
Seq. No.
                  36499
Seq. ID
                  LIB3051-104-Q1-K1-H4
Method
                  BLASTX
                  q1710530
NCBI GI
```

```
Match length
% identity
                  61
NCBI Description
                  60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256
                  ribosomal protein L27a - Arabidopsis thaliana
                  >gi 1107487 emb CAA63025 (X91959) 60S ribosomal protein
                  L27a [Arabidopsis thaliana]
Seq. No.
                  36500
Seq. ID
                  LIB3051-104-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  q1843462
BLAST score
                  160
```

% identity 44
NCBI Description (L10211) isoliquiritigenin 2'-O-methyltransferase [Medicago sativa]

Seq. No. 36501

E value

Match length

Seq. ID LIB3051-105-Q1-K1-A3
Method BLASTN
NCBI GI g12139
BLAST score 66

7.0e-11

111

E value 1.0e-28
Match length 131
% identity 94

NCBI Description Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and trnG coding for ribosomal protein S2, one CF(1) and three CF(0) subunits of ATP synthase and tRNA-Arg and tRNA-Gly

Seq. No. 36502

Seq. ID LIB3051-105-Q1-K1-B11

Method BLASTN
NCBI GI g170007
BLAST score 150
E value 7.0e-79
Match length 326
% identity 87

NCBI Description Soybean 18 kD late embryogenesis abundant (Lea) protein

mRNA, complete cds

Seq. No. 36503

Seq. ID LIB3051-105-Q1-K1-B12

Method BLASTN
NCBI GI g1786114
BLAST score 49
E value 9.0e-19
Match length 89
% identity 89

NCBI Description Vigna unguiculata phosphoinositide-specific phospholipase C

mRNA, complete cds

Seq. No. 36504

Seq. ID LIB3051-105-Q1-K1-B8

Method BLASTX NCBI GI g2252866 BLAST score 161

```
E value
Match length
                   77
% identity
                   58
NCBI Description
                   (AF013294) contains region of similarity to SYT
                   [Arabidopsis thaliana]
Seq. No.
                   36505
Seq. ID
                   LIB3051-105-Q1-K1-F4
Method
                   BLASTX
NCBI GI
                   g1362162
BLAST score
                   372
E value
                   1.0e-44
Match length
                   121
% identity
                   72
NCBI Description
                  beta-glucosidase BGQ60 precursor - barley >gi_804656
                   (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.
                   36506
Seq. ID
                   LIB3051-105-Q1-K1-F9
Method
                   BLASTX
NCBI GI
                   g2231046
BLAST score
                   171
E value
                   4.0e-12
Match length
                   124
% identity
                   40
NCBI Description
                  (Y12618) PPF-1 protein [Pisum sativum]
Seq. No.
                   36507
Seq. ID
                  LIB3051-105-Q1-K1-G1
Method
                  BLASTN
NCBI GI
                   g18764
BLAST score
                   367
                   0.0e+00
E value
Match length
                   374
                   99
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
Seq. No.
                  36508
                  LIB3051-106-Q1-K1-B2
Seq. ID
                  BLASTX
                  q2088653
                  225
                  1.0e-18
                  102
```

Method NCBI GI BLAST score E value Match length % identity

NCBI Description (AF002109) Hslpro-1 related protein isolog [Arabidopsis thaliana]

Seq. No. 36509

Seq. ID LIB3051-106-Q1-K1-D7 Method BLASTX

NCBI GI g1071924 BLAST score 150 E value 6.0e-10 Match length 89 % identity 46

NCBI Description Kunitz trypsin inhibitor precursor - soybean

```
>gi_510515_emb_CAA56343_ (X80039) Kunitz trypsin inhibitor [Glycine max]

Seq. No. 36510
Seq. ID LIB3051-106-Q1-K1-E4
Method BLASTN
NCBI GI g3747088
```

E value 3.0e-44
Match length 248
% identity 85

BLAST score

NCBI Description Glycine max NADP-dependent isocitrate dehydrogenase (IDH1)

mRNA, complete cds

 Seq. No.
 36511

 Seq. ID
 LIB3051-106-Q1-K1-F1

 Method
 BLASTN

 NCBI GI
 g166379

92

BLAST score 171
E value 2.0e-91
Match length 271
% identity 78

NCBI Description Alfalfa glucose-regulated endoplasmic reticular protein

mRNA, complete cds

Seq. No. 36512

Seq. ID LIB3051-106-Q1-K1-F6

Method BLASTN
NCBI GI g170065
BLAST score 273
E value 1.0e-152
Match length 453
% identity 18

NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP2)

gene, complete cds

Seq. No. 36513

Seq. ID LIB3051-106-Q1-K1-H10

Method BLASTX
NCBI GI g3482967
BLAST score 310
E value 1.0e-28
Match length 105
% identity 61

NCBI Description (AL031369) Protein phosphatase 2C-like protein [Arabidopsis

thaliana] >gi\_4559345\_gb\_AAD23006.1\_AC006585\_1 (AC006585)

protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 36514

Seq. ID LIB3051-107-Q1-K1-A10

Method BLASTX
NCBI GI g2621916
BLAST score 267
E value 2.0e-23
Match length 111
% identity 45

NCBI Description (AE000860) conserved protein [Methanobacterium



## thermoautotrophicum]

```
Seq. No.
                  36515
Seq. ID
                  LIB3051-107-Q1-K1-D1
Method
                  BLASTN
NCBI GI
                  g1218003
BLAST score
                  126
                  1.0e-64
E value
                  289
Match length
                  87
% identity
NCBI Description Glycine max dynamin-like protein SDL5A mRNA, complete cds
                  36516
Seq. No.
Seq. ID
                  LIB3051-107-Q1-K1-E2
Method
                  BLASTN
NCBI GI
                  g479059
BLAST score
                  347
                  0.0e+00
E value
Match length
                  359
                  99
% identity
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
                  36517
Seq. No.
                  LIB3051-107-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2842480
BLAST score
                  126
                  1.0e-14
E value
Match length
                  82
                  61
% identity
                  (AL021749) ADP, ATP carrier-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  36518
Seq. No.
Seq. ID
                  LIB3051-107-Q1-K1-F6
Method
                  BLASTN
                  g303900
NCBI GI
BLAST score
                  248
E value
                  1.0e-137
Match length
                  418
                  31
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
Seq. No.
                  36519
                  LIB3051-107-Q1-K1-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1212811
                  39
BLAST score
E value
                  9.0e-13
Match length
                  131
% identity
                  83
NCBI Description C.arietinum mRNA for seed imbibition protein
Seq. No.
                  36520
```

LIB3051-107-Q1-K1-G8 Seq. ID

Method BLASTX NCBI GI g3201680

```
BLAST score 243
E value 1.0e-20
Match length 124
% identity 41
NCBI Description (AF060941) extra-large G-protein [Arabidopsis thaliana]
```

Method BLASTX
NCBI GI g3643597
BLAST score 454
E value 4.0e-45
Match length 143
% identity 66

NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]

 Seq. No.
 36522

 Seq. ID
 LIB3051-108-Q1-K1-C1

 Method
 BLASTX

Method BLASTX
NCBI GI g2673917
BLAST score 515
E value 2.0e-52

Match length 129 % identity 42

NCBI Description (AC002561) putative ATP-dependent RNA helicase [Arabidopsis

tkaliana]

Seq. No. 36523

Seq. ID LIB3051-108-Q1-K1-C12

Method BLASTX
NCBI GI g2252863
BLAST score 469
E value 5.0e-47
Match length 134
% identity 41

NCBI Description (AF013294) similar to nucleolin protein [Arabidopsis

thaliana]

Seq. No. 36524

Seq. ID LIB3051-108-Q1-K1-C6

Method BLASTX
NCBI GI g2895866
BLAST score 205
E value 4.0e-16
Match length 95
% identity 45

NCBI Description (AF045770) methylmalonate semi-aldehyde dehydrogenase

[Oryza sativa]

Seq. No. 36525

Seq. ID LIB3051-108-Q1-K1-D10

Method BLASTX
NCBI GI g3377820
BLAST score 363
E value 1.0e-34
Match length 93
% identity 74

NCBI Description

```
(AF076275) contains similarity to coatomer zeta chains
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  36526
Seq. ID
                  LIB3051-108-Q1-K1-D9
                  BLASTX
Method
NCBI GI
                  g3913420
                  289
BLAST score
E value
                  5.0e-26
                  118
Match length
                  53
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                  (SAMDC) >gi 1421752 (U60592) S-adenosylmethionine
                  decarboxylase [Pisum sativum]
Seq. No.
                  36527
Seq. ID
                  LIB3051-108-Q1-K1-G3
Method
                  BLASTN
NCBI GI
                  g3452180
BLAST score
                  63
E value
                  6.0e-27
Match length
                  195
% identity
                  84
                  Glycine soja cv 342-633A clone 1 26S-18S ribosomal RNA
NCBI Description
                  intergenic spacer region
Seq. No.
                  36528
Seq. ID
                  LIB3051-109-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g3212865
BLAST score
                  150
E value
                  1.0e-09
                  50
Match length
% identity
                  62
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  36529
Seq. ID
                  LIB3051-109-Q1-K1-C12
Method
                  BLASTN
NCBI GI
                  g18749
BLAST score
                  232
E value
                  1.0e-128
Match length
                  296
                  95
% identity
NCBI Description G.max mRNA for seed maturation polypeptide
Seq. No.
                  36530
                  LIB3051-109-Q1-K1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g166929
BLAST score
                  76
E value
                  7.0e-35
Match length
                  96
                  95
% identity
```

complete cds

A.thaliana ubiquitin extension protein (UBQ1) gene,

Method

NCBI GI

E value

BLAST score

BLASTN

191

g2253383

1.0e-103

```
Seq. No.
Seq. ID
                  LIB3051-110-Q1-K1-B10
                  BLASTX
Method
NCBI GI
                  g2244759
                  120
BLAST score
                  4.0e-18
E value
                  88
Match length
                  68
% identity
                  (Z97335) selenium-binding protein [Arabidopsis thaliana]
NCBI Description
                  36532
Seq. No.
Seq. ID
                  LIB3051-110-Q1-K1-C7
                  BLASTX
Method
                  q1245182
NCBI GI
                   235
BLAST score
                   9.0e-20
E value
                   99
Match length
                   49
% identity
                  (U49398) sterol delta-7 reductase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   36533
                  LIB3051-110-Q1-K1-E12
Seq. ID
                  BLASTN
Method
                  g3334664
NCBI GI
                   260
BLAST score
                   1.0e-144
E value
Match length
                   260
                   100
% identity
NCBI Description G.max mRNA for putative cytochrome P450, clone CP5
                   36534
Seq. No.
                   LIB3051-110-Q1-K1-E2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1304226
BLAST score
                   60
                   3.0e-25
E value
Match length
                   201
                   86
% identity
                  Soybean mRNA for epoxide hydrolase, complete cds
NCBI Description
                   36535
Seq. No.
Seq. ID
                   LIB3051-110-Q1-K1-E9
Method
                   BLASTX
                   g3724087
NCBI GI
                   351
BLAST score
                   2.0e-33
E value
Match length
                   122
% identity
                   52
                   (AJ011840) 1-deoxyxylulose 5-phosphate synthase
NCBI Description
                   [Catharanthus roseus]
Seq. No.
                   36536
Seq. ID
                   LIB3051-110-Q1-K1-F6
```

5581

```
Match length
                  92
% identity
                  Glycine max biotin carboxylase precursor (accC-2) mRNA,
NCBI Description
                  complete cds
                  36537
Seq. No.
                  LIB3051-111-Q1-K1-B3
Seq. ID
Method
                  BLASTX
                  q4309741
NCBI GI
BLAST score
                  152
                  7.0e-10
E value
Match length
                  63
% identity
                  48
                  (AC006439) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  36538
Seq. No.
                  LIB3051-111-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g595768
BLAST score
                  142
                  6.0e-09
E value
Match length
                  45
% identity
                  60
                  (U13866) non-functional lacZ alpha peptide [Cloning vector]
NCBI Description
                  36539
Seq. No.
                  LIB3051-111-Q1-K1-D10
Seq. ID
Method
                  BLASTN
                  g169936
NCBI GI
                  277
BLAST score
                  1.0e-154
E value
                   423
Match length
% identity
                   97
NCBI Description Glycine max chalcone synthase (chs7) gene, complete cds
                   36540
Seq. No.
Seq. ID
                  LIB3051-111-Q1-K1-E12
                  BLASTX
```

Method BLASTX
NCBI GI g1709454
BLAST score 220
E value 5.0e-18
Match length 70
% identity 67

NCBI Description PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR

(PDHE1-B) >gi 1336097 (U56697) pyruvate dehydrogenase

Elbeta [Pisum sativum]

Seq. No. 36541

Seq. ID LIB3051-112-Q1-K1-A1

Method BLASTX
NCBI GI g2921320
BLAST score 106
E value 3.0e-10
Match length 62
% identity 66

NCBI Description (AF034110) beta-1,3-glucanase 5 [Glycine max]

E value

Match length

2.0e-24 95

```
Seq. No.
Seq. ID
                  LIB3051-112-Q1-K1-B6
                  BLASTN
Method
                  g4039114
NCBI GI
BLAST score
                   43
                  3.0e-15
E value
                  190
Match length
                  83
% identity
                  Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds
NCBI Description
                   36543
Seq. No.
                   LIB3051-112-Q1-K1-E1
Seq. ID
                   BLASTN
Method
                   q19272
NCBI GI
                   80
BLAST score
                   2.0e-37
E value
                   140
Match length
                   89
% identity
                  Tomato LeEF-1 mRNA for elongation factor 1 alpha
NCBI Description
                   36544
Seq. No.
Seq. ID
                   LIB3051-112-Q1-K1-E4
Method
                   BLASTX
                   q4191616
NCBI GI
                   250
BLAST score
                   1.0e-21
E value
                   66
Match length
% identity
                   67
                   (AF120334) GTP-binding protein NGB [Homo sapiens]
NCBI Description
                   36545
Seq. No.
Seq. ID
                   LIB3051-112-Q1-K1-F1
Method
                   BLASTX
NCBI GI
                   g4063746
                   160
BLAST score
                   5.0e-11
E value
                   83
Match length
                   45
% identity
                   (AC005851) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
                   36546
Seq. No.
Seq. ID
                   LIB3051-113-Q1-K1-A8
                   BLASTX
Method
NCBI GI
                   g3445201
BLAST score
                   266
                   3.0e-23
E value
                   90
Match length
                   59
% identity
                   (AC004786) unknown protein [Arabidopsis thaliana]
NCBI Description
                   36547
Seq. No.
Seq. ID
                   LIB3051-113-Q1-K1-A9
                   BLASTX
Method
                   q3158372
NCBI GI
BLAST score
                   275
```

```
% identity
                  (AF035383) polyubiquitin [Arabidopsis thaliana]
NCBI Description
                  36548
Seq. No.
                  LIB3051-113-Q1-K1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2827082
                  168
BLAST score
                  5.0e-12
E value
Match length
                  65
                   58
% identity
NCBI Description (AF020272) malate dehydrogenase [Medicago sativa]
Seq. No.
                  36549
                  LIB3051-113-Q1-K1-F3
Seq. ID
Method
                  BLASTX
                  g3915737
NCBI GI
BLAST score
                   187
                   1.0e-14
E value
                   68
Match length
                   63
% identity
                   IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (KAP
NCBI Description
                   ALPHA) >gi_3228370 (AF017252) importin alpha [Lycopersicon
                   esculentum]
Seq. No.
                   36550
                   LIB3051-113-Q1-K1-F5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4510352
BLAST score
                   185
                   8.0e-14
E value
                   115
Match length
% identity
                   (AC006921) putative salt-inducible protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   36551
                   LIB3051-113-Q1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4006917
BLAST score
                   336
                   9.0e-32
E value
Match length
                   94
% identity
                   61
```

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No.

36552

Seq. ID LIB3051-113-Q1-K1-H4

Method BLASTX
NCBI GI g3063455
BLAST score 228
E value 7.0e-19
Match length 57
% identity 70

NCBI Description (AC003981) F22013.17 [Arabidopsis thaliana]

2

```
LIB3051-114-Q1-K1-A11
Seq. ID
                  BLASTN
Method
                  g256634
NCBI GI
                  42
BLAST score
                  2.0e-14
E value
Match length
                  58
% identity
                   45
                  KTi1=Kunitz trypsin inhibitor KTi1, KTi2=Kunitz trypsin
NCBI Description
                   inhibitor KTi2 [soybeans, Genomic, 3269 nt]
Seq. No.
Seq. ID
                   LIB3051-114-Q1-K1-E2
Method
                   BLASTN
                   g3452136
NCBI GI
BLAST score
                   162
                   6.0e-86
E value
                   182
Match length
% identity
                   98
                   Glycine max mRNA for glucose-6-phosphate-dehydrogenase,
NCBI Description
                   partial
                   36555
Seq. No.
Seq. ID
                   LIB3051-115-Q1-K1-A10
Method
                   BLASTN
                   q3885514
NCBI GI
                   66
BLAST score
                   1.0e-28
E value
                   134
Match length
% identity
                   87
                   Medicago sativa clone MS56 unknown mRNA
NCBI Description
                   36556
Seq. No.
Seq. ID
                   LIB3051-115-Q1-K1-A6
                   BLASTX
Method
NCBI GI
                   g1171978
                   235
BLAST score
                   1.0e-19
E value
                   108
Match length
% identity
                   44
                   POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
NCBI Description
                   (PABP 2) >gi_304109 (L19418) poly(A)-binding protein
                   [Arabidopsis thaliana] >gi 2911051 emb_CAA17561_ (AL021961)
                   poly(A)-binding protein [Arabidopsis thaliana]
                   36557
 Seq. No.
                   LIB3051-115-Q1-K1-B10
Seq. ID
                   BLASTX
Method
                   g267082
NCBI GI
                   166
 BLAST score
                   1.0e-11
 E value
                   90
 Match length
                   40
 % identity
                   TUBULIN BETA-8 CHAIN >gi_320189_pir _JQ1592 tubulin beta-8
 NCBI Description
                   chain - Arabidopsis thaliana >gi 166908 (M84705) beta-8
                   tubulin [Arabidopsis thaliana]
```

36558

```
LIB3051-115-Q1-K1-F11
Seq. ID
                  BLASTX
Method
                  g531829
NCBI GI
                  141
BLAST score
                  6.0e-09
E value
Match length
                  69
% identity
                  52
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
                  36559
Seq. No.
                  LIB3051-115-Q1-K1-G8
Seq. ID
Method
                  BLASTX
                  q3925363
NCBI GI
                  557
BLAST score
                  2.0e-57
E value
Match length
                  139
                  77
% identity
                  (AF067961) homeodomain protein [Malus domestica]
NCBI Description
Seq. No.
                  36560
Seq. ID
                  LIB3051-116-Q1-K1-A8
Method
                  BLASTX
                  g4249416
NCBI GI
                   352
BLAST score
                   2.0e-33
E value
                   131
Match length
                   53
% identity
                   (AC006072) putative exoribonuclease (also contains
NCBI Description
                   zinc-finger C2H2-type domain) [Arabidopsis thaliana]
                   36561
Seq. No.
                   LIB3051-116-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   g2507421
NCBI GI
                   140
BLAST score
                   1.0e-08
E value
                   61
Match length
                   51
% identity
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi 1800277
NCBI Description
                   (U81042) translation initiation factor [Arabidopsis
                   thaliana] >gi 4490709 emb_CAB38843.1_ (AL035680)
                   translation initiation factor [Arabidopsis thaliana]
                   36562
Seq. No.
Seq. ID
                   LIB3051-116-Q1-K1-F7
                   BLASTX
Method
                   g3334405
NCBI GI
                   239
BLAST score
                   2.0e-20
E value
                   69
Match length
                   72
% identity
                   VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
NCBI Description
                   >gi 2267583 (AF009338) vacuolar H+-ATPase subunit E
                   [Gossypium hirsutum]
```

36563

```
LIB3051-116-Q1-K1-G9
Seq. ID
                  BLASTX
Method
                  g2832625
NCBI GI
                  184
BLAST score
                  1.0e-13
E value
                   91
Match length
                   41
% identity
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   36564
                  LIB3051-117-Q1-K1-A11
Seq. ID
Method
                  BLASTX
                   q3643598
NCBI GI
                   145
BLAST score
                   3.0e-09
E value
                   50
Match length
% identity
                   58
                   (AC005395) putative poly(A) polymerase [Arabidopsis
NCBI Description
                   thaliana]
                   36565
Seq. No.
Seq. ID
                   LIB3051-117-Q1-K1-A2
                   BLASTX
Method
                   g2317907
NCBI GI
                   271
BLAST score
                   4.0e-24
E value
                   76
Match length
                   71
% identity
                  (U89959) Mago Nashi-like protein [Arabidopsis thaliana]
NCBI Description
                   36566
Seq. No.
                   LIB3051-117-Q1-K1-A7
Seq. ID
                   {\tt BLASTX}
Method
                   g445126
NCBI GI
                   134
BLAST score
                   7.0e-15
E value
                   88
Match length
                   59
% identity
NCBI Description heat shock protein HSP81-1 [Arabidopsis thaliana]
                   36567
Seq. No.
Seq. ID
                   LIB3051-117-Q1-K1-C8
                   BLASTN
Method
                   g1617035
NCBI GI
BLAST score
                   49
                   2.0e-18
E value
                   89
Match length
                   89
% identity
NCBI Description V.unguiculata mRNA for Ted2 protein
                   36568
Seq. No.
Seq. ID
                   LIB3051-117-Q1-K1-C9
Method
                   BLASTX
                   q1403522
NCBI GI
BLAST score
                   311
E value
                   1.0e-28
                   111
Match length
```

% identity

NCBI Description (X57187) chitinase [Phaseolus vulgaris]

Seq. No.

36569

Seq. ID

LIB3051-117-Q1-K1-D1

Method NCBI GI BLASTX g746510

BLAST score

156

E value Match length 2.0e-10 42

62

% identity NCBI Description

(U23517) similar to ubiquitin conjugating enzyme

[Caenorhabditis elegans]

Seq. No.

36570

Seq. ID

LIB3051-117-Q1-K1-D3

Method NCBI GI BLASTN g2909421

BLAST score E value Match length 40 2.0e-13 170

57

% identity

NCBI Description Cicer arietinum mRNA for LEA protein (clone CapLEA-2)

Seq. No.

Seq. ID

LIB3051-117-Q1-K1-D7

BLASTX Method q2832664 NCBI GI BLAST score 205 3.0e-16 E value 104 Match length

% identity

(AL021710) pollen-specific protein - like [Arabidopsis NCBI Description

thaliana]

Seq. No.

36572

Seq. ID

LIB3052-001-Q1-B1-C7

Method BLASTN NCBI GI g1401239 185 BLAST score 1.0e-100 E value 193 Match length 99 % identity

Glycine max 7S seed globulin precursor, mRNA, complete cds NCBI Description

Seq. No.

36573

Seq. ID

LIB3052-001-Q1-B1-D8

BLASTN Method g736001 NCBI GI 320 BLAST score 1.0e-180 E value 324 Match length 100 % identity

G.soja (SH1) Gy5 mRNA for glycinin NCBI Description

Seq. No.

36574

Seq. ID

LIB3052-001-Q1-B1-E6

```
BLASTX
Method
NCBI GI
                  q4191791
                   339
BLAST score
                   5.0e-32
E value
                   80
Match length
                   78
% identity
                   (AC005917) putative sf21 {Helianthus annuus} protein
NCBI Description
                   [Arabidopsis thaliana]
                   36575
Seq. No.
                   LIB3052-001-Q1-B1-F9
Seq. ID
                   BLASTX
Method
                   q3075392
NCBI GI
                   309
BLAST score
                   2.0e-28
E value
                   90
Match length
% identity
                   (AC004484) putative steroid dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   36576
Seq. No.
                   LIB3052-001-Q1-B1-G11
Seq. ID
                   BLASTX
Method
                   g1946367
NCBI GI
BLAST score
                   163
                   2.0e-11
E value
                   66
Match length
                   47
% identity
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
                   36577
Seq. No.
                   LIB3052-001-Q1-B1-H11
Seq. ID
                   BLASTN
Method
NCBI GI
                   g218264
                   314
BLAST score
E value
                   1.0e-177
Match length
                   314
                   100
 % identity
NCBI Description Glycine max mRNA for glycinin A2Bla subunit, complete cds
                   36578
 Seq. No.
                   LIB3052-001-Q1-B1-H3
 Seq. ID
                   BLASTX
Method
                   g2204224
 NCBI GI
 BLAST score
                   384
 E value
                    3.0e-37
                   115
 Match length
                    64
 % identity
 NCBI Description (Y13849) alpha-galactosidase [Hordeum vulgare]
                    36579
 Seq. No.
                    LIB3052-002-Q1-B1-B3
 Seq. ID
                    BLASTN
 Method
                    g2970653
 NCBI GI
                    174
 BLAST score
```

4.0e-93

218

E value

Match length

% identity Vigna unguiculata ferritin subunit cowpea2 precursor, mRNA, NCBI Description nuclear gene encoding chloroplast protein, complete cds

Seq. No.

LIB3052-002-Q1-B1-B4 Seq. ID

Method BLASTN q18535 NCBI GI 170 BLAST score 6.0e-91 E value 242 Match length 93 % identity

NCBI Description Soybean mRNA for the alpha subunit of beta-conglycinin

36581 Seq. No.

LIB3052-002-Q1-B1-B8 Seq. ID

Method BLASTX g3328221 NCBI GI 171 BLAST score 3.0e-12 E value 38 Match length 87

% identity (AF076920) thioredoxin peroxidase [Secale cereale] NCBI Description

Seq. No. 36582

LIB3052-002-Q1-B1-C3 Seq. ID

BLASTX Method q2842494 NCBI GI 457 BLAST score 1.0e-45 E value 103 Match length % identity

(AL021749) prohibitin-like protein [Arabidopsis thaliana] NCBI Description >gi\_4097688 (U66591) prohibitin 1 [Arabidopsis thaliana]

>gi\_4097694 (U66594) prohibitin 1 [Arabidopsis thaliana]

36583 Seq. No.

LIB3052-002-Q1-B1-E11 Seq. ID

BLASTX Method NCBI GI g2961372 173 BLAST score 1.0e-12 E value 57 Match length 61 % identity

(AL022141) putative ribosomal protein L8 [Arabidopsis NCBI Description

thaliana] >gi\_3036817\_emb\_CAA18507\_ (AL022373) ribosomal

protein L2 [Arabidopsis thaliana]

Seq. No. 36584

LIB3052-002-Q1-B1-E3 Seq. ID

Method BLASTN q170009 NCBI GI 336 BLAST score 0.0e+00E value 385 Match length 96 % identity

NCBI Description Soybean late embryogenesis abundant (LEA) protein mRNA,

NCBI GI



```
36585
Seq. No.
                  LIB3052-002-Q1-B1-H3
Seq. ID
                  BLASTN
Method
                  g169972
NCBI GI
                  391
BLAST score
                  0.0e+00
E value
                  395
Match length
                  100
% identity
NCBI Description Soybean glycinin A-la-B-x subunit mRNA, complete cds
                  36586
Seq. No.
                  LIB3052-004-Q1-N1-B8
Seq. ID
                  BLASTN
Method
                   g531828
NCBI GI
BLAST score
                   38
                   4.0e-12
E value
                   110
Match length
                   84
% identity
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                   36587
                   LIB3052-004-Q1-N1-F2
Seq. ID
Method
                   BLASTN
                   g169972
NCBI GI
BLAST score
                   36
                   4.0e-11
E value
Match length
                   68
                   88
% identity
NCBI Description Soybean glycinin A-la-B-x subunit mRNA, complete cds
                   36588
Seq. No.
                   LIB3052-004-Q1-N1-H5
Seq. ID
Method
                   BLASTN
                   q169972
NCBI GI
                   81
BLAST score
                   4.0e-38
E value
                   129
Match length
                   91
% identity
                   Soybean glycinin A-la-B-x subunit mRNA, complete cds
NCBI Description
                   36589
Seq. No.
                   LIB3052-007-Q1-B1-A10
Seq. ID
                   BLASTN
Method
                   g170007
NCBI GI
                   53
BLAST score
                   3.0e-21
E value
                   145
Match length
                   84
 % identity
                   Soybean 18 kD late embryogenesis abundant (Lea) protein
NCBI Description
                   mRNA, complete cds
                   36590
 Seq. No.
 Seq. ID
                   LIB3052-007-Q1-B1-C11
                   BLASTN
 Method
```

g256428

```
BLAST score
                   0.0e+00
E value
                   393
Match length
                   97
% identity
```

KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and NCBI Description Forrest, mRNA, 1259 nt]

36591 Seq. No. Seq. ID

LIB3052-007-Q1-B1-C4

Method BLASTX q1076610 NCBI GI BLAST score 169 9.0e-14E value 106 Match length % identity

cathepsin B-like cysteine proteinase (EC 3.4.22.-) - Aztec NCBI Description tobacco >gi\_609175\_emb\_CAA57522\_ (X81995) cathepsin B-like

cysteine proteinase [Nicotiana rustica]

36592 Seq. No.

LIB3052-007-Q1-B1-C8 Seq. ID

Method BLASTX NCBI GI g1709970 BLAST score 279 6.0e-25 E value Match length 98 58 % identity

60S RIBOSOMAL PROTEIN L10A NCBI Description

36593 Seq. No.

LIB3052-007-Q1-B1-C9 Seq. ID

BLASTX Method NCBI GI q3860277 199 BLAST score 1.0e-15 E value 80 Match length 53 % identity

(AC005824) putative ribosomal protein L10 [Arabidopsis NCBI Description thaliana] >gi 4314394 gb AAD15604\_ (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

36594 Seq. No.

LIB3052-007-Q1-B1-F6 Seq. ID

BLASTN Method g18571 NCBI GI 246 BLAST score 1.0e-136 E value 346 Match length 93 % identity

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

36595 Seq. No.

LIB3052-007-Q1-B1-G10 Seq. ID

BLASTN Method g18638 NCBI GI BLAST score 63 4.0e-27 E value



Match length 175 % identity 84

NCBI Description Soybean Gy3 gene for glycinin subunit G3

Seq. No. 36596

Seq. ID LIB3052-007-Q1-B1-G2

Method BLASTN
NCBI GI g18628
BLAST score 171
E value 2.0e-91
Match length 203
% identity 96

NCBI Description Soybean mRNA for A5A4B3 subunits of glycinin

>gi 2170692\_dbj E02461\_E02461 cDNA encoding glycinine

subunit A5A4B3 precursor

Seq. No. 36597

Seq. ID LIB3052-007-Q1-B1-H5

Method BLASTN
NCBI GI g476215
BLAST score 79
E value 2.0e-36
Match length 203
% identity 85

NCBI Description Glycine max Century 84 p24 oleosin isoform B gene, complete

cds

Seq. No. 36598

Seq. ID LIB3052-007-Q1-B1-H9

Method BLASTN
NCBI GI g1326160
BLAST score 56
E value 1.0e-22
Match length 118
% identity 97

NCBI Description Phaseolus vulgaris dehydrin mRNA, complete cds

Seq. No. 36599

Seq. ID LIB3052-007-Q1-N1-E5

Method BLASTN
NCBI GI g170023
BLAST score 37
E value 1.0e-11
Match length 85
% identity 86

NCBI Description Glycine max maturation-associated protein (MAT9) mRNA,

complete cds

Seq. No. 36600

Seq. ID LIB3052-007-Q1-N1-E8

Method BLASTX
NCBI GI g548900
BLAST score 172
E value 2.0e-12
Match length 63
% identity 60

NCBI Description SUCROSE-BINDING PROTEIN PRECURSOR (SBP)



>gi\_322691\_pir\_\_JQ1730 62K sucrose-binding protein
precursor - soybean >gi\_170064 (L06038) glucose binding
protein [Glycine max]

 Seq. No.
 36601

 Seq. ID
 LIB3052-007-Q1-N1-G1

 Method
 BLASTN

 NCBI GI
 g4249567

 BLAST score
 41

 E value
 2.0e-14

 Match length
 53

NCBI Description Glycine max A5A4B3 glycinin gene, complete cds

Seq. No. 36602

% identity

Seq. ID LIB3052-008-Q1-N1-C8

94

Method BLASTX
NCBI GI g1199804
BLAST score 154
E value 9.0e-11
Match length 57
% identity 54

NCBI Description (X95639) transmembrane channel protein [Brassica oleracea]

Seq. No. 36603

Seq. ID LIB3052-008-Q1-N1-C9

Method BLASTN
NCBI GI g2270989
BLAST score 66
E value 9.0e-29
Match length 130
% identity 88

NCBI Description Glycine max dehydrin (GmPM12) mRNA, complete cds

Seq. No. 36604

Seq. ID LIB3052-008-Q1-N1-D11

Method BLASTN
NCBI GI g18621
BLAST score 77
E value 1.0e-35
Match length 129
% identity 90

NCBI Description Soybean DNA for glycinin A2B1a subunit

Seq. No. 36605

Seq. ID LIB3052-008-Q1-N1-E2

Method BLASTN
NCBI GI g18628
BLAST score 36
E value 5.0e-11
Match length 60
% identity 90

NCBI Description Soybean mRNA for A5A4B3 subunits of glycinin

>gi\_2170692\_dbj\_E02461\_E02461 cDNA encoding glycinine

subunit A5A4B3 precursor

```
LIB3052-008-Q1-N1-H11
Seq. ID
                  BLASTX
Method
                  g4510397
NCBI GI
                  169
BLAST score
                  2.0e-12
E value
Match length
                  61
                  61
% identity
                  (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
NCBI Description
                  36607
Seq. No.
                  LIB3052-009-Q1-N1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q72296
                  153
BLAST score
                  1.0e-10
E value
                   64
Match length
% identity
                   47
                  glycinin chain AlaBx precursor - soybean
NCBI Description
                   >gi 18615_emb_CAA26723_ (X02985) glycinin precursor
                   [Glycine max]
Seq. No.
                   36608
                   LIB3052-009-Q1-N1-D12
Seq. ID
                   BLASTX
Method
                   q868156
NCBI GI
                   186
BLAST score
                   4.0e-14
E value
Match length
                   45
                   82
% identity
                   (U26538) similar to mipB gene product in Mesembryanthemum
NCBI Description
                   crystallinum, encoded by Genbank Accession Number L36097;
                   MIP homolog; Method: conceptual translation supplied by
                   author. [Mesembryanthemum crystallinum]
                   36609
Seq. No.
                   LIB3052-009-Q1-N1-D2
Seq. ID
                   BLASTX
Method
                   g2129597
NCBI GI
BLAST score
                   156
                   9.0e-11
E value
                   41
Match length
                   76
% identity
                   glutamate dehydrogenase 1 - Arabidopsis thaliana
NCBI Description
                   >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis
                   tha\overline{l}iana] >gi 1293095 (U53527) glutamate dehydrogenase 1
                   [Arabidopsis thaliana]
                   36610
Seq. No.
Seq. ID
                   LIB3052-009-Q1-N1-D7
                   BLASTX
Method
                   q2344898
NCBI GI
BLAST score
                   241
                   1.0e-20
E value
                   51
Match length
% identity
                   (AC002388) 60S ribosomal protein L30 isolog [Arabidopsis
NCBI Description
```

thaliana]



```
36611
Seq. No.
                  LIB3052-011-Q1-N1-A1
Seq. ID
                  BLASTN
Method
                  g169962
NCBI GI
BLAST score
                  51
                  7.0e-20
E value
                  135
Match length
% identity
                  Soybean 16 kDa seed maturation protein (gGmpm9) gene exons
NCBI Description
                  1-2, complete cds
Seq. No.
                  36612
                  LIB3052-011-Q1-N1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1170746
BLAST score
                  154
                  2.0e-12
E value
                   98
Match length
                   52
% identity
                  DESICCATION PROTECTANT PROTEIN LEA14 HOMOLOG >gi 472850
NCBI Description
                   (U08108) putative desiccation protectant protein, homolog
                   of Lea14, GenBank Accession Number M88321 [Glycine max]
Seq. No.
                   LIB3052-011-Q1-N1-C5
Seq. ID
Method
                   BLASTN
                   g4097879
NCBI GI
BLAST score
                   82
                   3.0e-38
E value
Match length
                   210
% identity
                   90
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   36614
Seq. No.
Seq. ID
                   LIB3052-011-Q1-N1-C7
                   BLASTN
Method
                   q4249565
NCBI GI
                   52
BLAST score
                   2.0e-20
E value
                   268
Match length
                   84
% identity
                  Glycine max A3B4 glycinin gene, complete cds
NCBI Description
Seq. No.
                   36615
                   LIB3052-011-Q1-N1-C9
Seq. ID
                   BLASTN
Method
                   g210811
NCBI GI
BLAST score
                   151
                   2.0e-79
E value
                   387
Match length
                   85
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
```

Seq. No. 36616

NCBI Description

complete middle component (M) RNA

```
LIB3052-011-Q1-N1-D12
Seq. ID
                  BLASTN
Method
                  g4097879
NCBI GI
                  114
BLAST score
                  3.0e-57
E value
                  388
Match length
                  83
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  36617
Seq. No.
                  LIB3052-011-Q1-N1-D7
Seq. ID
Method
                  BLASTN
                  q4097879
NCBI GI
                  59
BLAST score
                  1.0e-24
E value
Match length
                  119
                  87
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                  36618
Seq. ID
                  LIB3052-011-Q1-N1-E11
Method
                  BLASTX
                  g1076485
NCBI GI
BLAST score
                  218
                   8.0e-18
E value
Match length
                   78
% identity
                   60
                  SAM-synthetase - chickpea (fragment)
NCBI Description
                   >qi 732576 emb CAA59508 (X85252) SAM-synthetase [Cicer
                   arietinum]
                   36619
Seq. No.
                   LIB3052-011-Q1-N1-E12
Seq. ID
                   BLASTX
Method
                   g138364
NCBI GI
                   479
BLAST score
                   3.0e-48
E value
Match length
                   133
                   72
% identity
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi 75639 pir__GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
                   36620
Seq. No.
```

Seq. ID LIB3052-011-Q1-N1-E9

Method BLASTX
NCBI GI g4539465
BLAST score 135
E value 7.0e-10
Match length 115
% identity 43

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Match length

123

```
LIB3052-011-Q1-N1-F10
Seq. ID
                  BLASTN
Method '
NCBI GI
                  q479059
BLAST score
                  184
                  4.0e-99
E value
Match length
                  364
                  88
% identity
                  G.max (Fiskeby V) mRNA for cysteine endopeptidase
NCBI Description
Seq. No.
                  36622
Seq. ID
                  LIB3052-011-Q1-N1-F9
Method
                  BLASTN
                  g479059
NCBI GI
BLAST score
                  166
                  2.0e-88
E value
Match length
                  318
                  88
% identity
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
Seq. No.
                  36623
Seq. ID
                  LIB3052-011-Q1-N1-G2
Method
                  BLASTN
NCBI GI
                  g3097320
                  47
BLAST score
                  2.0e-17
E value
Match length
                  165
                  85
% identity
NCBI Description Glycine max gene for Bd 30K, complete cds
Seq. No.
                  36624
Seq. ID
                  LIB3052-011-Q1-N1-H1
Method
                  BLASTN
NCBI GI
                  g1431744
                  71
BLAST score
E value
                  8.0e-32
Match length
                  127
% identity
                  89
NCBI Description
                  Glycine max sucrose binding protein (sbp) mRNA, complete
                  cds
Seq. No.
                  36625
Seq. ID
                  LIB3052-011-Q1-N1-H5
Method
                  BLASTN
NCBI GI
                  g311697
BLAST score
                  87
                  3.0e-41
E value
Match length
                  220
                  47
% identity
NCBI Description G.max Lea protein mRNA, complete CDS
Seq. No.
                  36626
Seq. ID
                  LIB3052-012-Q1-N1-B6
Method
                  BLASTX
NCBI GI
                  q2344896
BLAST score
                  180
E value
                  3.0e-13
```



```
% identity
NCBI Description
                  (AC002388) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   36627
Seq. ID
                  LIB3052-012-Q1-N1-C1
Method
                   BLASTN
NCBI GI
                   q169972
BLAST score
                   177
                   3.0e-95
E value
Match length
                   205
                   97
% identity
                  Soybean glycinin A-1a-B-x subunit mRNA, complete cds
NCBI Description
Seq. No.
                   36628
Seq. ID
                  LIB3052-012-Q1-N1-F11
Method
                  BLASTX
NCBI GI
                   g4512685
BLAST score
                   164
E value
                   2.0e-11
Match length
                   116
% identity
                   33
NCBI Description
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
                   >gi 4559325 gb AAD22987.1 AC007087 6 (AC007087)
                  hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   36629
Seq. ID
                  LIB3052-013-Q1-N1-A5
Method
                  BLASTN
NCBI GI
                   g414976
BLAST score
                   149
E value
                   2.0e-78
Match length
                   225
% identity
                   92
NCBI Description
                  Glycine max Shi-shi 51 kDa seed maturation protein
                   (pGmPM10) mRNA, complete cds
Seq. No.
                   36630
Seq. ID
                  LIB3052-013-Q1-N1-D4
Method
                  BLASTX
NCBI GI
                   q3337367
BLAST score
                   257
E value
                   2.0e-22
Match length
                  92
% identity
                  55
NCBI Description
                  (AC004481) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  36631
Seq. ID
                  LIB3052-013-Q1-N1-G2
Method
                  BLASTX
NCBI GI
                  g4102839
BLAST score
                  425
```

E value 6.0e-42Match length 97 % identity 75

NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

```
LIB3052-013-Q1-N1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2760844
BLAST score
                   117
                   1.0e-14
E value
Match length
                   74
% identity
                   61
NCBI Description
                  (AC003105) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   36633
Seq. ID
                  LIB3052-013-Q1-N1-H11
Method
                   BLASTX
NCBI GI
                   q4006888
BLAST score
                   204
E value
                   4.0e-16
Match length
                   61
% identity
                   64
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   36634
Seq. ID
                  LIB3052-014-Q1-N1-B5
Method
                  BLASTX
NCBI GI
                   g229707
BLAST score
                   457
                   6.0e-46
E value
Match length
                   98
% identity
                   84
NCBI Description Bean pod mottle virus
Seq. No.
                   36635
Seq. ID
                  LIB3052-014-Q1-N1-G12
Method
                  BLASTN
NCBI GI
                   q4097879
BLAST score
                   189
E value
                   1.0e-102
Match length
                   401
% identity
                   87
NCBI Description
                  Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
Seq. No.
                   36636
Seq. ID
                  LIB3052-014-Q1-N1-G7
Method
                   BLASTX
NCBI GI
                   g4218005
BLAST score
                   200
                   6.0e-16
E value
Match length
                   66
                   55
% identity
NCBI Description
                   (AC006135) putative vicilin storage protein (globulin-like)
                   [Arabidopsis thaliana]
Seq. No.
                   36637
Seq. ID
                  LIB3052-014-Q1-N1-H12
Method
                  BLASTX
NCBI GI
                  g4097880
BLAST score
                  157
E value
                  1.0e-10
```



Match length 85 % identity 45

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 36638

Seq. ID LIB3052-014-Q1-N1-H8

Method BLASTN
NCBI GI g18535
BLAST score 370
E value 0.0e+00
Match length 373
% identity 100

NCBI Description Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No. 36639

Seq. ID LIB3052-015-Q1-N1-D12

Method BLASTN
NCBI GI g210811
BLAST score 76
E value 7.0e-35
Match length 246
% identity 83

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 36640

Seq. ID LIB3052-015-Q1-N1-F4

Method BLASTX
NCBI GI g4104561
BLAST score 187
E value 4.0e-14
Match length 113
% identity 39

NCBI Description (AF036960) subtilisin-like protease [Glycine max]

Seq. No. 36641

Seq. ID LIB3052-015-Q1-N1-G7

Method BLASTN
NCBI GI g1786114
BLAST score 99
E value 2.0e-48
Match length 267
% identity 84

NCBI Description Vigna unguiculata phosphoinositide-specific phospholipase C

mRNA, complete cds

Seq. No. 36642

Seq. ID LIB3052-015-Q1-N1-H11

Method BLASTX
NCBI GI g1946364
BLAST score 245
E value 8.0e-21
Match length 70
% identity 66

NCBI Description (U93215) lipase isolog [Arabidopsis thaliana]



LIB3052-015-Q1-N1-H5 Seq. ID Method BLASTN q1930069 NCBI GI 132 BLAST score 5.0e-68 E value Match length 168 95 % identity NCBI Description Oryza sativa proteasome alpha subunit mRNA, complete cds 36644 Seq. No. LIB3052-016-Q1-N1-A12 Seq. ID Method BLASTN g169928 NCBI GI BLAST score 33 3.0e-09 E value 89 Match length 84 % identity Glycine max alpha'-type beta conglycinin storage protein NCBI Description gene, complete cds, clone ch4A 36645 Seq. No. LIB3052-016-Q1-N1-A6 Seq. ID Method BLASTX NCBI GI q4097880 BLAST score 230 2.0e-23 E value Match length 84 73 % identity (U70866) polyprotein [Bean pod mottle virus] NCBI Description 36646 Seq. No. LIB3052-016-Q1-N1-A9 Seq. ID BLASTX Method NCBI GI g4097880 430 BLAST score E value 1.0e-42 Match length 104 % identity 83 (U70866) polyprotein [Bean pod mottle virus] NCBI Description 36647 Seq. No. LIB3052-016-Q1-N1-B7 Seq. ID BLASTX Method .q2194136 NCBI GI BLAST score 166 1.0e-11 E value 79 Match length 39 % identity (AC002062) Strong similarity to Zea mays retrotransposon NCBI Description Hopscotch polyprotein (gb\_U12626). [Arabidopsis thaliana]

36648 Seq. No.

LIB3052-016-Q1-N1-C5 Seq. ID

Method BLASTX NCBI GI g2842490 163 BLAST score 3.0e-11E value

```
Match length
                  72
% identity
                  (AL021749) heat-shock protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  36649
Seq. ID
                  LIB3052-016-Q1-N1-C6
Method
                  BLASTN
NCBI GI
                  g56539
BLAST score
                  84
                  2.0e-39
E value
                  207
Match length
% identity
                  95
                  R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                  >gi 206360 gb J00764 RATPRLHR5 Rat (hooded) prolactin gene
                  : exon v and flanks
Seq. No.
Seq. ID
                  LIB3052-016-Q1-N1-D10
Method
                  BLASTN
NCBI GI
                  g476213
BLAST score
                  67
E value
                  2.0e-29
Match length
                  162
% identity
                  90
                  Glycine max Century 84 p24 oleosin isoform A gene, complete
NCBI Description
Seq. No.
                  36651
                  LIB3052-016-Q1-N1-D11
Seq. ID
Method
                  BLASTX
                  g3176098
NCBI GI
BLAST score
                  139
E value
                  1.0e-08
                  80
Match length
% identity
                  38
                  (Y15036) annexin [Medicago truncatula]
NCBI Description
Seq. No.
                  36652
Seq. ID
                  LIB3052-016-Q1-N1-E11
Method
                  BLASTX
NCBI GI
                  g1762436
BLAST score
                  240
                  1.0e-20
E value
Match length
                  75
% identity
                   (U60277) acyl-acyl carrier protein desaturase [Asclepias
NCBI Description
                  syriaca]
                  36653
Seq. No.
Seq. ID
                  LIB3052-016-Q1-N1-E9
Method
                  BLASTN
NCBI GI
                  g218264
BLAST score
                  175
```

5603

NCBI Description Glycine max mRNA for glycinin A2B1a subunit, complete cds

7.0e-94

263 92

E value Match length

% identity



```
Seq. No.
                  36654
Seq. ID
                  LIB3052-016-Q1-N1-F10
Method
                  BLASTX
                  q138364
NCBI GI
                  196
BLAST score
E value
                  1.0e-28
                  102
Match length
                  67
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
                  36655
Seq. No.
                  LIB3052-016-Q1-N1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4097880
BLAST score
                  263
                  2.0e-44
E value
                  131
Match length
% identity
                  76
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                  36656
                  LIB3052-016-Q1-N1-F5
Seq. ID
Method
                  BLASTN
                  a18634
NCBI GI
BLAST score
                   61
                   6.0e-26
E value
                  81
Match length
                   94
% identity
NCBI Description Soybean Gyl gene for glycinin subunit G1
                   36657
Seq. No.
Seq. ID
                   LIB3052-016-Q1-N1-G1
Method
                  BLASTN
NCBI GI
                   q18571
BLAST score
                   213
                   1.0e-116
E value
                   249
Match length
% identity
                   96
NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II
                   36658
Seq. No.
                   LIB3052-016-Q1-N1-G10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g806555
BLAST score
                   57
                   1.0e-23
E value
Match length
                   122
                   93
% identity
NCBI Description G.soja mRNA for glycinin
```

Seq. No. 36659

Seq. ID LIB3052-016-Q1-N1-H5

Method BLASTN

```
NCBI GI
                  q4097879
BLAST score
                  173
                  2.0e-92
E value
                  379
Match length
                  86
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                  36660
                  LIB3052-017-Q1-N1-D5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q210811
BLAST score
                  51
E value
                  1.0e-19
                  103
Match length
                   88
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                   36661
Seq. No.
                   LIB3052-017-Q1-N1-E10
Seq. ID
Method
                  BLASTN
                   g169928
NCBI GI
BLAST score
                   284
                   1.0e-159
E value
Match length
                   395
                   86
% identity
                  Glycine max alpha'-type beta conglycinin storage protein
NCBI Description
                   gene, complete cds, clone ch4A
                   36662
Seq. No.
                   LIB3052-017-Q1-N1-E11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g311697
BLAST score
                   79
E value
                   1.0e-36
Match length
                   195
                   85
% identity
NCBI Description G.max Lea protein mRNA, complete CDS
                   36663
Seq. No.
                   LIB3052-017-Q1-N1-F3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g18571
BLAST score
                   368
                   0.0e+00
E value
Match length
                   388
                   99
% identity
NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II
                   36664
Seq. No.
                   LIB3053-001-Q1-B1-A12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g456713
BLAST score
                   101
```

5605

1.0e-49

321

E value Match length

% identity 61 NCBI Description Glycine max gene for ubiquitin, complete cds

Seq. No. 36665

Seq. ID LIB3053-001-Q1-B1-B3

Method BLASTN
NCBI GI g1055367
BLAST score 392
E value 0.0e+00
Match length 392
% identity 100

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 36666

Seq. ID LIB3053-001-Q1-B1-D11

Method BLASTX
NCBI GI g1652203
BLAST score 149
E value 1.0e-09
Match length 80
% identity 39

NCBI Description (D90903) hypothetical protein [Synechocystis sp.]

Seq. No. 36667

Seq. ID LIB3053-001-Q1-B1-F2

Method BLASTN
NCBI GI 9454847
BLAST score 166
E value 2.0e-88
Match length 272
% identity 98

NCBI Description Glycine max ribosomal protein S11 gene, complete cds

Seq. No. 36668

Seq. ID LIB3053-001-Q1-B1-G12

Method BLASTX
NCBI GI g3184289
BLAST score 277
E value 1.0e-24
Match length 62
% identity 85

NCBI Description (AC004136) hypothetical protein [Arabidopsis thaliana]

Seq. No. 36669

Seq. ID LIB3053-001-Q1-B1-H1

Method BLASTN
NCBI GI g1055367
BLAST score 244
E value 1.0e-135
Match length 264
% identity 98

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 36670

Seq. ID LIB3053-002-Q1-B1-B4

```
BLASTX
Method
NCBI GI
                  q2702281
                  156
BLAST score
                  2.0e-10
E value
                  58
Match length
                  57
% identity
                  (AC003033) putative protein disulfide isomerase precursor
NCBI Description
                   [Arabidopsis thaliana]
                  36671
Seq. No.
                  LIB3053-002-Q1-B1-B5
Seq. ID
                  BLASTX
Method
                  q4115379
NCBI GI
BLAST score
                  266
                  2.0e-23
E value
                   96
Match length
                   56
% identity
                   (AC005967) putative carbonyl reductase [Arabidopsis
NCBI Description
                   thaliana]
                   36672
Seq. No.
                   LIB3053-002-Q1-B1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2462929
BLAST score
                   179
                   3.0e-13
E value
                   64
Match length
                   50
% identity
NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]
                   36673
Seq. No.
                   LIB3053-002-Q1-B1-F2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2104680
                   53
BLAST score
E value
                   6.0e-21
Match length
                   219
                   85
% identity
NCBI Description V.faba mRNA for putative transciption factor (1556bp)
                   36674
Seq. No.
                   LIB3053-002-Q1-B1-G4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g303900
BLAST score
                   286
                   1.0e-160
E value
                   343
Match length
                   29
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
```

Seq. No. 36675

Seq. ID LIB3053-002-Q1-B1-G9

Method BLASTX
NCBI GI g3702608
BLAST score 282
E value 2.0e-25
Match length 87

```
% identity
                  (AJ224165) shaggy kinase 7 [Petunia x hybrida]
NCBI Description
                  36676
Seq. No.
                  LIB3053-002-Q1-B1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q727263
BLAST score
                  50
                   4.0e-19
E value
                  90
Match length
% identity
                   14
                  Phaseolus vulgaris hydroxyproline-rich glycoprotein
NCBI Description
                  precursor gene, complete cds and promoter region
Seq. No.
                   36677
                  LIB3053-003-Q1-N1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2224901
                   172
BLAST score
                   2.0e-12
E value
                   65
Match length
                   54
% identity
                  (U67134) PcMYB1 protein [Petroselinum crispum]
NCBI Description
                   36678
Seq. No.
Seq. ID
                   LIB3053-003-Q1-N1-B8
Method
                   BLASTX
                   q4467116
NCBI GI
BLAST score
                   211
                   7.0e-17
E value
                   120
Match length
                   40
% identity
                   (AL035538) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   36679
Seq. No.
                   LIB3053-003-Q1-N1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4100433
BLAST score
                   326
                   2.0e-30
E value
Match length
                   126
                   52
% identity
                  (AF000378) beta-glucosidase [Glycine max]
NCBI Description
Seq. No.
                   36680
                   LIB3053-003-Q1-N1-H2
Seq. ID
Method
                   BLASTN
```

Method BLASIN
NCBI GI g904153
BLAST score 63
E value 5.0e-27
Match length 163
% identity 85

NCBI Description Glycine max FAD2-2 microsomal omega-6 desaturase mRNA,

complete cds

Seq. No.

36681

Seq. ID

LIB3053-004-Q1-N1-C9

NCBI GI

BLAST score

g206371

42

```
BLASTX
Method
                  g1903367
NCBI GI
                  179
BLAST score
                   4.0e-13
E value
                  76
Match length
                   42
% identity
                   (ACO00104) ESTs gb N65789, gb_T04628 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                   36682
Seq. No.
Seq. ID
                  LIB3053-004-Q1-N1-F3
Method
                  BLASTN
                  g169157
NCBI GI
                  124
BLAST score
                   3.0e-63
E value
                   224
Match length
% identity
                   89
                  Pisum sativum serine hydroxymethyltransferase mRNA,
NCBI Description
                   complete cds
Seq. No.
                   36683
Seq. ID
                  LIB3053-004-Q1-N1-G12
Method
                  BLASTN
                   q56539
NCBI GI
BLAST score
                   71
                   1.0e-31
E value
                   186
Match length
% identity
                   91
                  R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                   >gi 206360 gb J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and \overline{f}lanks
                   36684
Seq. No.
Seq. ID
                   LIB3053-005-Q1-N1-C12
                   BLASTX
Method
NCBI GI
                   q4097587
BLAST score
                   164
                   2.0e-11
E value
                   48
Match length
                   56
% identity
NCBI Description
                  (U64926) NTGP5 [Nicotiana tabacum]
Seq. No.
                   36685
                   LIB3053-005-Q1-N1-D7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q984678
BLAST score
                   175
                   1.0e-12
E value
                   98
Match length
                   42
% identity
                   (X62995) lipoamide dehydrogenase [Pisum sativum]
NCBI Description
Seq. No.
                   36686
Seq. ID
                   LIB3053-005-Q1-N1-E11
Method
                   BLASTN
```

```
E value
                  175
Match length
                  86
% identity
                  Rat(Sprague-Dawley) prolactin gene:exons IV,V and flanks
NCBI Description
Seq. No.
                  36687
                  LIB3053-005-Q1-N1-E2
Seq. ID
                  BLASTN
Method
                  g3309268
NCBI GI
                  138
BLAST score
                  1.0e-71
E value
Match length
                  330
% identity
                  Glycine max ferric leghemoglobin reductase-2 precursor
NCBI Description
                  mRNA, complete cds
Seq. No.
                  36688
                  LIB3053-005-Q1-N1-F3
Seq. ID
Method
                  BLASTX
                   g4314378
NCBI GI
                  196
BLAST score
E value
                   4.0e-15
Match length
                  88
% identity
                   45
                   (AC006232) putative lipase [Arabidopsis thaliana]
NCBI Description
                   36689
Seq. No.
Seq. ID
                   LIB3053-005-Q1-N1-H10
Method
                   BLASTN
                   g56539
NCBI GI
                   75
BLAST score
                   4.0e-34
E value
```

Match length 169

95 % identity

R.norvegicus gene encoding prolactin, exon 5 NCBI Description

>gi 206360 gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

36690 Seq. No.

LIB3053-005-Q1-N1-H2 Seq. ID

BLASTN Method g56539 NCBI GI BLAST score 63 6.0e-27 E value 202 Match length 87 % identity

R.norvegicus gene encoding prolactin, exon 5 NCBI Description

>gi\_206360\_gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

36691 Seq. No.

Seq. ID LIB3053-006-Q1-N1-C7

Method BLASTX g116395 NCBI GI BLAST score 278 7.0e-25 E value Match length 87

```
% identity
NCBI Description CHALCONE SYNTHASE (NARINGENIN-CHALCONE SYNTHASE)
                  >gi 629662_pir S42523 naringenin-chalcone synthase (EC
                  2.3.1.74) - parsley >gi 20514_emb_CAA24779_ (V01538)
                  chalcone synthase [Petroselinum crispum]
                  >qi 223820 prf 1001151A synthase, chalcone [Petroselinum
                  crispum]
Seq. No.
                  36692
Seq. ID
                  LIB3053-006-Q1-N1-C8
Method
                  BLASTX
                  g2465406
NCBI GI
                  278
BLAST score
                  7.0e-25
E value
                  98
Match length
                  54
% identity
                  (AF020709) chalcone synthase [Vitis vinifera]
NCBI Description
                  36693
Seq. No.
                  LIB3053-006-Q1-N1-E5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g20728
                  86
BLAST score
                  1.0e-40
E value
                  293
Match length
                  86
% identity
                  Pea chloroplast GAPA mRNA encoding
NCBI Description
                  glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A
                   (EC 1.2.1.13)
                  36694
Seq. No.
Seq. ID
                  LIB3053-006-Q1-N1-E7
Method
                  BLASTN
NCBI GI
                  g1053215
                  390
BLAST score
                  0.0e+00
E value
                  398
Match length
                  99
% identity
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                  nuclear gene encoding chloroplast protein, complete cds
Seq. No.
                   36695
Seq. ID
                  LIB3053-006-Q1-N1-F12
                  BLASTN
Method
NCBI GI
                  g1675195
BLAST score
                  128
```

1.0e-65 E value Match length 262 % identity

Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, NCBI Description

complete cds

Seq. No. 36696

Seq. ID LIB3053-007-Q1-N1-D6

BLASTN Method NCBI GI g56539 75 BLAST score

```
E value
                   3.0e-34
                  200
Match length
                  94
% identity
                  R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                  >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                  : exon v and flanks
                  36697
Seq. No.
                  LIB3053-007-Q1-N1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3435305
BLAST score
                  77
                  3.0e-35
E value
                  281
Match length
                  83
% identity
NCBI Description Medicago sativa glycolate oxidase mRNA, partial cds
Seq. No.
                   36698
                  LIB3053-007-Q1-N1-E7
Seq. ID
Method
                  BLASTN
                   g456713
NCBI GI
                   294
BLAST score
E value
                   1.0e-165
                   367
Match length
                   30
% identity
NCBI Description Glycine max gene for ubiquitin, complete cds
Seq. No.
                   36699
                   LIB3053-007-Q1-N1-F8
Seq. ID
Method
                   BLASTX
                   g2244876
NCBI GI
                   158
BLAST score
E value
                   1.0e-10
                   135
Match length
% identity
                   27
                  (Z97338) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   36700
Seq. No.
                   LIB3053-007-Q1-N1-G11
Seq. ID
                   BLASTX
Method
                   g3860258
NCBI GI
                   225
BLAST score
                   1.0e-18
E value
                   122
Match length
                   41
 % identity
                   (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                   36701
 Seq. No.
                   LIB3053-008-Q1-N1-D10
 Seq. ID
                   BLASTN
Method
                   g2218149
 NCBI GI
```

Method BLASTN
NCBI GI g2218149
BLAST score 36
E value 6.0e-11
Match length 136
% identity 83

NCBI Description Vigna unguiculata type IIIa membrane protein cp-wap11 mRNA,

complete cds



```
36702
Seq. No.
                  LIB3053-009-Q1-N1-A4
Seq. ID
                  BLASTX
Method
                  g2673917
NCBI GI
                  180
BLAST score
                  7.0e-21
E value
                  107
Match length
                  56
% identity
                  (AC002561) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                  thaliana]
                  36703
Seq. No.
                  LIB3053-009-Q1-N1-B6
Seq. ID
Method
                  BLASTX
                  g2407800
NCBI GI
BLAST score
                  231
                   3.0e-19
E value
Match length
                   88
                   62
% identity
NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
Seq. No.
                   36704
                   LIB3053-009-Q1-N1-C2
Seq. ID
Method
                   BLASTN
                   g1055367
NCBI GI
BLAST score
                   152
                   5.0e-80
E value
Match length
                   335
                   88
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   36705
Seq. No.
Seq. ID
                   LIB3053-009-Q1-N1-C8
                   BLASTN
Method
                   g255578
NCBI GI
                   105
BLAST score
                   6.0e-52
E value
                   253
Match length
% identity
                   small auxin up RNA gene cluster: orf X10A [Glycine
NCBI Description
                   max=soybeans, cv. Wayne, Genomic, 666 nt]
                   36706
Seq. No.
                   LIB3053-009-Q1-N1-F2
Seq. ID
                   BLASTX
Method
                   g3337356
NCBI GI
                   138
BLAST score
                   1.0e-08
E value
                   63
Match length
                   54
% identity
                  (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
```

36707

LIB3053-009-Q1-N1-F3

Seq. No.

Seq. ID

```
Method
                  BLASTN
                  q456713
NCBI GI
                  361
BLAST score
                  0.0e+00
E value
                  385
Match length
                  29
% identity
NCBI Description Glycine max gene for ubiquitin, complete cds
Seq. No.
                  LIB3053-009-Q1-N1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q144312
BLAST score
                   169
                   3.0e-18
E value
                   107
Match length
% identity
                   56
                  (J01566) 13.8 kd ORF [Plasmid ColE1]
NCBI Description
Seq. No.
                   LIB3053-010-Q1-N1-A4
Seq. ID
Method
                   BLASTX
                   g2244997
NCBI GI
BLAST score
                   140
E value
                   1.0e-08
                   107
Match length
                   36
% identity
                  (Z97341) unnamed protein product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   LIB3053-010-Q1-N1-A7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g206371
BLAST score
                   83
                   8.0e-39
E value
Match length
                   300
                   92
% identity
NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV,V and flanks
Seq. No.
                   36711
                   LIB3053-010-Q1-N1-D9
Seq. ID
                   BLASTN
Method
                   g1053215
NCBI GI
BLAST score
                   312
                   1.0e-175
E value
                   351
Match length
                   98
% identity
                   Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
```

Seq. No. 36712

Seq. ID LIB3053-010-Q1-N1-E7

Method BLASTN
NCBI GI g1055367
BLAST score 400
E value 0.0e+00
Match length 404
% identity 100

nuclear gene encoding chloroplast protein, complete cds

```
Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
                  36713
Seq. No.
                  LIB3053-010-Q1-N1-F1
Seq. ID
Method
                  BLASTX
                  q629669
NCBI GI
BLAST score
                  141
                  1.0e-08
E value
Match length
                  87.
% identity
                   41
NCBI Description hypothetical protein - tomato
                   36714
Seq. No.
                  LIB3053-011-Q1-N1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3461828
BLAST score
                   152
                   6.0e-10
E value
                   71
Match length
                   44
% identity
                  (AC004138) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   36715
                   LIB3053-011-Q1-N1-E4
Seq. ID
                   BLASTX
Method
                   g1834387
NCBI GI
                   183
BLAST score
                   7.0e-14
E value
                   71
Match length
                   59
% identity
NCBI Description (Y11022) chalcone synthase [Betula pendula]
                   36716
Seq. No.
                   LIB3053-011-Q1-N1-F5
Seq. ID
                   BLASTN
Method
                   q18646
NCBI GI
                   119
BLAST score
                   2.0e-60
E value
                   226
Match length
                   90
% identity
NCBI Description Soybean mRNA for HMG-Y related protein, variant A
Seq. No.
                   36717
                   LIB3053-011-Q1-N1-G12
Seq. ID
                   BLASTX
Method
                   g3114573
NCBI GI
                   497
BLAST score
                   2.0e-50
E value
                   133
Match length
                   66
 % identity
                   (AF019383) 1-deoxyxylulose-5-phosphate synthase [Mentha x
NCBI Description
                   piperita]
                   36718
 Seq. No.
 Seq. ID
                   LIB3053-012-Q1-N1-B2
                   BLASTX
Method
```

```
NCBI GI
                  q2828293
BLAST score
                  167
                  1.0e-11
E value
                  40
Match length
% identity
                 (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 36719

LIB3053-012-Q1-N1-B8 Seq. ID

BLASTX Method NCBI GI q267120 BLAST score 208 E value 2.0e-16 107 Match length 46 % identity

THIOREDOXIN F-TYPE PRECURSOR (TRX-F) >gi\_100070\_pir\_\_S20929 NCBI Description

thioredoxin f precursor - garden pea >gi 20907 emb CAA45098 (X63537) thioredoxin F [Pisum

sativum] >gi\_1388086 (U35830) thioredoxin f [Pisum sativum]

Seq. No. 36720

LIB3053-012-Q1-N1-E7 Seq. ID

BLASTN Method q170075 NCBI GI BLAST score 87 3.0e-41 E value 195 Match length 91 % identity

NCBI Description Soybean calmodulin (SCaM-4) mRNA, complete cds

Seq. No. 36721

LIB3053-012-Q1-N1-E9 Seq. ID

BLASTX Method NCBI GI g3550467 133 BLAST score E value 2.0e-16 Match length 96 58 % identity

(AJ005286) cp31AHv protein [Hordeum vulgare] NCBI Description

Seq. No.

36722

LIB3053-013-Q1-N1-B4 Seq. ID Method BLASTN

NCBI GI g399647 BLAST score 54 2.0e-21 E value Match length 142 85 % identity

Lycopersicon esculentum (DB244) meloidogyne-induced giant NCBI Description

cell protein mRNA, 3' end

36723 Seq. No.

LIB3053-013-Q1-N1-B5 Seq. ID

Method BLASTX NCBI GI g4567283 BLAST score 232 1.0e-19 E value



Match length 76 % identity 59

NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

Seq. No. 36724

Seq. ID LIB3053-013-Q1-N1-C7

Method BLASTN
NCBI GI g758693
BLAST score 47

E value 3.0e-17
Match length 174
% identity 82

NCBI Description Catharanthus roseus S-adenosyl-L-methionine decarboxylase

proenzyme mRNA, complete cds

Seq. No. 36725

Seq. ID LIB3053-013-Q1-N1-D10

Method BLASTX
NCBI GI g2911067
BLAST score 352
E value 2.0e-33
Match length 109
% identity 65

NCBI Description (AL021960) UV-damaged DNA-binding protein- like

[Arabidopsis thaliana]

Seq. No. 36726

Seq. ID LIB3053-013-Q1-N1-E2

Method BLASTN
NCBI GI g255451
BLAST score 79
E value 2.0e-36
Match length 175
% identity 86

NCBI Description CH5B=chitinase [Phaseolus vulgaris=beans, cv Saxa, Genomic,

4704 nt]

Seq. No. 36727

Seq. ID LIB3053-013-Q1-N1-E9

Method BLASTN
NCBI GI g56539
BLAST score 95
E value 5.0e-46
Match length 281
% identity 95

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi 206360\_gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 36728

Seq. ID LIB3053-014-Q1-N1-B2

Method BLASTX
NCBI GI g1644388
BLAST score 291
E value 3.0e-26
Match length 134
% identity 43





```
(U72654) flavonoid 3'5'-hydroxylase [Eustoma grandiflorum]
NCBI Description
                  36729
Seq. No.
                  LIB3053-014-Q1-N1-B5
Seq. ID
                  BLASTX
Method
                  g4567225
NCBI GI
                  209
BLAST score
                  6.0e-17
E value
                  52
Match length
                  77
% identity
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]
                  36730
Seq. No.
                  LIB3053-014-Q1-N1-F2
Seq. ID
                  BLASTX
Method
                  g3885334
NCBI GI
                  172
BLAST score
                  3.0e-12
E value
                  56
Match length
                  59
% identity
                  (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                   thaliana]
                   36731
Seq. No.
                  LIB3055-001-Q1-B1-B1
Seq. ID
                  BLASTX
Method
                   g2245378
NCBI GI
                   212
BLAST score
                   4.0e-17
E value
                   44
Match length
                   86
% identity
                  (U83245) auxin response factor 1 [Arabidopsis thaliana]
NCBI Description
                   36732
Seq. No.
                   LIB3055-001-Q1-B1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3204106
                   264
BLAST score
E value
                   3.0e-23
Match length
                   106
% identity
                   52
                   (AJ006763) putative beta-amilase [Cicer arietinum]
NCBI Description
                   36733
Seq. No.
                   LIB3055-001-Q1-B1-B5
Seq. ID
                   BLASTX
Method
                   g2244780
NCBI GI
BLAST score
                   139
E value
                   4.0e-19
Match length
                   87
% identity
                   (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   36734
Seq. No.
                   LIB3055-001-Q1-B1-D6
Seq. ID
```

BLASTX

g3047082

Method

NCBI GI



BLAST score E value 1.0e-18 Match length 57 72 % identity

NCBI Description (AF058914) similar to Vigna radiata pectinacetylesterase

precursor (GB:X99348) [Arabidopsis thaliana]

36735 Seq. No.

LIB3055-001-Q1-B1-D9 Seq. ID

Method BLASTN g340697 NCBI GI BLAST score 77 2.0e-35 E value Match length 185 % identity 85

NCBI Description Soybean chloroplast 16S/23S ribosomal intergenic spacer DNA

36736 Seq. No.

LIB3055-001-Q1-B1-E3 Seq. ID

Method BLASTX q4049399 NCBI GI 155 BLAST score E value 2.0e-10 Match length 62 % identity 48

NCBI Description (Y09581) FRO2 [Arabidopsis thaliana]

Seq. No. 36737

LIB3055-001-Q1-B1-F4 Seq. ID

BLASTX Method NCBI GI g267069 BLAST score 139 9.0e-09 E value Match length 44 % identity 61

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 36738

LIB3055-001-Q1-B1-G6 Seq. ID

BLASTN Method g3219360 NCBI GI BLAST score 38 E value 3.0e-12 Match length 70 % identity 89

NCBI Description Glycine max biotin carboxylase precursor (accC-3) mRNA,

nuclear gene encoding chloroplast protein, complete cds

Seq. No. 36739

Seq. ID LIB3055-001-Q1-B1-G8

Method BLASTX NCBI GI g547886 245 BLAST score E value 5.0e-21



Match length 10% identity 55% NCBI Description M

MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)

(ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME) >qi 542102 pir S42939 malate dehydrogenase

(oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) precursor - Flaveria pringlei >gi\_1084444\_pir\_\_S52016 malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flaveria pringlei >gi\_459441\_emb\_CAA54986\_

(X78069) malate dehydrogenase (oxaloacetate decarboxylating) (NADP+) [Flaveria pringlei]

Seq. No. 36740

Seq. ID LIB3055-001-Q1-B1-H11

Method BLASTX
NCBI GI g309673
BLAST score 338
E value 7.0e-32
Match length 103
% identity 74

NCBI Description (L19651) light harvesting protein [Pisum sativum]

Seq. No. 36741

Seq. ID LIB3055-001-Q1-B1-H3

Method BLASTX
NCBI GI g1086252
BLAST score 202
E value 5.0e-16
Match length 94
% identity 45

% identity 45

NCBI Description sucrose cleavage protein - Potato >gi\_707001\_bbs\_157931

(S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]

[Solanum tuberosum]

Seq. No. 36742

Seq. ID LIB3055-001-Q1-B1-H4

Method BLASTN
NCBI GI g1055367
BLAST score 197
E value 1.0e-107
Match length 225
% identity 97

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 36743

Seq. ID LIB3055-002-Q1-B1-D12

Method BLASTN
NCBI GI g1360633
BLAST score 71
E value 1.0e-31
Match length 174
% identity 88

NCBI Description V.sativa mRNA for protein binding to ENOD12B promoter

Seq. No. 36744



```
LIB3055-002-Q1-B1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4337025
                  281
BLAST score
                   3.0e-25
E value
                   97
Match length
% identity
NCBI Description (AF123253) AIM1 protein [Arabidopsis thaliana]
                  36745
Seq. No.
Seq. ID
                  LIB3055-002-Q1-B1-G1
Method
                  BLASTX
NCBI GI
                   q309673
                   305
BLAST score
                   2.0e-39
E value
                   117
Match length
% identity
NCBI Description (L19651) light harvesting protein [Pisum sativum]
                   36746
Seq. No.
                   LIB3055-002-Q1-B1-G10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q18551
BLAST score
                   307
                   1.0e-172
E value
                   358
Match length
% identity
                   Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                   protein
                   36747
Seq. No.
                   LIB3055-003-Q1-N1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3860256
BLAST score
                   449
                   1.0e-44
E value
                   124
Match length
                   68
% identity
                   (AC005824) putative tRNA isopentenylpyrophosphate
NCBI Description
                   transferase [Arabidopsis thaliana]
                   36748
Seq. No.
                   LIB3055-003-Q1-N1-C2
Seq. ID
Method
                   BLASTN
                   g1556445
NCBI GI
                   96
BLAST score
                   1.0e-46
E value
Match length
                   232
                   85
% identity
NCBI Description Hordeum vulgare alpha tubulin (tubA) mRNA, complete cds
                   36749
Seq. No.
                   LIB3055-004-Q1-N1-B12
Seq. ID
                   {\tt BLASTN}
Method
```

5621

g18644

4.0e-25

60

NCBI GI

E value

BLAST score

```
Match length 240 % identity 86
```

NCBI Description Soybean mRNA for HMG-1 like protein

Seq. No.

36750

Seq. ID LIB3055-004-Q1-N1-C12

Method BLASTN
NCBI GI g170053
BLAST score 60
E value 2.0e-25
Match length 106
% identity 90

NCBI Description Soybean ribosomal protein S11 mRNA, 3' end

Seq. No.

36751

Seq. ID LIB3055-004-Q1-N1-C9

Method BLASTN
NCBI GI g310575
BLAST score 267
E value 1.0e-148
Match length 408
% identity 94

NCBI Description Glycine max nodulin-26 mRNA, complete cds

Seq. No.

36752

Seq. ID LIB3055-004-Q1-N1-D12

Method BLASTX
NCBI GI g4063751
BLAST score 223
E value 3.0e-18
Match length 137
% identity 39

NCBI Description (AC005851) putative white protein [Arabidopsis thaliana]

>gi\_4510409\_gb\_AAD21495.1\_ (AC006929) putative white

protein [Arabidopsis thaliana]

Seq. No. 36753

Seq. ID LIB3055-004-Q1-N1-D2

Method BLASTX
NCBI GI g2281627
BLAST score 216
E value 2.0e-17
Match length 62
% identity 61

NCBI Description (AF003094) AP2 domain containing protein RAP2.1

[Arabidopsis thaliana]

Seq. No. 36754

Seq. ID LIB3055-004-Q1-N1-D8

Method BLASTX
NCBI GI g2104535
BLAST score 120
E value 8.0e-12
Match length 45
% identity 84

NCBI Description (AF001308) T10M13.13 [Arabidopsis thaliana]

```
Seq. No.
Seq. ID
                   LIB3055-004-Q1-N1-E8
Method
                   BLASTX
                   g2465923
NCBI GI
                   270
BLAST score
                   9.0e-24
E value
                   129
Match length
                   18
% identity
                   (AF024648) receptor-like serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
                   36756
Seq. No.
                   LIB3055-004-Q1-N1-H8
Seq. ID
                   BLASTN
Method
                   q4220645
NCBI GI
                   102
BLAST score
                   4.0e-50
E value
Match length
                   246
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MYA6, complete sequence [Arabidopsis thaliana]
                   36757
Seq. No.
Seq. ID
                   LIB3055-005-Q1-N1-C8
                   BLASTN
Method
NCBI GI
                   q303900
                   346
BLAST score
                   0.0e + 00
E value
Match length
                   411
                   31
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
Seq. No.
                   LIB3055-005-Q1-N1-D11
Seq. ID
Method
                   BLASTX
                   g4234955
NCBI GI
BLAST score
                   149
                   2.0e-09
E value
                   144
Match length
 % identity
                   33
                   (AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]
NCBI Description
                   36759
 Seq. No.
                   LIB3055-005-Q1-N1-E2
 Seq. ID
Method
                   BLASTN
                    g1053215
 NCBI GI
 BLAST score
                    360
E value
                    0.0e + 00
                    396
Match length
                    98
 % identity
```

Seq. No. 36760

NCBI Description

Seq. ID LIB3055-005-Q1-N1-F8

Method BLASTX NCBI GI g1175014

Glycine max chlorophyll a/b-binding protein (cab3) mRNA,

nuclear gene encoding chloroplast protein, complete cds



BLAST score 180 E value 8.0e-14 Match length 48 % identity 75

NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 2B >gi\_629543\_pir\_\_S44085 plasma membrane intrinsic protein 2b - Arabidopsis thaliana >gi\_472879\_emb\_CAA53478\_ (X75884) plasma membrane intrinsic

protein 2b [Arabidopsis thaliana]

Seq. No. 36761

Seq. ID LIB3055-005-Q1-N1-H1

Method BLASTX
NCBI GI g231573
BLAST score 260
E value 1.0e-22
Match length 101
% identity 54

NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)

>gi\_99970\_pir\_\_S24757 asparaginase (EC 3.5.1.1) -

narrow-leaved blue lupine >gi\_19135\_emb\_CAA43099\_ (X60691) developing seed L-asparaginase [Lupinus angustifolius]

Seq. No. 36762

Seq. ID LIB3055-006-Q1-N1-B12

Method BLASTX
NCBI GI 94455313
BLAST score 215
E value 2.0e-17
Match length 93
% identity 46

NCBI Description (AL035528) fatty acid elongase-like protein (cer2-like)

[Arabidopsis thaliana]

Seq. No. 36763

Seq. ID LIB3055-006-Q1-N1-B9

Method BLASTX
NCBI GI g2769642
BLAST score 606
E value 4.0e-63
Match length 144
% identity 77

NCBI Description (Z97215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon

esculentum]

Seq. No. 36764

Seq. ID LIB3055-006-Q1-N1-E12

Method BLASTX
NCBI GI g2244865
BLAST score 175
E value 9.0e-13
Match length 73
% identity 41

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 36765

Seq. ID LIB3055-006-Q1-N1-E5

Method BLASTX

```
g3548802
NCBI GI
BLAST score
                  336
                  2.0e-31
E value
Match length
                  125
                  54
% identity
                  (AC005313) axi 1-like protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4335769 gb AAD17446 (AC006284) putative axil protein
                  [Nicotiana tabacum] [Arabidopsis thaliana]
Seq. No.
                  36766
                  LIB3055-006-Q1-N1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3047104
BLAST score
                  271
                  7.0e-24
E value
                  82
Match length
% identity
                  66
NCBI Description
                  (AF058919) No definition line found [Arabidopsis thaliana]
                  36767
Seq. No.
                  LIB3055-007-Q1-N1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4467126
BLAST score
                  596
E value
                  5.0e-62
Match length
                  133
% identity
                  90
NCBI Description
                  (AL035538) guanine nucleotide-exchange protein-like
                  [Arabidopsis thaliana]
                  36768
Seq. No.
Seq. ID
                  LIB3055-007-Q1-N1-C1
Method
                  BLASTX
NCBI GI
                  q2642443
BLAST score
                  447
E value
                  2.0e-44
Match length
                  136
                  57
% identity
NCBI Description (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  36769
Seq. ID
                  LIB3055-007-Q1-N1-E2
Method
                  BLASTN
NCBI GI
                  q1370202
BLAST score
                  198
```

NCBI GI g1370202
BLAST score 198
E value 1.0e-107
Match length 314
% identity 91

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAN1A

Seq. No. 36770

Seq. ID LIB3055-007-Q1-N1-E6

Method BLASTX
NCBI GI g1657374
BLAST score 508
E value 1.0e-51
Match length 123

```
% identity
NCBI Description
                  (X96853) endo-beta-1,4-glucanase [Prunus persica]
                   >gi 1657380 emb CAA65600 (X96856) endo-beta-1,4-glucanase
                   [Prunus persica]
                  36771
Seq. No.
                  LIB3055-007-Q1-N1-H5
Seq. ID
Method
                  BLASTX
                  g2190553
NCBI GI
                  169
BLAST score
                   4.0e-12
E value
Match length
                  77
% identity
                   47
NCBI Description
                  (ACO01229) Strong similarity to Arabidopsis
                   zeta-crystallin-like protein (gb_Z49268). [Arabidopsis
                   thaliana]
Seq. No.
                   36772
                  LIB3055-008-Q1-N1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1871177
BLAST score
                  301
E value
                  1.0e-27
Match length
                   76
% identity
NCBI Description
                  (U90439) unknown protein [Arabidopsis thaliana]
Seq. No.
                  36773
                  LIB3055-008-Q1-N1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3033512
BLAST score
                  161
E value
                  2.0e-85
Match length
                  387
% identity
                  86
NCBI Description
                  Phaseolus vulgaris rubisco activase (Rcal) mRNA, complete
                  cds
Seq. No.
                   36774
Seq. ID
                  LIB3055-008-Q1-N1-C9
Method
                  BLASTN
NCBI GI
                  g1055367
BLAST score
                  407
                  0.0e + 00
E value
Match length
                  411
                  100
% identity
```

Glycine max ribulose-1,5-bisphosphate carboxylase small NCBI Description

subunit mRNA, complete cds

36775 Seq. No. Seq. ID LIB3055-008-Q1-N1-D4 Method BLASTX

NCBI GI q1507699 BLAST score 181 E value 2.0e-13 Match length 49 % identity 69

```
(L81119) COL2 [Arabidopsis thaliana] >gi 1507701 (L81120)
NCBI Description
                  COL2 [Arabidopsis thaliana]
Seq. No.
                  36776
Seq. ID
                  LIB3055-008-Q1-N1-E7
Method
                  BLASTX
NCBI GI
                  q4027897
                  484
BLAST score
E value
                  6.0e-49
Match length
                  113
% identity
                  77
NCBI Description (AF049353) alpha-expansin precursor [Nicotiana tabacum]
Seq. No.
                  36777
                  LIB3055-009-Q1-N1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2245107
BLAST score
                  291
E value
                  3.0e-26
Match length
                  86
                  44
% identity
NCBI Description (Z97343) thioesterase homolog [Arabidopsis thaliana]
                  36778
Seq. No.
                  LIB3055-009-Q1-N1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g556835
BLAST score
                  109
E value
                  3.0e-54
                  328
Match length
% identity
                  89
NCBI Description P.vulgaris mRNA for profilin
Seq. No.
                  36779
Seq. ID
                  LIB3055-010-Q1-N1-A4
Method
                  BLASTX
NCBI GI
                  g2148014
BLAST score
                  140
E value
                  8.0e-09
Match length
                  46
                  25
% identity
NCBI Description rhodopsin - Alloteuthis subulata
Seq. No.
                  36780
                  LIB3055-010-Q1-N1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2267139
BLAST score
                  170
E value
                  4.0e-12
```

Match length 55 % identity 64

NCBI Description (AF008910) ubiquitin-conjugating enzyme [Prunus armeniaca]

Seq. No. 36781

Seq. ID LIB3055-010-Q1-N1-B9

Method BLASTN NCBI GI g1053215



BLAST score 228 E value 1.0e-125 Match length 284 % identity 95

NCBI Description Glycine max chlorophyll a/b-binding protein (cab3) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 36782

Seq. ID LIB3055-010-Q1-N1-C6

Method BLASTX
NCBI GI g4455235
BLAST score 243
E value 4.0e-21
Match length 52
% identity 88

NCBI Description (AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA

SUBUNIT-like [Arabidopsis thaliana]

Seq. No. 36783

Seq. ID LIB3055-010-Q1-N1-E4

Method BLASTN
NCBI GI g2961299
BLAST score 92
E value 3.0e-44
Match length 224
% identity 85

NCBI Description Cicer arietinum mRNA for ribosomal protein L24

Seq. No. 36784

Seq. ID LIB3055-010-Q1-N1-G1

Method BLASTX
NCBI GI g3242709
BLAST score 174
E value 2.0e-14
Match length 80
% identity 57

NCBI Description (AC003040) putative guanine nucleotide-binding protein

[Arabidopsis thaliana]

Seq. No. 36785

Seq. ID LIB3055-010-Q1-N1-G4

Method BLASTN
NCBI GI g300418
BLAST score 74
E value 1.0e-33
Match length 106
% identity 92

NCBI Description aspartate aminotransferase isozyme 5 [Glycine max=soybeans,

cv. Century, mRNA, 1755 nt]

Seq. No. 36786

Seq. ID LIB3055-010-Q1-N1-H5

Method BLASTX
NCBI GI g4204312
BLAST score 499
E value 1.0e-50
Match length 136



% identity

(AC003027) 1cl prt seq No definition line found NCBI Description

[Arabidopsis thaliana]

36787 Seq. No.

LIB3055-011-Q1-N1-A5 Seq. ID

BLASTX Method g4512657 NCBI GI 401 BLAST score 4.0e-39 E value 125 Match length % identity 62

(AC006931) putative APG protein [Arabidopsis thaliana] NCBI Description

>gi\_4544463\_gb\_AAD22370.1\_AC006580\_2 (AC006580) putative

APG isolog protein [Arabidopsis thaliana]

Seq. No. 36788

LIB3055-011-Q1-N1-C5 Seq. ID

Method BLASTX NCBI GI g4191789 476 BLAST score E value 6.0e-48Match length 129 % identity 77

(AC005917) putative transmembrane transport protein NCBI Description

[Arabidopsis thaliana]

Seq. No. 36789

LIB3055-011-Q1-N1-D7 Seq. ID

Method BLASTX g1143511 NCBI GI BLAST score 110 E value 5.0e-11 Match length 88 % identity 49

(Z47076) Ser/Thr protein phosphatase homologous to PPX NCBI Description

[Malus domestica] >gi\_1586034\_prf\_\_2202340A Ser/Thr protein

phosphatase [Malus domestica]

36790 Seq. No.

LIB3055-011-Q1-N1-E9 Seq. ID

BLASTN Method g1381675 NCBI GI BLAST score 80 5.0e-37 E value 80 Match length 100 % identity

Glycine max small GTP-binding protein (sra1) mRNA, partial NCBI Description

cds

36791 Seq. No.

Seq. ID LIB3055-011-Q1-N1-F11

BLASTX Method g4191789 NCBI GI 284 BLAST score 6.0e-26 E value 95 Match length

```
% identity
                                                                             (AC005917) putative transmembrane transport protein
NCBI Description
                                                                              [Arabidopsis thaliana]
                                                                             36792
Seq. No.
                                                                             LIB3055-011-Q1-N1-F2
Seq. ID
Method
                                                                             BLASTX
                                                                             g114200
NCBI GI
                                                                             226
BLAST score
                                                                             9.0e-19
E value
                                                                             79
Match length
 % identity
                                                                             SHIKIMATE KINASE PRECURSOR >gi 100253 pir S21584 shikimate
NCBI Description
                                                                              kinase precursor - tomato >gi_19349_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA}}45121_{emb_C\overline{AA
                                                                              shikimate kinase precursor [Lycopersicon esculentum]
 Seq. No.
                                                                              LIB3055-012-Q1-N1-E10
 Seq. ID
                                                                              BLASTX
 Method
 NCBI GI
                                                                              q2827699
                                                                               231
 BLAST score
                                                                               3.0e-19
 E value
                                                                               78
 Match length
                                                                               63
  % identity
                                                                              (AL021684) predicted protein [Arabidopsis thaliana]
  NCBI Description
                                                                               36794
  Seq. No.
                                                                               LIB3055-012-Q1-N1-F9
  Seq. ID
                                                                               BLASTN
  Method
                                                                               q508303
  NCBI GI
                                                                                73
  BLAST score
                                                                               7.0e-33
  E value
                                                                               173
  Match length
                                                                                86
   % identity
  NCBI Description Alfalfa bimodular protein (corC) mRNA, complete cds
                                                                                36795
   Seq. No.
                                                                                LIB3055-012-Q1-N1-G10
   Seq. ID
   Method
                                                                                BLASTN
   NCBI GI
                                                                                g1142620
                                                                                 50
   BLAST score
```

4.0e-19 E value

108 Match length 93 % identity

Phaseolus vulgaris phaseolin G-box binding protein PG2 NCBI Description (PG2) mRNA, partial cds

36796 Seq. No.

LIB3055-012-Q1-N1-H1 Seq. ID

BLASTX Method q4510373 NCBI GI 183 BLAST score 1.0e-13 E value 71 Match length 52 % identity

(AC007017) putative harpin-induced protein [Arabidopsis NCBI Description

thaliana]

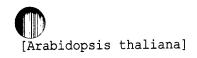
Seq. No.

36802



```
36797
Seq. No.
                  LIB3055-012-Q1-N1-H9
Seq. ID
                  BLASTX
Method
                  g3236238
NCBI GI
                  208
BLAST score
                  6.0e-23
E value
                  74
Match length
                  77
% identity
                   (AC004684) putative ARF1 GTPase activating protein
NCBI Description
                   [Arabidopsis thaliana] >gi_4519792 dbj BAA75744.1
                   (AB017876) Aspl [Arabidopsis thaliana]
                  36798
Seq. No.
                  LIB3055-013-Q1-N1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g18551
                  127
BLAST score
                   4.0e-65
E ♥alue
                   143
Match length
                   97
% identity
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                  protein
                   36799
Seq. No.
                   LIB3055-013-Q1-N1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2739010
BLAST score
                   220
E value
                   3.0e-18
Match length
                   81
                   59
% identity
                  (AF022464) CYP77A3p [Glycine max]
NCBI Description
                   36800
Seq. No.
                   LIB3055-013-Q1-N1-A8
Seq. ID
Method
                   BLASTX
                   q2062167
NCBI GI
BLAST score
                   224
                   2.0e-18
E value
                   95
Match length
                   51
% identity
                   (AC001645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                   thaliana]
                   36801
Seq. No.
                   LIB3055-013-Q1-N1-B3
Seq. ID
Method
                   BLASTX
                   g2924781
NCBI GI
                   478
BLAST score
                   3.0e-48
E value
                   128
Match length
% identity
                   (AC002334) putative cellulose synthase [Arabidopsis
NCBI Description
                   thaliana]
```

```
LIB3055-013-Q1-N1-D9
Seq. ID
                  BLASTX
Method
                  g1173223
NCBI GI
                  237
BLAST score
                   4.0e-20
E value
                  91
Match length
% identity
                   60
                  40S RIBOSOMAL PROTEIN S11 >gi 454848 (L28831) ribosomal
NCBI Description
                  protein S11 [Glycine max]
Seq. No.
                   36803
Seq. ID
                   LIB3055-013-Q1-N1-E4
Method
                   BLASTN
                   q20728
NCBI GI
                   39
BLAST score
                   1.0e-12
E value
                   99
Match length
% identity
                   90
                   Pea chloroplast GAPA mRNA encoding
NCBI Description
                   glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A
                   (EC 1.2.1.13)
                   36804
Seq. No.
                   LIB3055-013-Q1-N1-F7
Seq. ID
                   BLASTN
Method
                   q56539
NCBI GI
                   91
BLAST score
                   1.0e-43
E value
Match length
                   206
                   94
% identity
                   R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                   >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
                   36805
Seq. No.
                   LIB3055-013-Q1-N1-G7
Seq. ID
                   BLASTX
Method
                   g2791276
NCBI GI
                   170
BLAST score
                   4.0e-12
E value
                   80
Match length
                   49
 % identity
                   (Z95327) Cleavage Stimulation Factor (CF-1, Polyadenylation
NCBI Description
                   Factor) 64 kD subunit [Homo sapiens]
                   36806
 Seq. No.
                   LIB3056-001-Q1-B1-C6
 Seq. ID
                   BLASTX
 Method
                   g1703200
 NCBI GI
                   116
 BLAST score
                   7.0e-12
 E value
                   58
Match length
                   67
 % identity
                   PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase
 NCBI Description
                   [Arabidopsis thaliana] >gi 642130_dbj_BAA08214_ (D45353)
                   protein kinase [Arabidopsis thaliana]
                   >gi 4220516 emb_CAA22989_ (AL035356) protein kinase (AFC2)
```



```
36807
Seq. No.
                  LIB3056-001-Q1-B1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3687389
                  365
BLAST score
                  5.0e-35
E value
                  110
Match length
                  68
% identity
                  (Y16124) putative cullin protein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  36808
                  LIB3056-001-Q1-B1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2654093
BLAST score
                   44
E value
                   1.0e-15
                   164
Match length
                   82
% identity
                  Glycine max aspartate aminotransferase glyoxysomal isozyme
NCBI Description
                   AAT1 precursor and aspartate aminotransferase cytosolic
                   isozyme AAT2 (AAT) mRNA, complete cds
                   36809
Seq. No.
                   LIB3056-001-Q1-B1-F4
Seq. ID
                   BLASTN
Method
                   q56539
NCBI GI
BLAST score
                   84
                   2.0e-39
E value
                   232
Match length
                   93
% identity
                   R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                   >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
                   36810
Seq. No.
                   LIB3056-001-Q1-B1-G1
Seq. ID
Method
                   BLASTX
                   g2660670
NCBI GI
                   367
BLAST score
                   3.0e-35
E value
                   108
Match length
                   68
% identity
                   (AC002342) putative Cu2+-transporting ATPase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   36811
                   LIB3056-001-Q1-B1-G3
Seq. ID
Method
                   BLASTX
                   q549063
NCBI GI
BLAST score
                   267
                   1.0e-23
E value
                   79
Match length
                   65
 % identity
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
 NCBI Description
                   >gi 1072464 pir__A38958 IgE-dependent histamine-releasing
```

```
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
```

Seq. No. 36812

Seq. ID LIB3056-002-Q1-B1-A11

Method BLASTX
NCBI GI g4102600
BLAST score 128
E value 4.0e-13
Match length 116
% identity 51

NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]

21kd polypeptide [Oryza sativa]

Seq. No. 36813

Seq. ID LIB3056-002-Q1-B1-B11

Method BLASTN
NCBI GI g4039114
BLAST score 66
E value 1.0e-28
Match length 300
% identity 87

NCBI Description Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds

Seq. No. 36814

Seq. ID LIB3056-002-Q1-B1-F5

Method BLASTN
NCBI GI g56539
BLAST score 76
E value 1.0e-34
Match length 310
% identity 91

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi\_206360\_gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 36815

Seq. ID LIB3056-002-Q1-B1-G2

Method BLASTX
NCBI GI g417744
BLAST score 316
E value 2.0e-29
Match length 89
% identity 73

NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) >gi\_169663 (M81885)

S-adenosylhomocysteine hydrolase [Petroselinum crispum]

Seq. No. 36816

Seq. ID LIB3056-002-Q1-B1-H2

Method BLASTX
NCBI GI g3372230
BLAST score 204
E value 4.0e-16
Match length 62
% identity 63

NCBI Description (AF017074) RNA polymerase I, II and III 16.5 kDa subunit

[Arabidopsis thaliana]

NCBI Description



```
36817
Seq. No.
                  LIB3056-003-Q1-N1-A3
Seq. ID
                  BLASTN
Method
                  g56539
NCBI GI
                  87
BLAST score
                  2.0e-41
E value
                  219
Match length
                  92
% identity
                  R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                  >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                  : exon v and flanks
                  36818
Seq. No.
                  LIB3056-003-Q1-N1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1856971
                  263
BLAST score
                   4.0e-23
E value
                  89
Match length
% identity
                   (D26058) This gene is specifically expressed at the S phase
NCBI Description
                  during the cell cycle in the synchronous culture of
                  periwinkle cells. [Catharanthus roseus]
Seq. No.
                   36819
                   LIB3056-003-Q1-N1-B7
Seq. ID
Method
                   BLASTX
                   g4512685
NCBI GI
                   306
BLAST score
                   5.0e-28
E value
                   100
Match length
% identity
                   57
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4559325 gb AAD22987.1 AC007087_6 (AC007087)
                   hypothetical protein [Arabidopsis thaliana]
                   36820
Seq. No.
                   LIB3056-003-Q1-N1-C1
Seq. ID
                   BLASTX
Method
                   g2911073
NCBI GI
                   477
BLAST score
                   4.0e-48
E value
                   130
Match length
% identity
                   (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                   36821
Seq. No.
                   LIB3056-003-Q1-N1-C12
Seq. ID
                   BLASTN
Method
                   g56539
NCBI GI
BLAST score
                   68
                   6.0e-30
E value
                   169
Match length
% identity
                   R.norvegicus gene encoding prolactin, exon 5
```

>gi 206360\_gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene

NCBI GI

BLAST score



## : exon v and flanks

```
Seq. No.
                  36822
Seq. ID
                  LIB3056-003-Q1-N1-E11
Method
                  BLASTN
NCBI GI
                  q2879810
BLAST score
                  88
E value
                  8.0e-42
Match length
                  268
% identity
                  84
NCBI Description Lupinus luteus mRNA for ribosomal protein L30
Seq. No.
                  36823
                  LIB3056-003-Q1-N1-E8
Seq. ID
Method
                  BLASTX
                  g3395428
NCBI GI
BLAST score
                  326
                  2.0e-30
E value
Match length
                  91
                  69
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                  36824
Seq. No.
Seq. ID
                  LIB3056-003-Q1-N1-F2
Method
                  BLASTN
NCBI GI
                  q3860330
BLAST score
                  91
E value
                  1.0e-43
Match length
                  167
% identity
                  89
NCBI Description Cicer arietinum mRNA for hypothetical protein, clone Can106
Seq. No.
                  36825
Seq. ID
                  LIB3056-003-Q1-N1-G10
Method
                  BLASTX
NCBI GI
                  q4091806
BLAST score
                  163
                  2.0e-11
E value
Match length
                  57
                  32
% identity
NCBI Description (AF052585) CONSTANS-like protein 2 [Malus domestica]
Seq. No.
                  36826
                  LIB3056-003-Q1-N1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1418990
BLAST score
                  405
E value
                  1.0e-39
Match length
                  120
% identity
                  67
NCBI Description (Z75524) unknown [Lycopersicon esculentum]
Seq. No.
                  36827
Seq. ID
                  LIB3056-003-Q1-N1-H7
Method
                  BLASTX
```

g3786011

181

```
2.0e-13
```

E value 2.0e-13 Match length 68 % identity 84

NCBI Description (AC005499) putative elongation factor [Arabidopsis

thaliana]

Seq. No. 36828

Seq. ID LIB3056-003-Q1-N1-H9

Method BLASTX
NCBI GI g2765442
BLAST score 184
E value 7.0e-14
Match length 56
% identity 68

NCBI Description (Y15066) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 36829

Seq. ID LIB3056-004-Q1-N1-A11

Method BLASTN
NCBI GI g56539
BLAST score 91
E value 1.0e-43
Match length 268
% identity 94

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi 206360\_gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 36830

Seq. ID LIB3056-004-Q1-N1-A6

Method BLASTX
NCBI GI g2702277
BLAST score 328
E value 1.0e-30
Match length 77
% identity 78

NCBI Description (AC003033) putative cyclin g-associated kinase [Arabidopsis

thaliana] >gi\_2914689 (AC003974) putative cyclin

g-associated kinase [Arabidopsis thaliana]

Seq. No. 36831

Seq. ID LIB3056-004-Q1-N1-B4

Method BLASTN
NCBI GI g3021505
BLAST score 69
E value 9.0e-31
Match length 157
% identity 86

NCBI Description N.tabacum mRNA for NAD-dependent isocitrate dehydrogenase

Seq. No. 36832

Seq. ID LIB3056-004-Q1-N1-F3

Method BLASTN
NCBI GI g210811
BLAST score 106
E value 1.0e-52



Match length 258 % identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 36833

Seq. ID LIB3056-004-Q1-N1-F5

Method BLASTX
NCBI GI g2642154
BLAST score 156
E value 1.0e-10
Match length 62
% identity 56

NCBI Description (AC003000) unknown protein [Arabidopsis thaliana]

>gi 3790595 (AF079186) RING-H2 finger protein RHC2a

[Arabidopsis thaliana]

Seq. No. 36834

Seq. ID LIB3056-004-Q1-N1-F6

Method BLASTN
NCBI GI g1370197
BLAST score 87
E value 4.0e-41
Match length 315
% identity 82

NCBI Description L. japonicus mRNA for small GTP-binding protein, RAB8E

Seq. No. 36835

Seq. ID LIB3056-004-Q1-N1-G3

Method BLASTX
NCBI GI g1841540
BLAST score 144
E value 2.0e-09
Match length 71
% identity 46

NCBI Description (U87317) ATP citrate lyase [Drosophila melanogaster]

Seq. No. 36836

Seq. ID LIB3056-005-Q1-N1-E5

Method BLASTX
NCBI GI g2443878
BLAST score 163
E value 2.0e-11
Match length 81
% identity 53

NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No. 36837

Seq. ID LIB3056-005-Q1-N1-H3

Method BLASTX
NCBI GI g1621467
BLAST score 242
E value 7.0e-21
Match length 68
% identity 68

NCBI Description (U73106) laccase [Liriodendron tulipifera]

```
36838
Seq. No.
                  LIB3056-006-Q1-N1-A1
Seq. ID
                  BLASTX
Method
                   g1771162
NCBI GI
                   222
BLAST score
                   2.0e-18
E value
                   83
Match length
                   57
% identity
                   (X98930) SBT2 [Lycopersicon esculentum]
NCBI Description
                   >gi 3687307_emb_CAA07000_ (AJ006379) subtilisin-like
                   protease [Lycopersicon esculentum]
Seq. No.
                   36839
                   LIB3056-006-Q1-N1-E4
Seq. ID
Method
                   BLASTX
                   g2129739
NCBI GI
BLAST score
                   260
                   8.0e-23
E value
                   67
Match length
                   82
% identity
                   shaggy-like kinase etha - Arabidopsis thaliana
NCBI Description
                   >gi 1161512_emb_CAA64409_ (X94939) shaggy-like kinase etha
                   [Arabidopsis thaliana] >gi_1627516_emb_CAA70144_ (Y08947)
                   shaggy-like kinase etha [Arabidopsis thaliana]
                   36840
Seq. No.
                   LIB3056-006-Q1-N1-E5
Seq. ID
Method
                   BLASTX
                   g2245131
NCBI GI
                   175
BLAST score
                   1.0e-12
E value
                   70
Match length
% identity
                   56
                   (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   36841
Seq. No.
                   LIB3056-006-Q1-N1-F6
Seq. ID
                   BLASTN
Method
                   g1619904
NCBI GI
                   33
BLAST score
                   4.0e-09
E value
                   53
Match length
                   91
% identity
                   Glycine max thiol protease isoform A mRNA, partial cds
NCBI Description
                   36842
Seq. No.
                   LIB3056-006-Q1-N1-F7
Seq. ID
                   BLASTX
Method
                   q2827550
NCBI GI
                   433
BLAST score
                   7.0e-43
E value
                   136
Match length
                   58
 % identity
```

Seq. No. 36843

NCBI Description

[Arabidopsis thaliana]

(AL021635) leucine rich repeat receptor kinase-like protein

```
LIB3056-006-Q1-N1-G9
Seq. ID
                  BLASTX
Method
                  g2661840
NCBI GI
                  367
BLAST score
                  4.0e-35
E value
                  92
Match length
                  75
% identity
NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]
                  36844
Seq. No.
                  LIB3056-007-Q1-N1-B2
Seq. ID
                  BLASTN
Method
                  g3941288
NCBI GI
                  56
BLAST score
                  9.0e-23
E value
                  252
Match length
                  82
% identity
                  Pisum sativum similarity to SCAMP37 (psam2) mRNA, complete
NCBI Description
                  cds
                  36845
Seq. No.
                  LIB3056-007-Q1-N1-B3
Seq. ID
Method
                  BLASTX
                  q3941289
NCBI GI
                   208
BLAST score
                   3.0e-17
E value
                   118
Match length
                   49
% identity
                  (AF018093) similarity to SCAMP37 [Pisum sativum]
NCBI Description
                   36846
Seq. No.
                   LIB3056-007-Q1-N1-C2
Seq. ID
Method
                   BLASTX
                   g3805962
NCBI GI
                   178
BLAST score
                   4.0e-13
E value
                   111
Match length
                   38
% identity
NCBI Description (Y13772) laccase [Populus balsamifera subsp. trichocarpa]
                   36847
Seq. No.
                   LIB3056-007-Q1-N1-C7
Seq. ID
                   BLASTN
Method
                   q457569
NCBI GI
BLAST score
                   102
                   4.0e-50
E value
                   278
Match length
                   84
% identity
                   Soybean mRNA for endo-xyloglucan transferase, partial cds
NCBI Description
                   36848
Seq. No.
Seq. ID
                   LIB3056-007-Q1-N1-D6
                   BLASTX
Method
                   q3395440
NCBI GI
BLAST score
                   324
                   4.0e-30
E value
                   121
Match length
```

```
% identity
                 (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  36849
Seq. No.
                  LIB3056-007-Q1-N1-E11
Seq. ID
Method
                  BLASTN
                  g849135
NCBI GI
                  36
BLAST score
                  9.0e-11
E value
                   48
Match length
                   94
% identity
                  Vigna radiata vacuolar H+-ATPase subunit A mRNA, complete
NCBI Description
                   36850
Seq. No.
                   LIB3056-007-Q1-N1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2160166
                   142
BLAST score
                   2.0e-14
E value
                   99
Match length
                   47
% identity
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   LIB3056-007-Q1-N1-G11
Seq. ID
                   BLASTX
Method
                   q1076670
NCBI GI
BLAST score
                   216
                   1.0e-17
E value
                   73
Match length
                   64
% identity
                   NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                   >gi_668985_emb_CAA59062_ (X84319) NADH dehydrogenase
                   [Solanum tuberosum]
Seq. No.
                   36852
                   LIB3056-007-Q1-N1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2583118
                   227
BLAST score
                   9.0e-19
E value
Match length
                   75
                   63
% identity
                   (AC002387) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   36853
                   LIB3056-008-Q1-N1-A1
 Seq. ID
                   BLASTX
Method
                   g505136
NCBI GI
                   262
BLAST score
                   8.0e-23
 E value
                   90
Match length
                   58
 % identity
                   (D30794) ferredoxin [Oryza sativa]
 NCBI Description
```

36854

Seq. No.

· Service ·

Seq. ID LIB3056-008-Q1-N1-B10

Method BLASTX
NCBI GI g4512699
BLAST score 152
E value 6.0e-10
Match length 41
% identity 66

NCBI Description (AC006569) putative NADH-ubiquinone oxireductase

[Arabidopsis thaliana]

Seq. No. 36855

Seq. ID LIB3056-008-Q1-N1-B6

Method BLASTX
NCBI GI g3913425
BLAST score 542
E value 9.0e-56
Match length 114
% identity 93

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi\_2275203 (AC002337) RNA helicase isolog

[Arabidopsis thaliana]

Seq. No. 36856

Seq. ID LIB3056-008-Q1-N1-C11

Method BLASTX
NCBI GI g4490297
BLAST score 227
E value 8.0e-19
Match length 115
% identity 48

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 36857

Seq. ID LIB3056-008-Q1-N1-E1

Method BLASTN
NCBI GI g210811
BLAST score 132
E value 5.0e-68
Match length 332
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 36858

Seq. ID LIB3056-008-Q1-N1-E9

Method BLASTX
NCBI GI g4567250
BLAST score 194
E value 7.0e-15
Match length 86
% identity 47

NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No. 36859

Seq. ID LIB3056-008-Q1-N1-G1

Method BLASTX NCBI GI g3511223

E value

Match length

% identity

72

71

```
BLAST score
                  4.0e-11
E value
                  41
Match length
                  76
% identity
NCBI Description (AF069528) plant adhesion molecule 1 [Arabidopsis thaliana]
                  36860
Seq. No.
                  LIB3056-008-Q1-N1-G11
Seq. ID
                  BLASTN
Method
                  q473216
NCBI GI
BLAST score
                  39
                  7.0e-13
E value
Match length
                  87
                  86
% identity
NCBI Description P.sativum (little marvel) HSC71.0 mRNA
                  36861
Seq. No.
Seq. ID
                  LIB3056-008-Q1-N1-H4
                  BLASTN
Method
                  q1009206
NCBI GI
BLAST score
                   45
                   4.0e-16
E value
                   45
Match length
% identity
                   100
                  Miquartia guianensis Aubl. 18S ribosomal RNA gene, partial
NCBI Description
                   sequence
                   36862
Seq. No.
                   LIB3056-009-Q1-N1-B3
Seq. ID
Method
                   BLASTX
                   g3121825
NCBI GI
                   368
BLAST score
                   3.0e-35
E value
Match length
                   131
                   62
% identity
                   2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
NCBI Description
                   ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219)
                   bas1 protein [Spinacia oleracea]
                   36863
Seq. No.
                   LIB3056-009-Q1-N1-B4
Seq. ID
                   BLASTX
Method
                   g571484
NCBI GI
                   183
BLAST score
                   7.0e-14
E value
                   70
Match length
 % identity
                   57
                   (U16727) peroxidase precursor [Medicago truncatula]
NCBI Description
                   36864
Seq. No.
                   LIB3056-009-Q1-N1-C10
 Seq. ID
                   BLASTX
Method
                   g2789434
NCBI GI
                   286
BLAST score
                   1.0e-25
```

```
(AB001389) CLB1 [Lycopersicon esculentum]
NCBI Description
                  36865
Seq. No.
                  LIB3056-009-Q1-N1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4572674
BLAST score
                  143
                  7.0e-09
E value
                  32
Match length
                  84
% identity
                  (AC006954) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  36866
                  LIB3056-009-Q1-N1-E11
Seq. ID
                  BLASTN
Method
                  q56539
NCBI GI
                   49
BLAST score
                   1.0e-18
E value
                   139
Match length
                   88
% identity
                  R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                   >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
                   36867
Seq. No.
                   LIB3056-009-Q1-N1-E2
Seq. ID
                   BLASTX
```

Method q126959 NCBI GI BLAST score 198

6.0e-16 E value 64 Match length 64 % identity

TONOPLAST INTRINSIC PROTEIN, ROOT-SPECIFIC RB7-5A (RT-TIP) NCBI Description >gi 82192 pir\_ JQ1011 TobRB7-5A protein - common tobacco

>gi 100371 pir S13719 probable membrane channel protein common tobacco >gi\_20011\_emb\_CAA38634 (X54855) possible

membrane channel protein [Nicotiana tabacum]

36868 Seq. No.

LIB3056-009-Q1-N1-E3 Seq. ID

BLASTX Method g3158474 NCBI GI 388 BLAST score 1.0e-37 E value 97 Match length 75 % identity

(AF067184) aquaporin 1 [Samanea saman] NCBI Description

36869 Seq. No.

LIB3056-009-Q1-N1-E9 Seq. ID

BLASTX Method g2344901 NCBI GI 390 BLAST score 4.0e-38 E value 85 Match length 84 % identity

(AC002388) serine/threonine protein kinase isolog NCBI Description



## [Arabidopsis thaliana]

```
      Seq. No.
      36870

      Seq. ID
      LIB3056-009-Q1-N1-F4

      Method
      BLASTN

      NCBI GI
      g56539

      BLAST score
      43

      Example
      2.0e-15
```

E value 2.0e-15
Match length 103
% identity 85

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi\_206360\_gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 36871

Seq. ID LIB3056-009-Q1-N1-G3

Method BLASTX
NCBI GI g3395424
BLAST score 184
E value 6.0e-14
Match length 90
% identity 44

NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

>gi 3786024 (AC005499) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 36872

Seq. ID LIB3056-009-Q1-N1-G7

Method BLASTN
NCBI GI g347454
BLAST score 162
E value 6.0e-86
Match length 336
% identity 46

NCBI Description Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3'

end

Seq. No. 36873

Seq. ID LIB3056-009-Q1-N1-H12

Method BLASTN
NCBI GI g467551
BLAST score 294
E value 1.0e-165
Match length 330
% identity 97

NCBI Description Soybean mRNA for phosphoenolpyruvate carboxylase

Seq. No. 36874

Seq. ID LIB3056-010-Q1-N1-D11

Method BLASTX
NCBI GI g2827665
BLAST score 316
E value 4.0e-29
Match length 129
% identity 52

NCBI Description (AL021637) vacuolar sorting receptor-like protein

[Arabidopsis thaliana]



```
36875
Seq. No.
                  LIB3056-010-Q1-N1-G12
Seq. ID
                  BLASTX
Method
                  g1709970
NCBI GI
                  215
BLAST score
                  3.0e-17
E value
                  55
Match length
                  78
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L10A
                  36876
Seq. No.
                  LIB3056-011-Q1-N1-D1
Seq. ID
                  BLASTX
Method
                  q439493
NCBI GI
                  161
BLAST score
                  4.0e-11
E value
Match length
                  60
% identity
NCBI Description (D26086) zinc-finger protein [Petunia x hybrida]
                   36877
Seq. No.
                  LIB3056-011-Q1-N1-H12
Seq. ID
Method
                  BLASTN
                  q456713
NCBI GI
                   122
BLAST score
                   2.0e-62
E value
                   170
Match length
% identity
NCBI Description Glycine max gene for ubiquitin, complete cds
                   36878
Seq. No.
                   LIB3056-011-Q1-N1-H2
Seq. ID
Method
                   BLASTX
                   g2244806
NCBI GI
                   203
BLAST score
                   3.0e-16
E value
                   58
Match length
                   66
% identity
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
                   36879
Seq. No.
                   LIB3056-012-Q1-N1-B9
Seq. ID
Method
                   BLASTX
                   g1572819
NCBI GI
                   197
BLAST score
E value
                   3.0e-15
Match length
                   107
 % identity
                   43
                   (U70855) similar to the RAS gene family [Caenorhabditis
NCBI Description
                   elegans]
                   36880
 Seq. No.
                   LIB3056-012-Q1-N1-D2
 Seq. ID
                   BLASTN
 Method
```

5646

g18764

132

NCBI GI BLAST score



E value 4.0e-68 Match length 324 % identity 85

NCBI Description G.max tefS1 gene for elongation factor EF-1a

Seq. No.

36881

Seq. ID

LIB3056-012-Q1-N1-D4

Method BLASTX NCBI GI g2117937 BLAST score 383 5.0e-37 E value Match length 81 % identity 89

NCBI Description UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

barley >gi 1212996 emb CAA62689 (X91347) UDP-glucose

pyrophosphorylase [Hordeum vulgare]

Seq. No.

36882 Seq. ID

LIB3056-012-Q1-N1-E3

Method BLASTX NCBI GI g2493129 BLAST score 199 E value 1.0e-15 Match length 78 60 % identity

VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B NCBI Description

SUBUNIT) >gi 459198 (U07052) vacuolar H+-ATPase subunit B

[Gossypium hirsutum]

Seq. No. 36883

Seq. ID LIB3056-012-Q1-N1-E9

Method BLASTX NCBI GI g1946359 BLAST score 186 5.0e-14 E value Match length 93 % identity

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 36884

Seq. ID LIB3056-012-Q1-N1-G9

Method BLASTX NCBI GI g123601 BLAST score 458 8.0e-46 E value 138 Match length 64 % identity

NCBI Description HEAT SHOCK 70 KD PROTEIN >gi\_99913\_pir\_\_S14992 heat shock

protein, 70K - soybean >gi\_18663\_emb\_CAA44620\_ (X62799)

Heat Shock 70kD protein [Glycine max]

Seq. No. 36885

Seq. ID LIB3056-012-Q1-N1-H5

Method BLASTN NCBI GI g555615 BLAST score 80 E value 5.0e-37

```
Match length
                  83
% identity
                  Glycine max Mandarin cytokinin induced message (cim1) mRNA,
NCBI Description
                  complete cds
                  36886
Seq. No.
                  LIB3056-013-Q1-N1-B10
Seq. ID
                  BLASTX
Method
                  g1272349
NCBI GI
                   240
BLAST score
                   3.0e-20
E value
                   116
Match length
                   44
% identity
NCBI Description (U51740) secreted glycoprotein 3 [Ipomoea trifida]
                   36887
Seq. No.
                   LIB3056-013-Q1-N1-C8
Seq. ID
                   BLASTX
Method
                   g3355480
NCBI GI
                   208
BLAST score
                   2.0e-16
E value
                   107
Match length
                   41
% identity
                   (AC004218) Medicago nodulin N21-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   36888
Seq. No.
                   LIB3056-013-Q1-N1-G6
Seq. ID
                   BLASTX
Method
                   g2598597
NCBI GI
                   146
BLAST score
                   3.0e-09
E value
                   45
Match length
                   58
% identity
NCBI Description (Y15371) MtN5 [Medicago truncatula]
                   36889
Seq. No.
                   LIB3056-013-Q1-N1-H9
Seq. ID
                   BLASTN
Method
NCBI GI
                   q56539
BLAST score
                   54
                   2.0e-21
E value
Match length
                   201
 % identity
                   R.norvegicus gene encoding prolactin, exon 5
 NCBI Description
                   >gi 206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                    : exon v and flanks
                   36890
```

Seq. No.

Seq. ID LIB3056-014-Q1-N1-B7

Method BLASTX g2809246

NCBI GI BLAST score 341 3.0e-32 E value 105 Match length % identity 64

(AC002560) F2401.15 [Arabidopsis thaliana] NCBI Description



36891 Seq. No. Seq. ID LIB3056-014-Q1-N1-C12 Method BLASTX NCBI GI g3273764 BLAST score 157 1.0e-10 E value Match length 89 % identity 42 (AF061870) Dc3 promoter-binding factor-3 [Helianthus NCBI Description annuus] 36892 Seq. No. Seq. ID LIB3056-014-Q1-N1-C2 Method BLASTX NCBI GI q3249095 BLAST score 237 E value 4.0e-20 Match length 83 % identity 57 NCBI Description (AC003114) Contains similarity to dihydrofolate reductase (dfr1) gb\_L13703 from Schizosaccharomyces pombe. ESTs gb N37567 and gb T43002 come from this gene. [Arabidopsis thaliana] Seq. No. 36893 Seq. ID LIB3056-014-Q1-N1-F3 Method BLASTX NCBI GI g416731 BLAST score 184 E value 9.0e-14 Match length 89 % identity 40 POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi 82655 pir JQ1107 NCBI Description 18.3K protein precursor, pollen - maize >gi 255569 bbs 113677 (S44171) pollen specific protein [Zea mays=corn, Peptide, 170 aa] [Zea mays] >gi 1588669 prf 2209273A Zm13 [Zea mays] Seq. No. 36894 Seq. ID LIB3056-014-Q1-N1-G10 Method BLASTX NCBI GI g113603 BLAST score 246 3.0e-21E value Match length 95 52 % identity THIOL PROTEASE ALEURAIN PRECURSOR >gi 19021 emb CAA28804 NCBI Description (X05167) aleurain [Hordeum vulgare] 36895 Seq. No.

Seq. ID LIB3065-001-Q1-N1-A6

Method BLASTX
NCBI GI g2244754
BLAST score 223
E value 2.0e-18
Match length 75



Seq. No. 36896

Seq. ID LIB3065-001-Q1-N1-C12

Method BLASTX
NCBI GI g3550661
BLAST score 192
E value 5.0e-15
Match length 83
% identity 46

NCBI Description (AJ001310) 39 kDa EF-Hand containing protein [Solanum

tuberosum]

Seq. No. 36897

Seq. ID LIB3065-001-Q1-N1-C4

Method BLASTN
NCBI GI g56539
BLAST score 72
E value 3.0e-32
Match length 250
% identity 91

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi\_206360\_gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 36898

Seq. ID LIB3065-001-Q1-N1-F8

Method BLASTX
NCBI GI g135535
BLAST score 237
E value 3.0e-20
Match length 63
% identity 83

NCBI Description T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)

(CCT-ALPHA) >gi\_322602\_pir\_\_JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi\_217871\_dbj\_BAA01955\_ (D11351) t-complex polypeptide 1 homologue [Arabidopsis

thaliana] >gi 2326265\_dbj\_BAA21772\_ (D11352) CCT

alpha/TCP-1 [Arabidopsis thaliana]

Seq. No. 36899

Seq. ID LIB3065-002-Q1-N1-B1

Method BLASTN
NCBI GI g56539
BLAST score 95
E value 5.0e-46
Match length 276
% identity 95

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi\_206360\_gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 36900

Seq. ID LIB3065-002-Q1-N1-B3

Method BLASTN



NCBI GI g56539 BLAST score 39 E value 1.0e-12 Match length 246 % identity 87

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi 206360 gb J00764 RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 36901

Seq. ID LIB3065-002-Q1-N1-C3

Method BLASTN
NCBI GI g2760361
BLAST score 42
E value 2.0e-14
Match length 74
% identity 89

NCBI Description Arabidopsis thaliana 15.9 kDa subunit of RNA polymerase II

(RPB15.9) mRNA, complete cds

Seq. No. 36902

Seq. ID LIB3065-002-Q1-N1-C6

Method BLASTN
NCBI GI g170009
BLAST score 116
E value 1.0e-58
Match length 196
% identity 90

NCBI Description Soybean late embryogenesis abundant (LEA) protein mRNA,

complete cds

Seq. No. 36903

Seq. ID LIB3065-002-Q1-N1-D4

Method BLASTN
NCBI GI g18769
BLAST score 222
E value 1.0e-122
Match length 270
% identity 96

NCBI Description G.max mRNA Ti-a for Kunitz trypsin inhibitor subtype A

Seq. No. 36904

Seq. ID LIB3065-002-Q1-N1-D5

Method BLASTN
NCBI GI g56539
BLAST score 78
E value 7.0e-36
Match length 98
% identity 95

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi\_206360\_gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 36905

Seq. ID LIB3065-002-Q1-N1-E11

Method BLASTN NCBI GI g169972



BLAST score 4.0e-40 E value Match length 273 83 % identity

NCBI Description Soybean glycinin A-la-B-x subunit mRNA, complete cds

Seq. No. 36906

LIB3065-002-Q1-N1-E7 Seq. ID

BLASTX Method g3695393 NCBI GI BLAST score 186 5.0e-14 E value Match length 112 % identity 44

(AF096371) contains similarity to retroviral aspartyl NCBI Description

proteases (Pfam: rvp.hmm, score: 11.80) [Arabidopsis

thaliana]

Seq. No.

36907

LIB3065-002-Q1-N1-H12 Seq. ID

Method BLASTX NCBI GI q138364 BLAST score 196 E value 1.0e-28 97 Match length 70 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 36908

LIB3065-003-Q1-N1-A7 Seq. ID

BLASTN Method NCBI GI q256634 BLAST score 233 1.0e-128 E value Match length 396 45 % identity

NCBI Description KTil=Kunitz trypsin inhibitor KTil, KTi2=Kunitz trypsin

inhibitor KTi2 [soybeans, Genomic, 3269 nt]

36909 Seq. No.

Seq. ID LIB3065-003-Q1-N1-B9

Method BLASTN g206371 NCBI GI BLAST score 98 E value 1.0e-47 257 Match length % identity 96

NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks

36910 Seq. No.

Seq. ID LIB3065-003-Q1-N1-D4

Method BLASTN NCBI GI g56539 BLAST score 87



E value 3.0e-41
Match length 310
% identity 94

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>qi 206360 qb J00764 RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 36911

Seq. ID LIB3065-003-Q1-N1-D8

Method BLASTN
NCBI GI g18535
BLAST score 151
E value 1.0e-79
Match length 203
% identity 94

NCBI Description Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No. 36912

Seq. ID LIB3065-003-Q1-N1-F1

Method BLASTN
NCBI GI g56539
BLAST score 76
E value 1.0e-34
Match length 104
% identity 94

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi 206360 gb J00764 RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 36913

Seq. ID LIB3065-003-Q1-N1-G11

Method BLASTN
NCBI GI g2052028
BLAST score 51
E value 8.0e-20
Match length 147
% identity 84

NCBI Description G.max mRNA for glutathione transferase

Seq. No. 36914

Seq. ID LIB3065-003-Q1-N1-H9

Method BLASTN
NCBI GI g56539
BLAST score 87
E value 3.0e-41
Match length 271
% identity 93

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi\_206360\_gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 36915

Seq. ID LIB3065-004-Q1-N1-B5

Method BLASTN
NCBI GI g56539
BLAST score 65
E value 3.0e-28



```
Match length
% identity
                   92
                  R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                   >gi 206360 gb J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
                   36916
Seq. No.
                   LIB3065-004-Q1-N1-D7
Seq. ID
                   BLASTN
Method
                   q169972
NCBI GI
BLAST score
                   124
                   2.0e-63
E value
Match length
                   276
                   87
% identity
NCBI Description Soybean glycinin A-la-B-x subunit mRNA, complete cds
                   36917
Seq. No.
                   LIB3065-004-Q1-N1-E11
Seq. ID
Method
                   BLASTN
                   g170007
NCBI GI
                   204
BLAST score
                   1.0e-111
E value
                   336
Match length
% identity
                   Soybean 18 kD late embryogenesis abundant (Lea) protein
NCBI Description
                   mRNA, complete cds
                   36918
Seq. No.
                   LIB3065-004-Q1-N1-G5
Seq. ID
                   BLASTN
Method
                   g1199562
NCBI GI
                   74
BLAST score
                   1.0e-33
E value
Match length
                   150
% identity
                   Glycine max 34 kDa maturing seed vacuolar thiol protease
NCBI Description
                   mRNA, complete cds
                   36919
Seq. No.
                   LIB3065-004-Q1-N1-H10
 Seq. ID
Method
                   BLASTN
                   g256426
NCBI GI
BLAST score
                   287
E value
                   1.0e-160
Match length
                   344
                    95
 % identity
                   CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic,
 NCBI Description
                    3840 nt]
                    36920
 Seq. No.
                   LIB3065-005-Q1-N1-B11
 Seq. ID
                    BLASTN
 Method
```

g2618603

NCBI GI 48 BLAST score 6.0e-18 E value 64 Match length

94 % identity



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]

Seq. No. 36921

Seq. ID LIB3065-005-Q1-N1-C12

Method BLASTN
NCBI GI g18764
BLAST score 175
E value 9.0e-94
Match length 359
% identity 87

NCBI Description G.max tefS1 gene for elongation factor EF-la

Seq. No. 36922

Seq. ID LIB3065-005-Q1-N1-D12

Method BLASTX
NCBI GI g2792220
BLAST score 151
E value 8.0e-10
Match length 122
% identity 41

NCBI Description (AF032688) NBS-LRR type resistance protein [Oryza sativa]

Seq. No. 36923

Seq. ID LIB3065-005-Q1-N1-E2

Method BLASTX
NCBI GI g3668092
BLAST score 499
E value 1.0e-50
Match length 132
% identity 70

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 36924

Seq. ID LIB3065-005-Q1-N1-E5

Method BLASTX
NCBI GI g3461820
BLAST score 156
E value 2.0e-10
Match length 68
% identity 51

NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]

Seq. No. 36925

Seq. ID LIB3065-006-Q1-N1-B8

Method BLASTN
NCBI GI g1165321
BLAST score 66
E value 7.0e-29
Match length 182
% identity 54

NCBI Description Glycine max extensin (SbHRGP3) gene, complete cds

Seq. No. 36926

Seq. ID LIB3065-006-Q1-N1-H11

Method BLASTX NCBI GI g3980405

```
BLAST score
                  9.0e-15
E value
                  76
Match length
                  53
% identity
                 (AC004561) putative tropinone reductase [Arabidopsis
NCBI Description
                  thaliana]
                  36927
Seq. No.
                  LIB3065-006-Q1-N1-H8
Seq. ID
                  BLASTX
Method
                  q3413423
NCBI GI
                  267
BLAST score
                  2.0e-23
E value
                  93
Match length
                   53
% identity
NCBI Description (AJ006309) hypothetical protein [Arabidopsis thaliana]
                   36928
Seq. No.
                  LIB3065-007-Q1-N1-A4
Seq. ID
                   BLASTN
Method
                   g476215
NCBI GI
                   426
BLAST score
                   0.0e + 00
E value
                   458
Match length
                   99
% identity
                  Glycine max Century 84 p24 oleosin isoform B gene, complete
NCBI Description
                   36929
Seq. No.
                   LIB3065-007-Q1-N1-C2
Seq. ID
                   BLASTX
Method
                   g2493047
NCBI GI
                   277
BLAST score
                   1.0e-24
E value
                   105
Match length
                   61
% identity
                   ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >qi 294087 (L13320) F1-ATPase delta-prime subunit [Pisum
```

sativum]

36930 Seq. No.

LIB3065-007-Q1-N1-E2 Seq. ID

BLASTN Method q497119 NCBI GI BLAST score 183 2.0e-98 E value 335 Match length 89 % identity

Pisum sativum monodehydroascorbate reductase mRNA, complete NCBI Description

36931 Seq. No.

LIB3065-007-Q1-N1-E3 Seq. ID

Method BLASTX q633890 NCBI GI 295 BLAST score 1.0e-26 E value

```
Match length
% identity
                   (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
NCBI Description
                  vulgare]
                   36932
Seq. No.
                  LIB3065-008-Q1-N1-B1
Seq. ID
Method
                  BLASTN
                   g1053215
NCBI GI
                   363
BLAST score
                   0.0e + 00
E value
Match length
                   438
% identity
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                   nuclear gene encoding chloroplast protein, complete cds
                   36933
Seq. No.
                   LIB3065-008-Q1-N1-E1
Seq. ID
                   BLASTX
Method
                   g4049353
NCBI GI
                   400
BLAST score
                   5.0e-39
E value
Match length
                   116
% identity
                   (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   LIB3065-008-Q1-N1-H2
Seq. ID
Method
                   BLASTX
                   g4204297
NCBI GI
                   324
BLAST score
                   4.0e-30
E value
                   90
Match length
% identity
                   67
                   (AC003027) ADK1 [Arabidopsis thaliana]
NCBI Description
                   36935
 Seq. No.
                   LIB3065-009-Q1-N1-C10
 Seq. ID
Method
                   BLASTX
                   g541943
 NCBI GI
                   197
 BLAST score
                   3.0e-15
 E value
                   50
Match length
                   72
```

 Seq. No.
 36936

 Seq. ID
 LIB3065-009-Q1-N1-D3

 Method
 BLASTN

 NCBI GI
 g169964

 BLAST score
 140

BLAST score 140 E value 8.0e-73 Match length 330 % identity 87

NCBI Description Soybean glutathione reductase (GR) mRNA, complete cds

```
36937
Seq. No.
                  LIB3065-009-Q1-N1-E11
Seq. ID
                   BLASTX
Method
                   q4309918
NCBI GI
                   257
BLAST score
                   3.0e-22
E value
                   122
Match length
                   45
% identity
NCBI Description (AC006153) similar to Aquifex aeolicus GTP-binding protein;
                   similar to AE000771 (PID:g2984292) [Homo sapiens]
                   36938
Seq. No.
                   LIB3065-010-Q1-N1-A10
Seq. ID
                   BLASTX
Method
                   g2642213
NCBI GI
                   206
BLAST score
                   2.0e-16
E value
                   69
Match length
                   59
% identity
                   (AF030385) nitrate-induced NOI protein [Zea mays]
NCBI Description
                   >gi 2895781 (AF045033) nitrate-induced NOI protein [Zea
                   mays]
                   36939
Seq. No.
                   LIB3065-010-Q1-N1-A6
 Seq. ID
                   BLASTN
 Method
                   g829118
 NCBI GI
                   185
 BLAST score
                   1.0e-99
 E value
                   360
 Match length
                   88
 % identity
 NCBI Description P.vulgaris gene for cyclophilin
                   36940
 Seq. No.
                   LIB3065-010-Q1-N1-B9
 Seq. ID
                   BLASTX
 Method
                   g730463
 NCBI GI
 BLAST score
                   266
                   2.0e-23
 E value
                   91
 Match length
                    54
 % identity
                   60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
 NCBI Description
                   >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast
                    (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal
                    protein L37 [Saccharomyces cerevisiae]
                    ->gi 1420537_emb_CAA99454_ (Z75142) ORF YOR234c
                    [Saccharomyces cerevisiae]
                    36941
 Seq. No.
                    LIB3065-010-Q1-N1-D2
 Seq. ID
 Method
                    BLASTN
                    q310575
 NCBI GI
                    174
 BLAST score
                    3.0e-93
 E value
```

NCBI Description Glycine max nodulin-26 mRNA, complete cds

312

89

Match length % identity

NCBI GI

BLAST score



```
36942
Seq. No.
                  LIB3065-010-Q1-N1-E2
Seq. ID
                  BLASTX
Method
                  q4580469
NCBI GI
                  187
BLAST score
                  4.0e-14
E value
                  68
Match length
                  50
% identity
                  (AC006081) putative zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
                  36943
Seq. No.
                  LIB3065-010-Q1-N1-F2
Seq. ID
                  BLASTN
Method
                  q456713
NCBI GI
                  209
BLAST score
                  1.0e-114
E value
                  389
Match length
                   35
% identity
NCBI Description Glycine max gene for ubiquitin, complete cds
                   36944
Seq. No.
                   LIB3065-010-Q1-N1-G8
Seq. ID
                   BLASTX
Method
                   g3341443
NCBI GI
                   381
BLAST score
                   8.0e-37
E value
                   123
Match length
                   61
% identity
NCBI Description (AJ223074) acid phosphatase [Glycine max]
                   36945
Seq. No.
                   LIB3065-010-Q1-N1-G9
Seq. ID
                   BLASTN
Method
                   q516853
NCBI GI
                   188
BLAST score
                   1.0e-101
E value
                   324
Match length
% identity
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
                   36946
Seq. No.
                   LIB3065-011-Q1-N1-B6
Seq. ID
                   BLASTN
Method
                   g1498341
NCBI GI
                   59
BLAST score
                   2.0e-24
E value
                   126
Match length
                   87
 % identity
NCBI Description Glycine max actin (Soy117) gene, partial cds
                   36947
 Seq. No.
                   LIB3065-011-Q1-N1-B7
 Seq. ID
 Method
                   BLASTX
```

g4415942

365

```
E value
                  114
Match length
% identity
NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]
                  36948
Seq. No.
                  LIB3065-011-Q1-N1-C3
Seq. ID
                  BLASTX
Method
                  g4006878
NCBI GI
                   135
BLAST score
                   3.0e-14
E value
                   101
Match length
                   48
% identity
NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
                   36949
Seq. No.
                   LIB3065-011-Q1-N1-G2
Seq. ID
                   BLASTN
Method
                   g1694899
NCBI GI
                   54
BLAST score
                   1.0e-21
E value
                   138
Match length
                   85
% identity
NCBI Description P.sativum mRNA for Cop1 protein
                   36950
Seq. No.
                   LIB3065-011-Q1-N1-H6
Seq. ID
                   BLASTX
Method
                   g4406539
NCBI GI
                   192
BLAST score
                   1.0e-14
E value
                   100
Match length
                   42
% identity
NCBI Description (AF127804) ascorbate peroxidase [Glycine max]
Seq. No.
                   36951
                   LIB3065-012-Q1-N1-C6
Seq. ID
                   BLASTN
Method
                   q18551
NCBI GI
BLAST score
                   324
                   0.0e + 00
 E value
                   400
Match length
 % identity
                   Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
 NCBI Description
                   protein
                   36952
 Seq. No.
```

Seq. ID

LIB3065-012-Q1-N1-F4

Method BLASTN g210811 NCBI GI BLAST score 124 3.0e-63 E value 324 Match length 85 % identity

Bean pod mottle virus coat protein gene, complete cds, NCBI Description

complete middle component (M) RNA

```
Seq. No.
Seq. ID
                   LIB3065-013-Q1-N1-B12
Method
                   BLASTX
NCBI GI
                   q3258635
BLAST score
                   357
E value
                   7.0e - 34
Match length
                   130
% identity
                   54
NCBI Description
                  (AF041049) 4-coumarate: CoA ligase [Populus tremuloides]
Seq. No.
                   36954
                   LIB3065-013-Q1-N1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q401189
BLAST score
                   166
                   4.0e-12
E value
                   58
Match length
                   62
% identity
NCBI Description
```

WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN (WSI-TIP) (TURGOR-RESPONSIVE PROTEIN 7A) >gi 485511 pir S33617

trg-31 protein - garden pea >gi\_20426\_emb\_CAA79159\_

(Z18288) trg-31 [Pisum sativum]

Seq. No. 36955 Seq. ID LIB3065-013-Q1-N1-D7 Method BLASTX NCBI GI g2209087 BLAST score 143 5.0e-09

E value Match length 68 43 % identity

NCBI Description (AF000309) putative serine/threonine kinase [Colletotrichum

lindemuthianum]

Seq. No. 36956

Seq. ID LIB3065-013-Q1-N1-H7

BLASTN Method NCBI GI q4115338 BLAST score 86 E value 4.0e-41 Match length 106 % identity 35

NCBI Description Pisum sativum (Alaska) ubuquitin (PUB4) gene, complete cds

36957 Seq. No.

LIB3065-013-Q1-N1-H9 Seq. ID

Method BLASTX NCBI GI g1174613 BLAST score 162 E value 3.0e-11 Match length 70 % identity 41

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING

PROTEIN HOMOLOG 1) (TBP-1) >gi 556560 dbj BAA04614 (D17788) rice homologue of Tat binding protein [Oryza

sativa]



Seq. No. 36958

Seq. ID LIB3065-014-Q1-N1-A3

Method BLASTX
NCBI GI g2213867
BLAST score 454
E value 2.0e-45
Match length 104
% identity 84

NCBI Description (AF003124) fructose-biphosphate aldolase [Mesembryanthemum

crystallinum]

Seq. No. 36959

Seq. ID LIB3065-014-Q1-N1-A4

Method BLASTX
NCBI GI g4567235
BLAST score 328
E value 6.0e-31
Match length 86
% identity 65

NCBI Description (AC007119) putative phosphatidylinositol/phophatidylcholine

transfer protein [Arabidopsis thaliana]

Seq. No. 36960

Seq. ID LIB3065-014-Q1-N1-B8

Method BLASTN
NCBI GI g18551
BLAST score 161
E value 1.0e-85
Match length 213
% identity 94

NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

Seq. No. 36961

Seq. ID LIB3065-014-Q1-N1-C10

Method BLASTN
NCBI GI g2213870
BLAST score 50
E value 4.0e-19
Match length 126
% identity 85

NCBI Description Mesembryanthemum crystallinum poly(A)-binding protein mRNA,

partial cds

Seq. No. 36962

Seq. ID LIB3065-014-Q1-N1-C5

Method BLASTN
NCBI GI g1518539
BLAST score 121
E value 1.0e-61
Match length 213
% identity 89

NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds

Seq. No. 36963

Seq. ID LIB3065-014-Q1-N1-E7

Method BLASTX

```
g2829911
NCBI GI
BLAST score
                  178
E value
                   1.0e-13
Match length
                   50
% identity
                   68
                   (AC002291) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  36964
Seq. No.
                  LIB3065-015-Q1-N1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g18535
BLAST score
                  268
E value
                  1.0e-149
Match length
                  276
% identity
                  99
NCBI Description Soybean mRNA for the alpha subunit of beta-conglycinin
                  36965
Seq. No.
                  LIB3065-015-Q1-N1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1199562
BLAST score
                   244
E value
                   1.0e-135
Match length
                   299
                   99
% identity
NCBI Description
                  Glycine max 34 kDa maturing seed vacuolar thiol protease
                  mRNA, complete cds
Seq. No.
                   36966
Seq. ID
                  LIB3065-016-Q1-N1-B2
Method
                  BLASTN
NCBI GI
                   g56539
BLAST score
                   59
                   1.0e-24
E value
Match length
                   289
% identity
                   89
                  R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                   >gi 206360 gb J00764 RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
Seq. No.
                   36967
Seq. ID
                   LIB3065-016-Q1-N1-B6
                   BLASTN
Method
NCBI GI
                   q944829
BLAST score
                   37
                   7.0e-12
E value
                   120
```

Match length 84 % identity

NCBI Description G.max mRNA for 24 kDa oleosin isoform (clone P24/91)

36968 Seq. No. Seq. ID LIB3065-016-Q1-N1-C4 Method BLASTX NCBI GI q541943 BLAST score 188

E value 1.0e-14 Match length 67

Seq. No. 36969

Seq. ID LIB3065-016-Q1-N1-E6

Method BLASTN
NCBI GI g210811
BLAST score 167
E value 6.0e-89
Match length 370
% identity 87

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 36970

Seq. ID LIB3065-017-Q1-N1-A7

Method BLASTN
NCBI GI g1431744
BLAST score 212
E value 1.0e-116
Match length 244
% identity 97

NCBI Description Glycine max sucrose binding protein (sbp) mRNA, complete

cds

Seq. No. 36971

Seq. ID LIB3065-017-Q1-N1-C10

Method BLASTN
NCBI GI g1732555
BLAST score 148
E value 6.0e-78
Match length 188
% identity 95

NCBI Description Glycine max desiccation protective protein LEA5 (Lea5)

mRNA, complete cds

Seq. No. 36972

Seq. ID LIB3065-017-Q1-N1-D7

Method BLASTN
NCBI GI g256634
BLAST score 77
E value 3.0e-35
Match length 149
% identity 44

NCBI Description KTil=Kunitz trypsin inhibitor KTil, KTi2=Kunitz trypsin

inhibitor KTi2 [soybeans, Genomic, 3269 nt]

Seq. No. 36973

Seq. ID LIB3065-017-Q1-N1-E5

Method BLASTN
NCBI GI 956539
BLAST score 42
E value 2.0e-14
Match length 96
% identity 91

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi\_206360\_gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene : exon v and flanks

Seq. No. 36974

Seg. ID LIB3065-017-Q1-N1-G10

Method BLASTN
NCBI GI g311697
BLAST score 236
E value 1.0e-130
Match length 244
% identity 38

NCBI Description G.max Lea protein mRNA, complete CDS

Seq. No. 36975

Seq. ID LIB3065-017-Q1-N1-G5

Method BLASTN
NCBI GI g56539
BLAST score 52
E value 2.0e-20
Match length 271
% identity 86

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi\_206360\_gb\_J00764\_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 36976

Seq. ID LIB3065-017-Q1-N1-H2

Method BLASTX
NCBI GI g229707
BLAST score 470
E value 2.0e-47
Match length 106
% identity 81

NCBI Description Bean pod mottle virus

Seq. No. 36977

Seq. ID LIB3065-018-Q1-N1-B3

Method BLASTN
NCBI GI 94097879
BLAST score 46
E value 8.0e-17
Match length 110
% identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 36978

Seq. ID LIB3065-018-Q1-N1-C1

Method BLASTN
NCBI GI 94097879
BLAST score 51
E value 3.0e-20
Match length 79
% identity 91

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

```
Seq. No.
 Seq. ID
                    LIB3065-018-Q1-N1-E1
 Method
                    BLASTX
 NCBI GI
                    g4097880
 BLAST score
                    181
 E value
                    8.0e-14
 Match length
                    49
 % identity
                    73
                    (U70866) polyprotein [Bean pod mottle virus]
 NCBI Description
 Seq. No.
                    36980
                    LIB3065-018-Q1-N1-E6
 Seq. ID
 Method
                    BLASTX
                    g1515454
 NCBI GI
 BLAST score
                    240
                    2.0e-20
 E value
                    90
 Match length
 % identity
                    61
                    (U64448) lac repressor [Cloning vector pCMVLacI]
 NCBI Description
                    36981
 Seq. No.
                    LIB3065-018-Q1-N1-H10
 Seq. ID
 Method
                    BLASTN
                    g170007
 NCBI GI
 BLAST score
                    210
*E value
                    1.0e-115
                    282
 Match length
 % identity
 NCBI Description
                    Soybean 18 kD late embryogenesis abundant (Lea) protein
                    mRNA, complete cds
                    36982
 Seq. No.
 Seq. ID
                    LIB3065-018-Q1-N1-H11
 Method
                    BLASTN
                    g2305019
 NCBI GI
 BLAST score
                    42
                    2.0e-14
 E value
                    207
 Match length
                    86
  % identity
 NCBI Description
                    Glycine max 2S albumin pre-propeptide mRNA, complete cds
                    36983
 Seq. No.
 Seq. ID
                    LIB3065-018-Q1-N1-H5
 Method
                    BLASTN
 NCBI GI
                    q256428
 BLAST score
                    191
                    1.0e-103
 E value
 Match length
                    335
```

89 % identity

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

36984 Seq. No.

Seq. ID LIB3065-019-Q1-N1-A4

Method BLASTN NCBI GI g218264 BLAST score 297

```
E value 1.0e-166
Match length 312
```

% identity 99

NCBI Description Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No. 36985

Seq. ID LIB3065-019-Q1-N1-D11

Method BLASTN
NCBI GI g170023
BLAST score 100
E value 3.0e-49
Match length 211
% identity 88

NCBI Description Glycine max maturation-associated protein (MAT9) mRNA,

complete cds

Seq. No. 36986

Seq. ID LIB3065-019-Q1-N1-D4

Method BLASTN
NCBI GI g4097879
BLAST score 169
E value 4.0e-90
Match length 389
% identity 86

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 36987

Seq. ID LIB3065-019-Q1-N1-D8

Method BLASTX
NCBI GI g3056602
BLAST score 313
E value 9.0e-29
Match length 86
% identity 66

NCBI Description (AC004255) T1F9.23 [Arabidopsis thaliana]

Seq. No. 36988

Seq. ID LIB3065-019-Q1-N1-G5

Method BLASTX
NCBI GI g3451069
BLAST score 222
E value 4.0e-18
Match length 125
% identity 40

NCBI Description (AL031326) hypothetical protein [Arabidopsis thaliana]

Seq. No. 36989

Seq. ID LIB3065-019-Q1-N1-H4

Method BLASTN
NCBI GI g210811
BLAST score 61
E value 6.0e-26
Match length 174
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA



Seq. No. 36990

Seq. ID LIB3065-020-Q1-N1-A11

Method BLASTN
NCBI GI g4097879
BLAST score 124
E value 2.0e-63
Match length 332
% identity 84

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 36991

Seq. ID LIB3065-020-Q1-N1-A4

Method BLASTN
NCBI GI g210811
BLAST score 120
E value 5.0e-61
Match length 264
% identity 88

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 36992

Seq. ID LIB3065-020-Q1-N1-B1

Method BLASTN
NCBI GI g475599
BLAST score 40
E value 2.0e-13
Match length 52
% identity 94

NCBI Description Glycine max Century 84 BiP isoform B mRNA, complete cds

Seq. No. 36993

Seq. ID LIB3065-020-Q1-N1-B12

Method BLASTX
NCBI GI 9462195
BLAST score 282
E value 2.0e-25
Match length 77
% identity 73

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

>gi\_100682\_pir\_\_S21636 GOS2 protein - rice

>gi\_20238\_emb\_CAA36190\_ (X51910) GOS2 [Oryza sativa]

>gi\_3789950 (AF094774) translation initiation factor [Oryza

satīva]

Seq. No. 36994

Seq. ID LIB3065-020-Q1-N1-C4

Method BLASTN
NCBI GI g206371
BLAST score 55
E value 3.0e-22
Match length 197
% identity 87

NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV,V and flanks

```
36995
Seq. No.
                  LIB3065-020-Q1-N1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1657541
BLAST score
                  139
                  1.0e-08
E value
Match length
                  87
                   44
% identity
                  (U73857) lac repressor [Escherichia coli]
NCBI Description
Seq. No.
                  36996
                  LIB3065-021-Q1-N1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g81886
BLAST score
                  185
                   5.0e-20
E value
Match length
                  116
% identity
                   53
NCBI Description tonoplast intrinsic protein alpha - kidney bean
Seq. No.
                   36997
Seq. ID
                  LIB3065-021-Q1-N1-B2
Method
                  BLASTN
NCBI GI
                   g4097879
BLAST score
                   178
E value
                   2.0e-95
Match length
                   378
% identity
                   87
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                   36998
Seq. No.
Seq. ID
                  LIB3065-021-Q1-N1-G4
Method
                  BLASTN
NCBI GI
                   q18535
BLAST score
                   301
                   1.0e-169
E value
Match length
                   305
% identity
                   100
```

NCBI Description Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No. 36999

Seq. ID LIB3065-021-Q1-N1-H6

Method BLASTN
NCBI GI g4191813
BLAST score 155
E value 7.0e-82
Match length 319
% identity 87

NCBI Description Glycine max mRNA for alpha' subunit of beta-conglycinin,

complete cds

Seq. No. 37000

Seq. ID LIB3065-022-Q1-N1-A6

Method BLASTN NCBI GI g18614 BLAST score 201

```
E value 1.0e-109
Match length 336
% identity 91
```

NCBI Description Soybean mRNA for glycinin AlaBx precursor

>gi 2170694 dbj E02463 E02463 cDNA encoding glycinine

subunit AlaBlb precursor

```
      Seq. No.
      37001

      Seq. ID
      LIB3065-022-Q1-N1-B2

      Method
      BLASTN

      NCBI GI
      g169928

      BLAST score
      47
```

E value 1.0e-17
Match length 115
% identity 85

NCBI Description Glycine max alpha'-type beta conglycinin storage protein

gene, complete cds, clone ch4A

 Seq. No.
 37002

 Seq. ID
 LIB3065-022-Q1-N1-G3

 Method
 BLASTX

 NCBI GI
 g2832658

NCBI GI g283265 BLAST score 130 E value 1.0e-15 Match length 48 % identity 83

NCBI Description (AL021710) putative protein [Arabidopsis thaliana]

Seq. No. 37003

Seq. ID LIB3065-022-Q1-N1-G5

Method BLASTX
NCBI GI g3901091
BLAST score 319
E value 1.0e-29
Match length 75
% identity 68

NCBI Description (AJ006305) arbuscular mycorrhiza protein [Pisum sativum]

Seq. No. 37004

Seq. ID LIB3065-023-Q1-N1-B2

Method BLASTX
NCBI GI g115797
BLAST score 218
E value 9.0e-18
Match length 105
% identity 42

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-215) (LHCP) >gi\_100026\_pir\_\_S16592 chlorophyll a/b-binding protein - garden pea >gi\_20658\_emb\_CAA40365\_(X57082) chlorophyll a/b-binding protein [Pisum sativum]

Seq. No. 37005

Seq. ID LIB3065-023-Q1-N1-E2

Method BLASTN
NCBI GI g56539
BLAST score 47
E value 2.0e-17



Match length 248 % identity 88

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi 206360 gb J00764 RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 37006

Seq. ID LIB3065-023-Q1-N1-E4

Method BLASTX
NCBI GI g1679658
BLAST score 268
E value 2.0e-23
Match length 129
% identity 47

NCBI Description (U63726) gamma glutamyl hydrolase [Glycine max]

Seq. No. 37007

Seq. ID LIB3065-023-Q1-N1-E6

Method BLASTN
NCBI GI g18628
BLAST score 176
E value 2.0e-94
Match length 268
% identity 91

NCBI Description Soybean mRNA for A5A4B3 subunits of glycinin

>gi 2170692 dbj E02461 E02461 cDNA encoding glycinine

subunit A5A4B3 precursor

Seq. No. 37008

Seq. ID LIB3065-023-Q1-N1-F7

Method BLASTX
NCBI GI g121282
BLAST score 172
E value 2.0e-12
Match length 103
% identity 43

NCBI Description BETA-CONGLYCININ, BETA CHAIN PRECURSOR

>gi\_72290\_pir\_\_FWSYCB beta-conglycinin beta chain - soybean

>gi\_256427\_bbs\_114632 (S44893) CG4 beta-conglycinin

[soybeans, Forrest and Dare, Peptide, 439 aa] [Glycine max]

Seq. No. 37009

Seq. ID LIB3065-024-Q1-N1-B11

Method BLASTX
NCBI GI g3915826
BLAST score 421
E value 2.0e-41
Match length 98
% identity 79

NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 37010

Seq. ID LIB3065-024-Q1-N1-H3

Method BLASTN
NCBI GI g736001
BLAST score 126
E value 1.0e-64



```
Match length
% identity
                  89
NCBI Description
```

G.soja (SH1) Gy5 mRNA for glycinin

Seq. No. 37011 Seq. ID LIB3065-025-Q1-N1-C3 Method BLASTN NCBI GI g4097879

BLAST score 115 E value 4.0e-58 187 Match length 90 % identity

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

37012 Seq. No.

LIB3065-025-Q1-N1-C8 Seq. ID

BLASTN Method g476213 NCBI GI BLAST score 53 E value 3.0e-21 Match length 171 82 % identity

Glycine max Century 84 p24 oleosin isoform A gene, complete NCBI Description

cds

Seq. No. 37013

Seq. ID LIB3065-025-Q1-N1-C9

Method BLASTN NCBI GI g1685276 BLAST score 66 E value 7.0e-29 Match length 241 82

% identity

NCBI Description Assembly vector pNOMAD2, complete genomic sequence

Seq. No.

37014

Seq. ID LIB3065-025-Q1-N1-D11

BLASTX Method g3176874 NCBI GI BLAST score 296 2.0e-28 E value Match length 95 65 % identity

NCBI Description (AF065639) cucumisin-like serine protease [Arabidopsis

thaliana]

Seq. No. 37015

LIB3065-025-Q1-N1-D3 Seq. ID

Method BLASTN NCBI GI g169912 234 BLAST score 1.0e-129 E value Match length 250 98 % identity

NCBI Description Glycine max beta-amylase mRNA, complete cds



```
Seq. No.
                  LIB3065-025-Q1-N1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g18678
BLAST score
                  94
                  1.0e-45
E value
                  169
Match length
% identity
                  90
                  Soybean mRNA for lipoxygenase-3 (EC 1.13.11.12)
NCBI Description
                  37017
Seq. No.
                  LIB3065-025-Q1-N1-E7
Seq. ID
Method
                  BLASTN
                  q1401239
NCBI GI
BLAST score
                   65
E value
                  2.0e-28
Match length
                  133
% identity
                  89
                  Glycine max 7S seed globulin precursor, mRNA, complete cds
NCBI Description
Seq. No.
                   37018
Seg. ID
                  LIB3065-025-Q1-N1-F7
Method
                  BLASTN
                  g18540
NCBI GI
BLAST score
                  187
                  1.0e-101
E value
Match length
                  213
                   97
% identity
                  G.max BBI mRNA for proteinase inhibitor
NCBI Description
Seq. No.
                  37019
                  LIB3065-025-Q1-N1-G4
Seq. ID
                  BLASTN
Method
NCBI GI
                   q56539
BLAST score
                   95
E value
                   4.0e-46
Match length
                   155
                   95
% identity
                  R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                   >gi 206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
                   37020
Seq. No.
                  LIB3065-025-Q1-N1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                   q4097879
BLAST score
                   93
E value
                   7.0e-45
Match length
                   249
% identity
                   84
```

Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description

gene, complete cds

Seq. No. 37021

Seq. ID LIB3065-026-Q1-N1-A3

Method BLASTX NCBI GI g4097880



BLAST score 293 E value 9.0e-27 Match length 77 % identity 77

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

37022

Seq. ID LIB3065-026-Q1-N1-A5

Method BLASTX
NCBI GI 94097880
BLAST score 567
E value 1.0e-58
Match length 138
% identity 81

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

37023

Seq. ID LIB3065-026-Q1-N1-D2

Method BLASTN
NCBI GI g169972
BLAST score 407
E value 0.0e+00
Match length 407
% identity 100

NCBI Description Soybean glycinin A-la-B-x subunit mRNA, complete cds

Seq. No. 37024

Seq. ID LIB3065-026-Q1-N1-H4

Method BLASTX
NCBI GI g729880
BLAST score 388
E value 1.0e-37
Match length 76
% identity 93

NCBI Description CASEIN KINASE II BETA CHAIN (CK II) >gi\_1076299\_pir\_\_S47967 casein kinase II (EC 2.7.1.-) beta chain CKB1 - Arabidopsis

thaliana >gi\_468264 (L22563) casein kinase II beta subunit

CKB1 [Arabidopsis thaliana]

Seq. No. 37025

Seq. ID LIB3065-027-Q1-N1-E1

Method BLASTN
NCBI GI g1794171
BLAST score 56
E value 3.0e-23
Match length 115
% identity 88

NCBI Description Glycine max lipoxygenase-3 mRNA, complete cds

Seq. No. 37026

Seq. ID LIB3072-002-Q1-K1-A10

Method BLASTN
NCBI GI 9433898
BLAST score 166
E value 2.0e-88
Match length 318
% identity 88



H.sapiens mRNA for ribosomal protein L8 NCBI Description

>gi 4506662 ref NM 000973.1 RPL8 Homo sapiens ribosomal

protein L8 (RPL8) mRNA

37027 Seq. No.

LIB3072-002-Q1-K1-B12 Seq. ID

Method BLASTN NCBI GI g179707 BLAST score 34 9.0e-10 E value Match length 66 % identity 88

NCBI Description Human alpha-2 collagen type VI-a' gene, exon 1

37028 Seq. No.

Seq. ID LIB3072-002-Q1-K1-E10

Method BLASTN NCBI GI g306467 BLAST score 230 E value 1.0e-126 Match length 342 % identity 92

NCBI Description Human binding protein mRNA, partial cds

37029 Seq. No.

Seq. ID LIB3072-002-Q1-K1-E11

BLASTN Method NCBI GI g642031 BLAST score 68 E value 4.0e-30 Match length 187 85 % identity

NCBI Description Human microfibril-associated glycoprotein (MFAP2) mRNA,

complete cds. >gi 4505156 ref NM 002403.1 MFAP2 Homo

sapiens microfibrillar-associated protein 2 (MFAP2) mRNA

Seq. No. 37030

Seq. ID LIB3072-002-Q1-K1-E12

Method BLASTN NCBI GI q18571 BLAST score 54 E value 8.0e-22 Match length 110 87 % identity

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

37031 Seq. No.

LIB3072-002-Q1-K1-E9 Seq. ID

Method BLASTN NCBI GI q642031 BLAST score 38 E value 4.0e-12 Match length 50 % identity 94

NCBI Description Human microfibril-associated glycoprotein (MFAP2) mRNA, complete cds. >gi\_4505156\_ref\_NM\_002403.1\_MFAP2\_ Homo

sapiens microfibrillar-associated protein 2 (MFAP2) mRNA



```
37032
Seq. No.
                   LIB3072-002-Q1-K1-F10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g35217
BLAST score
                   53
E value
                   6.0e-21
Match length
                   164
% identity
                   85
NCBI Description
                   Human mRNA for protein p68
                   37033
Seq. No.
                   LIB3072-002-Q1-K1-H10
Seq. ID
Method
                   BLASTN
                   g339567
NCBI GI
                   144
BLAST score
                   3.0e-75
E value
Match length
                   303
% identity
                   88
                   Human transforming growth factor-beta induced gene product
NCBI Description
                   (BIGH3) mRNA, complete cds.
                   >gi_4507466_ref_NM_000358.1_TGFBI_ Homo sapiens transforming growth factor, beta-induced, 68kD (TGFBI) mRNA
                   >gi_996468_gb_I14045_I14045 Sequence 1 from patent US
Seq. No.
                   37034
Seq. ID
                   LIB3072-002-Q1-K1-H11
Method
                   BLASTN
NCBI GI
                   g433898
BLAST score
                   60
                   3.0e-25
E value
Match length
                   161
                   89
% identity
                   H.sapiens mRNA for ribosomal protein L8
NCBI Description
                   >gi 4506662 ref NM 000973.1 RPL8 Homo sapiens ribosomal
                   protein L8 (RPL8) mRNA
Seq. No.
                   37035
Seq. ID
                   LIB3072-003-Q1-K1-B10
Method
                   BLASTN
NCBI GI
                   g256428
BLAST score
                   99
                   1.0e-48
E value
Match length
                   167
                   90
% identity
NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
                   Forrest, mRNA, 1259 nt]
Seq. No.
                   37036
Seq. ID
                   LIB3072-003-Q1-K1-C11
                   BLASTN
Method
NCBI GI
                   q288618
BLAST score
                   33
E value
                   3.0e-09
                   93
Match length
```

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

84

% identity



```
37037
Seq. No.
                  LIB3072-003-Q1-K1-F11
Seq. ID
Method
                  BLASTN
                  g256428
NCBI GI
BLAST score
                  231
                  1.0e-127
E value
Match length
                  360
                  92
% identity
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                  Forrest, mRNA, 1259 nt]
Seq. No.
                  37038
                  LIB3072-003-Q1-K1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q18571
BLAST score
                  149
E value
                  3.0e-78
Match length
                  244
% identity
                  90
NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II
Seq. No.
                  37039
Seq. ID
                  LIB3072-004-Q1-K1-D5
Method
                  BLASTN
NCBI GI
                  q18571
BLAST score
                  172
                  6.0e-92
E value
                  344
Match length
                  88
% identity
NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II
                  37040
Seq. No.
Seq. ID
                  LIB3072-004-Q1-K1-E3
                  BLASTN
Method
NCBI GI
                  g256428
BLAST score
                  379
                  0.0e+00
E value
Match length
                  405
% identity
                  99
NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
                  Forrest, mRNA, 1259 nt]
                  37041
Seq. No.
                  LIB3072-004-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2506877
BLAST score
                  139
E value
                  8.0e-09
Match length
                  89
% identity
```

NCBI Description MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2) >gi\_454154 (L21998) mucin [Homo sapiens] >gi\_4505285\_ref\_NP\_002448.1\_pMUC2\_

mucin 2, intestinal/tracheal

Seq. No. 37042

Seq. ID LIB3072-004-Q1-K1-F2

```
BLASTN
Method
NCBI GI
                  q288618
BLAST score
                  349
E value
                  0.0e + 00
                  393
Match length
% identity
                  97
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                  37043
Seq. No.
Seq. ID
                  LIB3072-004-Q1-K1-F3
Method
                  BLASTN
NCBI GI
                  g18571
BLAST score
                   356
                  0.0e + 00
E value
Match length
                   379
% identity
                  98
NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II
                  37044
Seq. No.
                  LIB3072-004-Q1-K1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                   q2462264
BLAST score
                   35
E value
                   1.0e-10
                   47
Match length
                   94
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   37045
Seq. No.
                   LIB3072-007-Q1-E1-B6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g18571
BLAST score
                   320
                   1.0e-180
E value
Match length
                   356
% identity
                   97
NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II
Seq. No.
                   37046
Seq. ID
                   LIB3072-007-Q1-E1-D1
Method
                   BLASTX
NCBI GI
                   q3292829
BLAST score
                   157
                   4.0e-20
E value
                   96
Match length
                   50
% identity
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
                   37047
Seq. No.
                   LIB3072-007-Q1-E1-H10
```

Seq. ID

Method BLASTX NCBI GI g125723 BLAST score 145 E value 3.0e-09 Match length 65 43 % identity

NCBI Description KUNITZ-TYPE TRYPSIN INHIBITOR KTI2 PRECURSOR

NCBI Description

CanMT-2)



>gi\_81815\_pir\_\_JQ1092 trypsin inhibitor KTi2 (Kunitz) soybean >gi\_256636\_bbs\_115029 (S45035) Kunitz trypsin
inhibitor KTi2 [soybeans, Peptide, 204 aa] [Glycine max]

37048 Seq. No. Seq. ID LIB3072-008-Q1-E1-E3 Method BLASTN NCBI GI q170053 BLAST score 192 E value 1.0e-104 Match length 280 92 % identity Soybean ribosomal protein S11 mRNA, 3' end NCBI Description Seq. No. 37049 LIB3072-008-Q1-E1-E5 Seq. ID Method BLASTN NCBI GI g18571 BLAST score 137 E value 4.0e-71 Match length 281 87 % identity NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II Seq. No. 37050 LIB3072-008-Q1-E1-E7 Seq. ID Method BLASTN NCBI GI q256634 BLAST score 51 4.0e-20 E value Match length 131 42 % identity KTil=Kunitz trypsin inhibitor KTil, KTi2=Kunitz trypsin NCBI Description inhibitor KTi2 [soybeans, Genomic, 3269 nt] Seq. No. 37051 LIB3072-008-Q1-E1-F7 Seq. ID Method BLASTN g256428 NCBI GI BLAST score 143 E value 9.0e-75 Match length 281 % identity 88 KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and NCBI Description Forrest, mRNA, 1259 nt] 37052 Seq. No. LIB3072-009-Q1-E1-B7 Seq. ID Method BLASTN NCBI GI g2815245 BLAST score 66 E value 1.0e-28 Match length 242 % identity 82

C.arietinum mRNA for class I type 2 metallothionein (clone:



```
Seq. No.
                   37053
                   LIB3072-009-Q1-E1-F7
Seq. ID
Method
                   BLASTN
NCBI GI
                   q256428
BLAST score
                   348
E value
                   0.0e + 00
                   378
Match length
                   98
% identity
NCBI Description
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
                   Forrest, mRNA, 1259 nt]
                   37054
Seq. No.
                   LIB3072-010-Q1-E1-A8
Seq. ID
Method
                   BLASTN
NCBI GI
                   q288618
BLAST score
                   387
                   0.0e+00
E value
Match length
                   411
% identity
                   99
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
Seq. No.
                   37055
Seq. ID
                   LIB3072-010-Q1-E1-B5
Method
                   BLASTN
NCBI GI
                   g1944318
BLAST score
                   201
E value
                   1.0e-109
Match length
                   337
% identity
                   90
                  Glycine max mRNA for cysteine proteinase inhibitor,
NCBI Description
                   complete cds
                   37056
Seq. No.
Seq. ID
                   LIB3072-010-Q1-E1-E1
Method
                   BLASTX
NCBI GI
                   g595768
BLAST score
                   144
                   4.0e-09
E value
Match length
                   44
                   66
% identity
NCBI Description
                  (U13866) non-functional lacZ alpha peptide [Cloning vector]
                   37057
Seq. No.
                   LIB3072-010-Q1-E1-E9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g256428
BLAST score
                   240
                   1.0e-132
E value
Match length
                   302
                   95
% identity
```

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37058

LIB3072-011-Q1-E1-A8 Seq. ID

Method BLASTN NCBI GI g256428

BLAST score 387 E value 0.0e+00 Match length 405 % identity 99

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37059

Seq. ID LIB3072-011-Q1-E1-C10

Method BLASTN
NCBI GI g18747
BLAST score 171
E value 2.0e-91
Match length 302
% identity 90

NCBI Description G.max mRNA for a protein similar to potato tuber protein

p322 homolgous to Bowman-Birk Proteinase Inhibitor

Seq. No. 37060

Seq. ID LIB3072-011-Q1-E1-C9

Method BLASTN
NCBI GI g288618
BLAST score 386
E value 0.0e+00
Match length 410
% identity 99

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No. 37061

Seq. ID LIB3072-011-Q1-E1-D11

Method BLASTN
NCBI GI g18769
BLAST score 122
E value 4.0e-62
Match length 232

% identity 91

NCBI Description G.max mRNA Ti-a for Kunitz trypsin inhibitor subtype A

Seq. No. 37062

Seq. ID LIB3072-011-Q1-E1-E11

Method BLASTN
NCBI GI g288618
BLAST score 381
E value 0.0e+00
Match length 413
% identity 98

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No.

No. 37063

Seq. ID LIB3072-011-Q1-E1-F12

Method BLASTN
NCBI GI g288618
BLAST score 321
E value 0.0e+00
Match length 349
% identity 98

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No.

Seq. ID

37069

LIB3072-012-Q1-E1-G6



```
37064
Seq. No.
                  LIB3072-011-Q1-E1-H11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g169928
BLAST score
                   33
E value
                   3.0e-09
Match length
                   57
% identity
                   89
NCBI Description
                  Glycine max alpha'-type beta conglycinin storage protein
                   gene, complete cds, clone ch4A
                   37065
Seq. No.
Seq. ID
                  LIB3072-011-Q1-E1-H4
Method
                   BLASTN
                   g256428
NCBI GI
BLAST score
                   343
E value
                   0.0e+00
Match length
                   381
                   98
% identity
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                   Forrest, mRNA, 1259 nt]
Seq. No.
                   37066
Seq. ID
                   LIB3072-012-Q1-E1-B5
Method
                   BLASTN
NCBI GI
                   q256428
BLAST score
                   169
                   2.0e-90
E value
                   203
Match length
                   96
% identity
NCBI Description
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
                   Forrest, mRNA, 1259 nt]
                   37067
Seq. No.
Seq. ID
                   LIB3072-012-Q1-E1-D2
Method
                   BLASTN
NCBI GI
                   g256428
BLAST score
                   295
E value
                   1.0e-165
Match length
                   341
                   97
% identity
NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
                   Forrest, mRNA, 1259 nt]
                   37068
Seq. No.
                   LIB3072-012-Q1-E1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3094014
BLAST score
                   172
E value
                   3.0e-12
                   59
Match length
% identity
                   49
                 (AF060862) unknown [Homo sapiens]
NCBI Description
```

5682



```
BLASTN
Method
NCBI GI
                  q288618
BLAST score
                  353
E value
                  0.0e + 00
Match length
                  412
% identity
                  97
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
Seq. No.
                  37070
                  LIB3072-012-Q1-E1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q256428
BLAST score
                  381
                  0.0e + 00
E value
                  415
Match length
                  98
% identity
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                  Forrest, mRNA, 1259 nt]
Seq. No.
                  37071
```

Seq. ID LIB3072-013-Q1-E1-B11

Method BLASTN NCBI GI g170005 BLAST score 125 E value 3.0e-64 Match length 181 92 % identity

NCBI Description Soybean lectin (Le1) gene, complete cds

Seq. No. 37072

Seq. ID LIB3072-013-Q1-E1-B12

Method BLASTN NCBI GI g256428 BLAST score 116 E value 1.0e-58 Match length 250 % identity 87

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37073

LIB3072-014-Q1-E1-C2 Seq. ID

Method BLASTN NCBI GI g256428 BLAST score 191 E value 1.0e-103 Match length 300 % identity 91

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37074

Seq. ID LIB3072-014-Q1-E1-C9

Method BLASTX NCBI GI g4567226 BLAST score 186 E value 4.0e-14



```
Match length
% identity
                   50
```

NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

Seq. No.

37075

LIB3072-014-Q1-E1-D10 Seq. ID

Method BLASTN q288618 NCBI GI BLAST score 383 E value 0.0e+00411 Match length 98 % identity

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No.

37076

LIB3072-014-Q1-E1-E10 Seq. ID

Method BLASTN NCBI GI g256428 BLAST score 147 E value 3.0e-77 Match length 245 90 % identity

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No.

37077 Seq. ID LIB3072-014-Q1-E1-E7

Method BLASTX NCBI GI g2829751 BLAST score 212 6.0e-17 E value Match length 110 % identity 41

MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF) NCBI Description

>gi 1850559 (U88035) macrophage migration inhibitory factor [Brugia malayi] >gi 2190976 (AF002699) macrophage migration

inhibitory factor [Brugia malayi]

Seq. No. 37078

LIB3072-014-Q1-E1-F3 Seq. ID

Method BLASTN NCBI GI q169946 BLAST score 33 2.0e-09 E value Match length 57 % identity 89

NCBI Description Soybean protease inhibitor IV mRNA, complete cds

Seq. No.

37079

Seq. ID LIB3072-014-Q1-E1-H2

Method BLASTX NCBI GI g541950 BLAST score 141 E value 5.0e-09 Match length 60 % identity 52

NCBI Description SPCP1 protein - soybean >gi 310576 (L12257) nodulin-26



## [Glycine max]

Seq. No. 37080 Seq. ID

LIB3072-014-Q1-E1-H5

Method BLASTN NCBI GI q288618 BLAST score 93 5.0e-45 E value 193 Match length % identity 87

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

37081 Seq. No.

Seq. ID LIB3072-015-Q1-E1-B6

Method BLASTN g18769 NCBI GI 76 BLAST score E value 6.0e-35 Match length 136 % identity 89

NCBI Description G.max mRNA Ti-a for Kunitz trypsin inhibitor subtype A

Seq. No. 37082

Seq. ID LIB3072-015-Q1-E1-C6

Method BLASTN NCBI GI q18769 BLAST score 89 E value 2.0e-42 Match length 264 85 % identity

NCBI Description G.max mRNA Ti-a for Kunitz trypsin inhibitor subtype A

37083 Seq. No.

LIB3072-015-Q1-E1-C7 Seq. ID

BLASTN Method NCBI GI g18644 BLAST score 54 E value 1.0e-21 Match length 158 % identity 84

NCBI Description Soybean mRNA for HMG-1 like protein

Seq. No. 37084

LIB3072-015-Q1-E1-E12 Seq. ID

Method BLASTX NCBI GI g2144583 BLAST score 209 E value 9.0e-17 Match length 94 % identity 50

NCBI Description proteinase inhibitor (Bowman-Birk) D-II precursor - soybean

>gi\_18572\_emb\_CAA48657\_ (X68706) Bowman-Birk proteinase isoinhibitor D-II [Glycine max] >gi 288619 emb\_CAA48658 (X68707) Soybean Bowman-Birk proteinase isoinhibitor D-II [Glycine max] >gi\_743636\_prf\_\_2013215A Bowman-Birk protease

inhibitor [Glycine max]



```
Seq. No.
Seq. ID
                   LIB3072-015-Q1-E1-E7
Method
                   BLASTN
NCBI GI
                   g18571
BLAST score
                   51
E value
                   8.0e-20
Match length
                   148
                   88
% identity
                  G.max D-II mRNA for proteinase isoinhibitor D-II
NCBI Description
                   37086
Seq. No.
                   LIB3072-015-Q1-E1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1326161
BLAST score
                   240
                   3.0e-20
E value
Match length
                   67
% identity
                   81
NCBI Description
                  (U54703) dehydrin [Phaseolus vulgaris]
                   37087
Seq. No.
                   LIB3072-015-Q1-E1-H3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g531828
BLAST score
                   42
                   9.0e-15
E value
                   78
Match length
                   88
% identity
NCBI Description Cloning vector pSport1, complete cds
                   37088
Seq. No.
Seq. ID
                   LIB3072-015-Q1-E1-H7
Method
                   BLASTN
NCBI GI
                   g288618
BLAST score
                   363
                   0.0e+00
E value
Match length
                   399
                   98
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
Seq. No.
                   37089
Seq. ID
                   LIB3072-016-Q1-E1-B7
Method
                   BLASTN
NCBI GI
                   q170005
BLAST score
                   47
E value
                   8.0e-18
Match length
                   74
                   91
% identity
NCBI Description Soybean lectin (Le1) gene, complete cds
                   37090
Seq. No.
```

LIB3072-017-Q1-E1-A10 Seq. ID

Method BLASTX NCBI GI g136057 BLAST score 197 E value 2.0e-17 Match length 84



% identity 62

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi\_99499\_pir\_\_A32187 (S)-tetrahydroberberine oxidase Coptis japonica >gi 556171 (J04121) triosephosphate

isomerase [Coptis japonica]

Seq. No. 37091

Seq. ID LIB3072-017-Q1-E1-C11

Method BLASTN
NCBI GI g516165
BLAST score 40
E value 3.0e-13
Match length 72
% identity 89

NCBI Description S.tuberosum pPOM34 mRNA for mitochondrial 34kDa porin

Seq. No. 37092

Seq. ID LIB3072-017-Q1-E1-D10

Method BLASTN
NCBI GI g18571
BLAST score 50
E value 2.0e-19
Match length 110
% identity 86

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37093

Seq. ID LIB3072-017-Q1-E1-E11

Method BLASTN
NCBI GI g169974
BLAST score 165
E value 7.0e-88
Match length 285
% identity 90

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 37094

Seq. ID LIB3072-017-Q1-E1-F9

Method BLASTN
NCBI GI g288618
BLAST score 263
E value 1.0e-146
Match length 323
% identity 95

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No. 37095

Seq. ID LIB3072-017-Q1-E1-H10

Method BLASTN
NCBI GI g531828
BLAST score 45
E value 1.0e-16
Match length 77
% identity 90

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 37096

```
LIB3072-018-Q1-E1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g18571
BLAST score
                   302
E value
                   1.0e-169
Match length
                  353
% identity
                   96
NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II
Seq. No.
                  37097
                  LIB3072-018-Q1-E1-B4
Seq. ID
Method
                  BLASTN
                  g288618
NCBI GI
BLAST score
                  375
                  0.0e + 00
E value
                  414
Match length
                  98
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                  37098
Seq. No.
                  LIB3072-018-Q1-E1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                   q288618
BLAST score
                   333
E value
                   0.0e + 00
Match length
                   364
% identity
                   98
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                   37099
Seq. No.
Seq. ID
                  LIB3072-018-Q1-E1-C5
Method
                  BLASTN
                   g288618
NCBI GI
BLAST score
                   378
                   0.0e + 00
E value
Match length
                   410
                   98
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
Seq. No.
                   37100
                  LIB3072-018-Q1-E1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g288618
BLAST score
                  272
                  1.0e-151
E value
Match length
                  396
                   92
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
```

Seq. No. 37101

Seq. ID LIB3072-018-Q1-E1-F5

Method BLASTN
NCBI GI g18571
BLAST score 144
E value 2.0e-75
Match length 236
% identity 90



NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37102

Seq. ID LIB3072-018-Q1-E1-G11

Method BLASTN
NCBI GI g18636
BLAST score 78
E value 4.0e-36
Match length 190

NCBI Description Soybean Gy2 gene for glycinin subunit G2

Seq. No. 37103

% identity

Seq. ID LIB3072-018-Q1-E1-G4

85

Method BLASTN
NCBI GI g288618
BLAST score 385
E value 0.0e+00
Match length 413
% identity 98

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No. 37104

Seq. ID LIB3072-018-Q1-E1-H11

Method BLASTX
NCBI GI 94376872
BLAST score 162
E value 4.0e-11
Match length 59
% identity 49

NCBI Description (AE001642) Sugar Nucleotide Phosphorylase [Chlamydia

pneumoniae]

Seq. No. 37105

Seq. ID LIB3072-019-Q1-E1-B8

Method BLASTN
NCBI GI g18571
BLAST score 44
E value 9.0e-16
Match length 168
% identity 82

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37106

Seq. ID LIB3072-019-Q1-E1-C11

Method BLASTX
NCBI GI g2144583
BLAST score 116
E value 1.0e-12
Match length 70
% identity 57

NCBI Description proteinase inhibitor (Bowman-Birk) D-II precursor - soybean

>gi\_18572\_emb\_CAA48657\_ (X68706) Bowman-Birk proteinase
isoinhibitor D-II [Glycine max] >gi\_288619\_emb\_CAA48658\_
(X68707) Soybean Bowman-Birk proteinase isoinhibitor D-II
[Glycine max] >gi\_743636\_prf\_\_2013215A Bowman-Birk protease

inhibitor [Glycine max]



```
37107
Seq. No.
                   LIB3072-019-Q1-E1-D3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q18769
BLAST score
                   125
E value
                   6.0e-64
Match length
                   273
% identity
                   87
NCBI Description
                   G.max mRNA Ti-a for Kunitz trypsin inhibitor subtype A
                   37108
Seq. No.
                   LIB3072-019-Q1-E1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q825756
                   149
BLAST score
                   6.0e-10
E value
Match length
                   66
% identity
                   48
                   (U12391) beta-galactosidase alpha peptide [Cloning vector
NCBI Description
                   pSport2]
                   37109
Seq. No.
Seq. ID
                   LIB3072-019-Q1-E1-F1
Method
                   BLASTX
NCBI GI
                   q134145
                   140
BLAST score
                   8.0e-09
E value
Match length
                   52
                   56
% identity
                   STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE
NCBI Description
                   PROTEIN A) >gi_99886_pir__S08511 28K protein - soybean
                   >gi 169898 (M37530) 28 kDa protein [Glycine max] >gi 169975
                   (M76981) vegetative storage protein [Glycine max]
                   >gi_226867_prf__1609232B 28kD glycoprotein [Glycine max]
>gi_444325_prf__1906374A vegetative storage protein
                   [Glycine max]
                   37110
Seq. No.
                   LIB3072-019-Q1-E1-F6
Seq. ID
Method
                   BLASTN
                   g531828
NCBI GI
BLAST score
                   32
E value
                   7.0e-09
Match length
                   72
% identity
                   86
NCBI Description Cloning vector pSport1, complete cds
                   37111
Seq. No.
Seq. ID
                   LIB3072-019-Q1-E1-G2
Method
                   BLASTN
NCBI GI
                   g256428
BLAST score
                   288
E value
                   1.0e-161
                   378
Match length
                   94
% identity
```

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and



## Forrest, mRNA, 1259 nt]

```
Seq. No.
                  37112
Seq. ID
                  LIB3072-019-Q1-E1-G5
Method
                  BLASTX
                  g2144584
NCBI GI
                  150
BLAST score
                  3.0e-13
E value
                  70
Match length
                  60
% identity
                  trypsin inhibitor A (Kunitz) precursor - soybean
NCBI Description
                  >gi_18770_emb_CAA45777_ (X64447) trypsin inhibitor subtype
                  A [Glycine max]
                  37113
Seq. No.
                  LIB3072-019-Q1-E1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2144584
BLAST score
                  174
E value
                  5.0e-13
Match length
                  61
% identity
                  56
NCBI Description
                  trypsin inhibitor A (Kunitz) precursor - soybean
                  >gi_18770_emb_CAA45777_ (X64447) trypsin inhibitor subtype
                  A [Glycine max]
Seq. No.
                  37114
Seq. ID
                  LIB3072-020-Q1-E1-C6
Method
                  BLASTN
                  g256428
NCBI GI
                  379
BLAST score
E value
                  0.0e+00
Match length
                  413
                  98
% identity
NCBI Description
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
                  Forrest, mRNA, 1259 nt]
Seq. No.
                  37115
Seq. ID
                  LIB3072-020-Q1-E1-E9
Method
                  BLASTN
NCBI GI
                  g288618
                  291
BLAST score
                  1.0e-163
E value
Match length
                  383
% identity
                  94
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                  37116
Seq. No.
Seq. ID
                  LIB3072-020-Q1-E1-F3
Method
                  BLASTX
NCBI GI
                  q2144583
BLAST score
                  151
E value
                  4.0e-10
Match length
                  64
% identity
                  48
                  proteinase inhibitor (Bowman-Birk) D-II precursor - soybean
NCBI Description
                  >gi_18572_emb_CAA48657_ (X68706) Bowman-Birk proteinase
```

Method

NCBI GI

BLAST score

BLASTN

62

g169946



isoinhibitor D-II [Glycine max] >gi\_288619\_emb\_CAA48658\_(X68707) Soybean Bowman-Birk proteinase isoinhibitor D-II [Glycine max] >gi\_743636\_prf\_\_2013215A Bowman-Birk protease inhibitor [Glycine max]

```
Seq. No.
                   37117
Seq. ID
                   LIB3072-020-Q1-E1-F4
Method
                   BLASTX
NCBI GI
                   g2347189
BLAST score
                   274
E value
                   3.0e-24
Match length
                   86
% identity
                   58
                   (AC002338) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3150399 (AC004165) hypothetical protein [Arabidopsis
                   thaliana]
                   37118
Seq. No.
Seq. ID
                   LIB3072-020-Q1-E1-H3
Method
                   BLASTX
NCBI GI
                   g1710530
                   138
BLAST score
E value
                   1.0e-08
Match length
                   39
                   59
% identity
                   60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256
NCBI Description
                   ribosomal protein L27a - Arabidopsis thaliana >gi_1107487 emb_CAA63025 (X91959) 60S ribosomal protein
                   L27a [Arabidopsis thaliana]
Seq. No.
                   37119
Seq. ID
                   LIB3072-021-Q1-E1-A1
Method
                   BLASTN
NCBI GI
                   q256428
BLAST score
                   247
                   1.0e-137
E value
                   321
Match length
                   95
% identity
NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
                   Forrest, mRNA, 1259 nt]
Seq. No.
                   37120
                   LIB3072-021-Q1-E1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g633890
BLAST score
                   229
                   4.0e-19
E value
                   80
Match length
% identity
                   60
NCBI Description
                   (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
                   vulgare]
                   37121
Seq. No.
Seq. ID
                   LIB3072-021-Q1-E1-C11
```



E value 2.0e-26 Match length 177 % identity 84

NCBI Description Soybean protease inhibitor IV mRNA, complete cds

Seq. No. 37122

Seq. ID LIB3072-021-Q1-E1-E7

Method BLASTN
NCBI GI g18571
BLAST score 144
E value 2.0e-75
Match length 200
% identity 93

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37123

Seq. ID LIB3072-021-Q1-E1-F12

Method BLASTN
NCBI GI g18571
BLAST score 90
E value 4.0e-43
Match length 230
% identity 87

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37124

Seq. ID LIB3072-021-Q1-E1-G2

Method BLASTN
NCBI GI g288618
BLAST score 369
E value 0.0e+00
Match length 401
% identity 98

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No. 37125

Seq. ID LIB3072-021-Q1-E1-G6

Method BLASTN
NCBI GI g18571
BLAST score 302
E value 1.0e-169
Match length 358
% identity 96

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37126

Seq. ID LIB3072-021-Q1-E1-H5

Method BLASTN
NCBI GI g18571
BLAST score 154
E value 3.0e-81
Match length 286
% identity 89

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37127

Seq. ID LIB3072-022-Q1-E1-B5

```
Method
                  BLASTN
NCBI GI
                  g2564044
BLAST score
                  39
E value
                  1.0e-12
Match length
                  59
% identity
                  92
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19P17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  37128
Seq. ID
                  LIB3072-022-Q1-E1-C7
```

Method BLASTN NCBI GI g3021374 BLAST score 83 E value 5.0e-39 Match length 199 % identity 86

Glycine max mRNA for profilin, PRO1 NCBI Description

Seq. No. 37129

LIB3072-022-Q1-E1-D4 Seq. ID

Method BLASTN NCBI GI g18571 BLAST score 112 E value 4.0e-56 Match length 295 85 % identity

G.max D-II mRNA for proteinase isoinhibitor D-II NCBI Description

37130 Seq. No.

Seq. ID LIB3072-022-Q1-E1-E11

Method BLASTN NCBI GI g256428 BLAST score 195 1.0e-106 E value Match length 265 % identity 94

KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and NCBI Description

Forrest, mRNA, 1259 nt]

Seq. No. 37131

Seq. ID LIB3072-022-Q1-E1-E8

Method BLASTN NCBI GI q288618 BLAST score 330 E value 0.0e+00Match length 354 98 % identity

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

37132 Seq. No.

LIB3072-022-Q1-E1-G5 Seq. ID

Method BLASTN NCBI GI q288618 BLAST score 191 E value 1.0e-103 Match length 275



% identity 92

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No. 37133

Seq. ID LIB3072-022-Q1-E1-H4

Method BLASTX
NCBI GI g1064887
BLAST score 201
E value 8.0e-16
Match length 60
% identity 67

NCBI Description (X92955) pollen coat protein [Brassica oleracea]

Seq. No. 37134

Seq. ID LIB3072-023-Q1-E1-A8

Method BLASTN
NCBI GI g4191813
BLAST score 272
E value 1.0e-151
Match length 272
% identity 82

NCBI Description Glycine max mRNA for alpha' subunit of beta-conglycinin,

complete cds

Seq. No. 37135

Seq. ID LIB3072-023-Q1-E1-C11

Method BLASTN
NCBI GI g18540
BLAST score 133
E value 1.0e-68
Match length 295
% identity 87

NCBI Description G.max BBI mRNA for proteinase inhibitor

Seq. No. 37136

Seq. ID LIB3072-023-Q1-E1-C12

Method BLASTX
NCBI GI g267122
BLAST score 163
E value 2.0e-11
Match length 45
% identity 64

NCBI Description THIOREDOXIN H-TYPE (TRX-H) >gi 478400 pir JQ2242

thioredoxin h - Arabidopsis thaliana

>gi\_16552\_emb\_CAA78462\_ (Z14084) Thioredoxin H [Arabidopsis
thaliana] >gi\_1388080 (U35827) thioredoxin h [Arabidopsis

thaliana]

Seq. No. 37137

Seq. ID LIB3072-023-Q1-E1-E1

Method BLASTN
NCBI GI g256634
BLAST score 42
E value 5.0e-15
Match length 50
% identity 48

NCBI Description KTil=Kunitz trypsin inhibitor KTi1, KTi2=Kunitz trypsin





## inhibitor KTi2 [soybeans, Genomic, 3269 nt]

```
Seq. No.
                  37138
Seq. ID
                  LIB3072-023-Q1-E1-E10
Method
                  BLASTX
NCBI GI
                  q541943
BLAST score
                  154
                  2.0e-10
E value
Match length
                  50
                  60
% identity
NCBI Description
                  metallothionein - soybean >gi 228682 prf 1808316A
                  metallothionein-like protein [Glycine max]
Seq. No.
                  37139
Seq. ID
                  LIB3072-023-Q1-E1-F8
Method
                  BLASTN
NCBI GI
                  g18614
BLAST score
                  63
                  4.0e-27
E value
Match length
                  119
% identity \
                  89
NCBI Description
                  Soybean mRNA for glycinin AlaBx precursor
                  >gi_2170694_dbj_E02463_E02463 cDNA encoding glycinine
                  subunit AlaBlb precursor
                  37140
Seq. No.
Seq. ID
                  LIB3072-023-Q1-E1-G1
Method
                  BLASTX
                  g1871179
NCBI GI
BLAST score
                  194
                  3.0e-15
E value
                  78
Match length
% identity
NCBI Description (U90439) FMRFamide precursor isolog [Arabidopsis thaliana]
Seq. No.
                  37141
Seq. ID
                  LIB3072-023-Q1-E1-G4
Method
                  BLASTN
NCBI GI
                  q256428
BLAST score
                  289
E value
                  1.0e-161
Match length
                  402
% identity
                  94
NCBI Description
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
                  Forrest, mRNA, 1259 nt]
Seq. No.
                  37142
Seq. ID
                  LIB3072-024-Q1-E1-A3
Method
                  BLASTN
NCBI GI
                  g256428
BLAST score
                  339
E value
                  0.0e + 00
Match length
                  380
% identity
                  98
NCBI Description
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
```

Forrest, mRNA, 1259 nt]



```
Seq. No.
                  LIB3072-024-Q1-E1-B10
Seq. ID
                  BLASTN
Method
                  q256428
NCBI GI
                  318
BLAST score
                  1.0e-179
E value
Match length
                  368
                  97
% identity
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                  Forrest, mRNA, 1259 nt]
                  37144
Seq. No.
Seq. ID
                  LIB3072-024-Q1-E1-B11
Method
                  BLASTN
                  g169928
NCBI GI
BLAST score
                  141
                  1.0e-73
E value
                  161
Match length
% identity
                  97
NCBI Description Glycine max alpha'-type beta conglycinin storage protein
                  gene, complete cds, clone ch4A
                   37145
Seq. No.
Seq. ID
                  LIB3072-024-Q1-E1-C7
Method
                  BLASTN
NCBI GI
                  g256428
BLAST score
                   211
                  1.0e-115
E value
Match length
                   281
% identity
                   94
NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
                   Forrest, mRNA, 1259 nt]
Seq. No.
                   37146
                   LIB3072-024-Q1-E1-C8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g256428
                   255
BLAST score
                   1.0e-141
E value
Match length
                   341
                   94
% identity
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                   Forrest, mRNA, 1259 nt]
Seq. No.
                   37147
                   LIB3072-024-Q1-E1-D10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g288618
BLAST score
                   101
                   9.0e-50
E value
                   193
Match length
                   88
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
```

Seq. No. 37148

Seq. ID LIB3072-024-Q1-E1-D7

Method BLASTN

```
q531828
NCBI GI
BLAST score
                  41
E value
                  3.0e-14
                  109
Match length
                  84
% identity
NCBI Description Cloning vector pSport1, complete cds
                  37149
Seq. No.
                  LIB3072-024-Q1-E1-E4
Seq. ID
                  BLASTN
Method
                  g288618
NCBI GI
                  373
BLAST score
                  0.0e + 00
E value
Match length
                  401
                  98
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                  37150
Seq. No.
                  LIB3072-024-Q1-E1-F7
Seq. ID
                  BLASTN
Method
                  g288618
NCBI GI
                  338
BLAST score
                  0.0e + 00
E value
                  378
Match length
                  97
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                  37151
Seq. No.
                  LIB3072-025-Q1-E1-A2
Seq. ID
                  BLASTN
Method
                  g288618
NCBI GI
                   96
BLAST score
                   9.0e-47
E value
                   208
Match length
                   87
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                   37152
Seq. No.
Seq. ID
                   LIB3072-025-Q1-E1-E7
Method
                   BLASTN
                   g256428
NCBI GI
                   284
BLAST score
                   1.0e-159
E value
                   314
Match length
% identity
                   98
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                   Forrest, mRNA, 1259 nt]
Seq. No.
                   37153
                   LIB3072-025-Q1-E1-F3
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g3834310
BLAST score 312
E value 6.0e-33
Match length 113
% identity 73

NCBI Description (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD





gb\_D83004 from Homo sapiens. ESTs gb\_T88233, gb\_Z24464, gb\_N37265, gb\_H36151, gb\_Z34711, gb\_AA040983, and gb\_T22122 come from this gene. [Arabidopsis thaliana]

 Seq. No.
 37154

 Seq. ID
 LIB3072-025-Q1-E1-H10

 Method
 BLASTN

 NCRI CI
 256428

NCBI GI g256428 BLAST score 268

E value 1.0e-149 Match length 318 % identity 96

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37155

Seq. ID LIB3072-025-Q1-E1-H6

Method BLASTN
NCBI GI g2995813
BLAST score 33
E value 3.0e-09
Match length 53
% identity 91

NCBI Description Trifolium bejariense 18S ribosomal RNA gene, partial

sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence;

and 26S ribosomal RNA gene, partial sequence

Seq. No. 37156

Seq. ID LIB3072-026-Q1-E1-A10

Method BLASTN
NCBI GI g256428
BLAST score 146
E value 2.0e-76
Match length 284
% identity 88

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37157

Seq. ID LIB3072-026-Q1-E1-A7

Method BLASTN
NCBI GI g18535
BLAST score 94
E value 2.0e-45
Match length 206
% identity 86

NCBI Description Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No. 37158

Seq. ID LIB3072-026-Q1-E1-B11

Method BLASTN
NCBI GI g256428
BLAST score 213
E value 1.0e-116
Match length 302
% identity 93



NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and Forrest, mRNA, 1259 nt]

Seq. No. 37159

Seq. ID LIB3072-026-Q1-E1-C1

Method BLASTN
NCBI GI g18571
BLAST score 189
E value 1.0e-102
Match length 300
% identity 92

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37160

Seq. ID LIB3072-026-Q1-E1-C11

Method BLASTN
NCBI GI g256428
BLAST score 131
E value 9.0e-68
Match length 201
% identity 92

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37161

Seq. ID LIB3072-026-Q1-E1-C3

Method BLASTN
NCBI GI g296442
BLAST score 124
E value 2.0e-63
Match length 172
% identity 94

NCBI Description G.max ADR11 mRNA

Seq. No. 37162

Seq. ID LIB3072-026-Q1-E1-C9

Method BLASTN
NCBI GI g288618
BLAST score 259
E value 1.0e-144
Match length 319
% identity 95

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No. 37163

Seq. ID LIB3072-026-Q1-E1-D4

Method BLASTN
NCBI GI g256428
BLAST score 398
E value 0.0e+00
Match length 416
% identity 99

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37164

Seq. ID LIB3072-026-Q1-E1-E9



```
BLASTN
Method
NCBI GI
                  g2305019
BLAST score
                  178
                  2.0e-95
E value
Match length
                  338
                  89
% identity
NCBI Description Glycine max 2S albumin pre-propeptide mRNA, complete cds
                  37165
Seq. No.
Seq. ID
                  LIB3072-027-Q1-E1-A11
Method
                  BLASTN
                  q256428
NCBI GI
BLAST score
                  261
                  1.0e-145
E value
                  323
Match length
                  96
% identity
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                  Forrest, mRNA, 1259 nt]
                  37166
Seq. No.
Seq. ID
                  LIB3072-027-Q1-E1-D6
Method
                  BLASTN
NCBI GI
                  g288618
BLAST score
                  392
                  0.0e + 00
E value
Match length
                  416
                  99
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                  37167
Seq. No.
Seq. ID
                  LIB3072-027-Q1-E1-E3
Method
                  BLASTN
NCBI GI
                  q256428
BLAST score
                  299
                  1.0e-167
E value
                  385
Match length
                  95
% identity
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                  Forrest, mRNA, 1259 nt]
Seq. No.
                  37168
                  LIB3072-027-Q1-E1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q836895
BLAST score
                  32
                  9.0e-09
E value
Match length
                  68
                  87
% identity
NCBI Description Saccharomyces cerevisiae CSP2 gene, complete cds
                  37169
Seq. No.
Seq. ID
                  LIB3072-027-Q1-E1-E5
Method
                  BLASTN
```

NCBI GI g256428 BLAST score 340 E value 0.0e + 00Match length 386



% identity

KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and NCBI Description

Forrest, mRNA, 1259 nt]

37170 Seq. No.

Seq. ID LIB3072-028-Q1-E1-A5

Method BLASTN NCBI GI q169946 BLAST score 40 E value 1.0e-13 Match length 44 % identity 98

NCBI Description Soybean protease inhibitor IV mRNA, complete cds

37171 Seq. No.

Seq. ID LIB3072-028-Q1-E1-B6

Method BLASTN NCBI GI q531828 BLAST score 34 8.0e-10 E value Match length 58 % identity 90

NCBI Description Cloning vector pSport1, complete cds

Seq. No.

Seq. ID LIB3072-028-Q1-E1-C11

37172

Method BLASTN NCBI GI g498167 BLAST score 177 E value 5.0e-95 Match length 213 % identity 96

NCBI Description Soybean mRNA for leginsulin, complete cds

Seq. No.

37173

Seq. ID LIB3072-028-Q1-E1-C7 Method

BLASTN NCBI GI g256428 BLAST score 244 1.0e-135 E value Match length 302 % identity 95

KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and NCBI Description

Forrest, mRNA, 1259 nt]

37174 Seq. No.

Seq. ID LIB3072-028-Q1-E1-D5

Method BLASTN NCBI GI g18571 BLAST score 230 E value 1.0e-126 310 Match length 94 % identity

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37175

Seq. ID LIB3072-028-Q1-E1-E7



```
Method BLASTN
NCBI GI g18571
BLAST score 61
E value 6.0e-26
Match length 155
% identity 88
```

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37176

Seq. ID LIB3072-028-Q1-E1-F5

Method BLASTN
NCBI GI g18769
BLAST score 70
E value 4.0e-31
Match length 239
% identity 87

NCBI Description G.max mRNA Ti-a for Kunitz trypsin inhibitor subtype A

Seq. No. 37177

Seq. ID LIB3072-028-Q1-E1-G5

Method BLASTX
NCBI GI g4185511
BLAST score 150
E value 5.0e-10
Match length 44
% identity 68

NCBI Description (AF102822) actin depolymerizing factor 4 [Arabidopsis

thaliana]

Seq. No. 37178

Seq. ID LIB3072-028-Q1-E1-H3

Method BLASTN
NCBI GI g256428
BLAST score 214
E value 1.0e-117
Match length 304
% identity 93

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37179

Seq. ID LIB3072-028-Q1-E1-H8

Method BLASTN
NCBI GI g2055227
BLAST score 38
E value 4.0e-12
Match length 66
% identity 89

NCBI Description Glycine max mRNA for SRC1, complete cds

Seq. No. 37180

Seq. ID LIB3072-030-Q1-E1-E1

Method BLASTX
NCBI GI g3676826
BLAST score 142
E value 9.0e-09
Match length 135



```
% identity
NCBI Description (AF092449) mucin-like protein [Heterodera glycines]
Seq. No.
                  37181
Seq. ID
                  LIB3072-031-Q1-E1-H7
Method
                  BLASTX
NCBI GI
                  q4191814
BLAST score
                  147
E value
                  3.0e-09
Match length
                  133
% identity
                  39
NCBI Description (AB008680) alpha' subunit of beta-conglycinin [Glycine max]
Seq. No.
                  37182
Seq. ID
                  LIB3072-037-Q1-E1-A3
Method
                  BLASTN
NCBI GI
                  q18571
BLAST score
                  342
E value
                  0.0e+00
Match length
                  388
% identity
                  97
NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II
Seq. No.
                  37183
Seq. ID
                  LIB3072-037-Q1-E1-C2
Method
                  BLASTN
NCBI GI
                  q288618
BLAST score
                  255
E value
                  1.0e-141
Match length
                  351
                  93
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
Seq. No.
                  37184
Seq. ID
                  LIB3072-037-Q1-E1-D1
Method
                  BLASTX
NCBI GI
                  q4455194
BLAST score
                  158
E value
                  4.0e-11
Match length
                  43
% identity
                  70
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  37185
Seq. ID
                  LIB3072-037-Q1-E1-F4
Method
                  BLASTN
NCBI GI
                  g169946
BLAST score
                  60
E value
                  1.0e-25
```

Match length 140 % identity 91

NCBI Description Soybean protease inhibitor IV mRNA, complete cds

Seq. No. 37186

Seq. ID LIB3072-043-Q1-K1-E8

Method BLASTN NCBI GI g18571



```
BLAST score
E value
                   2.0e-41
Match length
                   179
% identity
                   87
NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II
Seq. No.
                   37187
Seq. ID
                   LIB3072-043-Q1-K1-F11
Method
                   BLASTN
NCBI GI
                   g3212846
BLAST score
                   74
E value
                   1.0e-33
Match length
                   230
% identity
                   83
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   37188
                   LIB3072-043-Q1-K1-F5
Seq. ID
Method
                  BLASTN
NCBI GI
                   g288618
BLAST score
                   387
E value
                   0.0e + 00
Match length
                   411
                  99
% identity
NCBI Description
                  G.max GB-D-II gene for proteinase inhibitor D-II
Seq. No.
                   37189
Seq. ID
                  LIB3072-043-Q1-K1-F8
Method
                  BLASTN
NCBI GI
                  g18769
BLAST score
                  50
                  3.0e-19
E value
Match length
                  114
% identity
                  87
NCBI Description
                  G.max mRNA Ti-a for Kunitz trypsin inhibitor subtype A
Seq. No.
                  37190
Seq. ID
                  LIB3072-043-Q1-K1-H8
Method
                  BLASTN
NCBI GI
                  g256428
BLAST score
                  265
E value
                  1.0e-147
Match length
                  363
% identity
                  93
NCBI Description
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
                  Forrest, mRNA, 1259 nt]
Seq. No.
                  37191
Seq. ID
                  LIB3072-044-Q1-K1-B10
Method
                  BLASTN
NCBI GI
                  g18571
```

Method BLASTN
NCBI GI g18571
BLAST score 171
E value 2.0e-91
Match length 259
% identity 92

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Match length

NCBI Description

% identity

46

83



```
37192
Seq. No.
Seq. ID
                   LIB3072-044-Q1-K1-B8
Method
                   BLASTX
NCBI GI
                   g125723
BLAST score
                   154
E value
                   4.0e-10
Match length
                   101
% identity
                   41
                   KUNITZ-TYPE TRYPSIN INHIBITOR KTI2 PRECURSOR
NCBI Description
                   >gi_81815_pir__JQ1092 trypsin inhibitor KTi2 (Kunitz) -
                   soybean >gi_256636_bbs_115029 (S45035) Kunitz trypsin
                   inhibitor KTi2 [soybeans, Peptide, 204 aa] [Glycine max]
Seq. No.
                   37193
Seq. ID
                   LIB3072-044-01-K1-B9
Method
                   BLASTN
NCBI GI
                   g168679
BLAST score
                   48
E value
                   3.0e-18
Match length
                   104
% identity
                   87
                  Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
NCBI Description
                   >gi_270687_gb_I03334_ Sequence 9 from Patent US
Seq. No.
                   37194
Seq. ID
                   LIB3072-044-Q1-K1-C11
Method
                   BLASTX
NCBI GI
                   g2500354
BLAST score
                   480
E value
                   2.0e-48
Match length
                   117
% identity
                   79
NCBI Description
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462
                   (AB001891) QM family protein [Solanum melongena]
Seq. No.
                   37195
Seq. ID
                  LIB3072-044-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                   g4539307
BLAST score
                  150
E value
                   6.0e-10
Match length
                  71
% identity
                   46
NCBI Description
                   (AL049480) putative acidic ribosomal protein [Arabidopsis
                  thaliana]
                  37196
Seq. No.
Seq. ID
                  LIB3072-044-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g4454464
BLAST score
                  147
                  2.0e-12
E value
```

(AC006234) unknown protein [Arabidopsis thaliana]

```
Seq. No.
Seq. ID
                  LIB3072-044-Q1-K1-D2
Method
                  BLASTN
NCBI GI
                  g2270991
BLAST score
                  106
E value
                  1.0e-52
Match length
                  266
                  85
% identity
NCBI Description
                  Glycine max metallothionein-II protein mRNA, complete cds
                  37198
Seq. No.
Seq. ID
                  LIB3072-044-Q1-K1-D5
Method
                  BLASTN
NCBI GI
                  g2924257
BLAST score
                  40
E value
                  5.0e-13
Match length
                  244
% identity
                  83
NCBI Description
                  Tobacco chloroplast genome DNA
Seq. No.
                  37199
Seq. ID
                  LIB3072-044-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  q3176098
BLAST score
                  188
E value
                  4.0e-14
```

% identity 40
NCBI Description (Y15036) annexin [Medicago truncatula]

Seq. No. 37200

Match length

Seq. ID LIB3072-044-Q1-K1-E7

139 40

Method BLASTN
NCBI GI g18571
BLAST score 164
E value 2.0e-87
Match length 236
% identity 92

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37201

Seq. ID LIB3072-044-Q1-K1-F8

Method BLASTN
NCBI GI g18571
BLAST score 103
E value 8.0e-51
Match length 315
% identity 83

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37202

Seq. ID LIB3072-044-Q1-K1-G12

Method BLASTN
NCBI GI g18571
BLAST score 144
E value 3.0e-75
Match length 280



% identity NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

37203 Seq. No.

LIB3072-044-Q1-K1-G8 Seq. ID

Method BLASTN NCBI GI g256428 BLAST score 294 1.0e-164 E value 388 Match length 94 % identity

KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and NCBI Description

Forrest, mRNA, 1259 nt]

Seq. No. 37204

LIB3072-044-Q1-K1-H7 Seq. ID

Method BLASTN g288618 NCBI GI BLAST score 127 E value 4.0e-65 Match length 267 87 % identity

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No. 37205

LIB3072-046-Q1-K1-A11 Seq. ID

Method BLASTN g18769 NCBI GI BLAST score 58 E value 4.0e-24 Match length 190 83 % identity

NCBI Description G.max mRNA Ti-a for Kunitz trypsin inhibitor subtype A

Seq. No.

LIB3072-046-Q1-K1-A5 Seq. ID

37206

Method BLASTN NCBI GI g18571 BLAST score 257 E value 1.0e-142 325 Match length 95 % identity

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No.

37207 Seq. ID LIB3072-046-Q1-K1-B6

Method BLASTN NCBI GI q18571 BLAST score 61 E value 9.0e-26 Match length 189 % identity 83

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No.

37208

Seq. ID LIB3072-046-Q1-K1-C3

Method BLASTX

E value Match length

% identity

244

95



```
NCBI GI
BLAST score
                    141
                    7.0e-09
E value
                    89
Match length
% identity
                    40
NCBI Description
                    (U12390) beta-galactosidase alpha peptide [cloning vector
                    pSport1]
Seq. No.
                    37209
Seq. ID
                    LIB3072-046-Q1-K1-C7
Method
                    BLASTX
NCBI GI
                    g81811
BLAST score
                    195
E value
                    4.0e-15
Match length
                    118
                    41
% identity
NCBI Description ribosomal protein S11 - soybean (fragment) >gi 170054
                     (M31024) ribosomal protein S11 [Glycine max]
Seq. No.
                    37210
Seq. ID
                    LIB3072-046-Q1-K1-D2
Method
                    BLASTN
NCBI GI
                    g18571
BLAST score
                    312
E value
                    1.0e-175
Match length
                    336
                    98
% identity
NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II
Seq. No.
                    37211
                    LIB3072-046-Q1-K1-D7
Seq. ID
Method
                    BLASTX
NCBI GI
                    g266972
BLAST score
                    143
E value
                    6.0e-09
Match length
                    54
% identity
                    52
                    40S RIBOSOMAL PROTEIN S29 >qi 631884 pir S30298 ribosomal
NCBI Description
                    protein S29 - rat >gi_1362934_pir__S55919 ribosomal protein S29 - human >gi_57133_emb_CAA41778_ (X59051) ribosomal protein S29 [Rattus norvegicus] >gi_550027 (U14973)
                    ribosomal protein S29 [Homo sapiens] >gi 1220361 (L31610)
                    homologous to antisense sequence of krev-1, anti oncogene
                     [Homo sapiens] >gi_1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi_1513230 (U66372) ribosomal protein S29
                     [Bos taurus] >gi 1096945 prf 2113200H ribosomal protein
                    S29 [Homo sapiens] >gi 4506717 ref NP 001023.1 pRPS29_
                    ribosomal protein S29
                    37212
Seq. No.
Seq. ID
                    LIB3072-046-Q1-K1-E1
Method
                    BLASTN
NCBI GI
                    g18571
BLAST score
                    172
                    5.0e-92
```





## NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

37213 Seq. No.

Seq. ID LIB3072-046-Q1-K1-E2

Method BLASTN NCBI GI q288618 BLAST score 268 1.0e-149 E value 329 Match length % identity 96

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No. 37214

LIB3072-046-Q1-K1-E3 Seq. ID

Method BLASTN a18769 NCBI GI BLAST score E value 3.0e-35 Match length 267 90 % identity

NCBI Description G.max mRNA Ti-a for Kunitz trypsin inhibitor subtype A

37215 Seq. No.

Seq. ID LIB3072-046-Q1-K1-E5

Method BLASTN g2879810 NCBI GI 169 BLAST score 4.0e-90 E value Match length 333 % identity 88

NCBI Description Lupinus luteus mRNA for ribosomal protein L30

37216 Seq. No.

Seq. ID LIB3072-046-Q1-K1-F7

Method BLASTX q548852 NCBI GI BLAST score 148 E value 6.0e-10 Match length 45 % identity 62

40S RIBOSOMAL PROTEIN S21 >gi\_481227\_pir\_\_S38357 ribosomal NCBI Description

protein S21 - rice >gi 303839 dbj BAA02158 (D12633) 40S

subunit ribosomal protein [Oryza sativa]

Seq. No. 37217

LIB3072-047-Q1-K1-A3 Seq. ID

Method BLASTN NCBI GI g18771 BLAST score 38 3.0e-12 E value 38 Match length 100 % identity

NCBI Description G.max mRNA Ti-b for Kunitz trypsin inhibitor subtype B

Seq. No.

37218 Seq. ID LIB3072-047-Q1-K1-C2

BLASTX Method



NCBI GI g125722 BLAST score 191 E value 1.0e-14 Match length 83 % identity 49

NCBI Description KUNITZ-TYPE TRYPSIN INHIBITOR KTI1 PRECURSOR

>gi\_81814\_pir\_\_JQ1091 trypsin inhibitor KTi1 (Kunitz) soybean >gi\_256635\_bbs\_115028 (S45035) Kunitz trypsin
inhibitor KTi1 [soybeans, Peptide, 203 aa] [Glycine max]

Seq. No. 37219

Seq. ID LIB3072-047-Q1-K1-C9

Method BLASTN
NCBI GI g288618
BLAST score 307
E value 1.0e-172
Match length 407
% identity 94

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No. 37220

Seq. ID LIB3072-047-Q1-K1-D7

Method BLASTN
NCBI GI g18540
BLAST score 88
E value 9.0e-42
Match length 162
% identity 89

NCBI Description G.max BBI mRNA for proteinase inhibitor

Seq. No. 37221

Seq. ID LIB3072-047-Q1-K1-E6

Method BLASTX
NCBI GI g1326161
BLAST score 197
E value 2.0e-15
Match length 61
% identity 75

NCBI Description (U54703) dehydrin [Phaseolus vulgaris]

Seq. No. 37222

Seq. ID LIB3072-047-Q1-K1-F10

Method BLASTX
NCBI GI g3688162
BLAST score 164
E value 2.0e-11
Match length 63
% identity 65

NCBI Description (AJ009672) centrin [Arabidopsis thaliana]

Seq. No. 37223

Seq. ID LIB3072-049-Q1-K1-A3

Method BLASTN
NCBI GI g18571
BLAST score 38
E value 4.0e-12
Match length 166

5711

: "



% identity 81
NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37224

Seq. ID LIB3072-049-Q1-K1-C4

Method BLASTN
NCBI GI g256428
BLAST score 371
E value 0.0e+00
Match length 389
% identity 99

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37225

Seq. ID LIB3072-049-Q1-K1-C5

Method BLASTN
NCBI GI g256428
BLAST score 178
E value 1.0e-95
Match length 256
% identity 93

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37226

Seq. ID LIB3072-049-Q1-K1-D2

Method BLASTN
NCBI GI g170067
BLAST score 55
E value 1.0e-22
Match length 103
% identity 88

NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP3)

gene, complete cds

Seq. No. 37227

Seq. ID LIB3072-049-Q1-K1-E6

Method BLASTN
NCBI GI g256428
BLAST score 121
E value 8.0e-62
Match length 195
% identity 91

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37228

Seq. ID LIB3072-049-Q1-K1-H6

Method BLASTN
NCBI GI g256428
BLAST score 226
E value 1.0e-124
Match length 292
% identity 95

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]



```
37229
Seq. No.
Seq. ID
                  LIB3072-050-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g422270
                  222
BLAST score
                  5.0e-31
E value
                  107
Match length
% identity
                  67
                  ubiquitin / ribosomal protein CEP52 - Sauroleishmania
NCBI Description
                  tarentolae >gi 312486 emb CAA51549 (X73118)
                  ubiquitin-fusion protein [Leishmania tarentolae]
                  37230
Seq. No.
Seq. ID
                  LIB3072-050-Q1-K1-B11
Method
                  BLASTN
                  g288618
NCBI GI
                  64
BLAST score
                  2.0e-27
E value
                  90
Match length
                  93
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                  37231
Seq. No.
Seq. ID
                  LIB3072-050-Q1-K1-B5
Method
                  BLASTN
NCBI GI
                  g169972
BLAST score
                  287
                  1.0e-160
E value
                  351
Match length
                  96
% identity
NCBI Description Soybean glycinin A-la-B-x subunit mRNA, complete cds
                  37232
Seq. No.
Seq. ID
                  LIB3072-050-Q1-K1-C11
Method
                  BLASTN
NCBI GI
                  g18571
BLAST score
                  376
                  0.0e + 00
E value
                  399
Match length
                  98
% identity
NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II
                  37233
Seq. No.
Seq. ID
                  LIB3072-050-Q1-K1-D10
Method
                  BLASTN
NCBI GI
                  a288618
BLAST score
                  365
                  0.0e + 00
E value
                  410
Match length
                   98
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
```

Seq. No. 37234

Seq. ID LIB3072-050-Q1-K1-E2

Method BLASTN NCBI GI g288618



37235

BLAST score 1.0e-165 E value 334 Match length 97 % identity

G.max GB-D-II gene for proteinase inhibitor D-II NCBI Description

Seq. No. Seq. ID

LIB3072-050-Q1-K1-F6

BLASTN Method NCBI GI g18571 BLAST score 35 E value 1.0e-10 115 Match length % identity 83

G.max D-II mRNA for proteinase isoinhibitor D-II NCBI Description

Seq. No.

37236

Seq. ID

LIB3072-050-Q1-K1-G6

Method BLASTN NCBI GI q18571 BLAST score 66 E value 6.0e-29 Match length 166 % identity 85

G.max D-II mRNA for proteinase isoinhibitor D-II NCBI Description

Seq. No. 37237

LIB3072-050-Q1-K1-G8 Seq. ID

Method BLASTN q12139 NCBI GI BLAST score 84 1.0e-39 E value 184

Match length 87 % identity

Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and NCBI Description trnG coding for ribosomal protein S2, one CF(1) and three

CF(O) subunits of ATP synthase and tRNA-Arg and tRNA-Gly

37238 Seq. No.

Seq. ID LIB3072-051-Q1-E1-A8

Method BLASTN NCBI GI g1277163 BLAST score 225 1.0e-123 E value 277 Match length 95 % identity

Glycine max cysteine proteinase inhibitor mRNA, partial cds NCBI Description

Seq. No.

37239

Seq. ID LIB3072-051-Q1-E1-B3

BLASTN Method NCBI GI g288618 BLAST score 241 1.0e-133 E value Match length 295 96 % identity

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Method

NCBI GI BLAST score BLASTX g2253442

231



```
37240
Seq. No.
Seq. ID
                  LIB3072-051-Q1-E1-E8
Method
                  BLASTN
NCBI GI
                  g288618
                  268
BLAST score
                  1.0e-149
E value
                  323
Match length
                  96
% identity
                  G.max GB-D-II gene for proteinase inhibitor D-II
NCBI Description
Seq. No.
                  37241
                  LIB3072-052-Q1-E1-A11
Seq. ID
Method
                  BLASTN
                  q1055367
NCBI GI
BLAST score
                  163
E value
                  1.0e-86
                  295
Match length
% identity
                  89
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
Seq. No.
                  37242
Seq. ID
                  LIB3072-052-Q1-E1-D2
Method
                  BLASTN
NCBI GI
                  g288618
BLAST score
                  140
                  7.0e-73
E value
                  308
Match length
                  86
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
Seq. No.
                  37243
Seq. ID
                  LIB3072-052-Q1-E1-D3
Method
                  BLASTN
NCBI GI
                  q288618
BLAST score
                  221
E value
                  1.0e-121
                  301
Match length
                  93
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
Seq. No.
                  37244
Seq. ID
                  LIB3072-052-Q1-E1-D8
                  BLASTN
Method
NCBI GI
                  g288618
BLAST score
                  375
E value
                  0.0e + 00
                  399
Match length
                  98
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
Seq. No.
                  37245
Seq. ID
                  LIB3072-053-Q1-E1-A2
```



E value 3.0e-19
Match length 55
% identity 64

NCBI Description (AF007784) LTCOR11 [Lavatera thuringiaca]

Seq. No. 37246

Seq. ID LIB3072-053-Q1-E1-A8

Method BLASTN
NCBI GI g288618
BLAST score 350
E value 0.0e+00
Match length 382
% identity 98

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No. 37247

Seq. ID LIB3072-053-Q1-E1-C7

Method BLASTN
NCBI GI g531828
BLAST score 46
E value 4.0e-17
Match length 94
% identity 87

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 37248

Seq. ID LIB3072-053-Q1-E1-D12

Method BLASTN
NCBI GI g256428
BLAST score 374
E value 0.0e+00
Match length 404
% identity 98

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37249

Seq. ID LIB3072-053-Q1-E1-G5

Method BLASTN
NCBI GI g18571
BLAST score 137
E value 3.0e-71
Match length 201
% identity 92

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No.

Seq. ID LIB3072-053-Q1-E1-H7

37250

Method BLASTN
NCBI GI g531828
BLAST score 33
E value 3.0e-09
Match length 73
% identity 86

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 37251



```
LIB3072-053-Q1-E1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g135859
                    140
BLAST score
                    7.0e-09
E value
Match length
                    52
% identity
                    62
                   TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                   >gi_282919_pir__S26742 tonoplast intrinsic protein - kidney bean >gi_21055_emb_CAA44669_ (X62873) tonoplast intrinsic
                   protein [Phaseolus vulgaris]
Seq. No.
                    37252
                   LIB3072-054-Q1-E1-B10
Seq. ID
                   BLASTN
Method
                    g18608
NCBI GI
BLAST score
                    77
                    2.0e-35
E value
                    189
Match length
% identity
                    85
                   Glycine max mRNA for glycinin >gi 2170693 dbj E02462 E02462
NCBI Description
                    cDNA encoding glycinine subunit A2B1a precursor
Seq. No.
                    37253
                    LIB3072-054-Q1-E1-B7
Seq. ID
Method
                    BLASTN
NCBI GI
                    q169972
BLAST score
                    228
                    1.0e-125
E value
                    280
Match length
% identity
                    95
                   Soybean glycinin A-1a-B-x subunit mRNA, complete cds
NCBI Description
Seq. No.
                    37254
Seq. ID
                   LIB3072-054-Q1-E1-C10
                   BLASTN
Method
NCBI GI
                    g288618
BLAST score
                    324
                    0.0e + 00
E value
                    364
Match length
                    97
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
Seq. No.
                    37255
Seq. ID
                   LIB3072-054-Q1-E1-C7
Method
                    BLASTN
NCBI GI
                    g18571
BLAST score
                    321
                    0.0e + 00
E value
```

353 Match length 98 % identity

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37256

Seq. ID LIB3072-054-Q1-E1-D10

Method BLASTN NCBI GI g18769



```
BLAST score 142
E value 3.0e-74
Match length 194
% identity 93
```

NCBI Description G.max mRNA Ti-a for Kunitz trypsin inhibitor subtype A

Seq. No. 37257

Seq. ID LIB3072-054-Q1-E1-E3

Method BLASTN
NCBI GI g1141781
BLAST score 118
E value 9.0e-60
Match length 260
% identity 73

NCBI Description Vigna radiata EM protein mRNA, complete cds

Seq. No. 37258

Seq. ID LIB3072-054-Q1-E1-E4

Method BLASTN
NCBI GI g288618
BLAST score 132
E value 3.0e-68
Match length 227
% identity 90

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No. 37259

Seq. ID LIB3072-054-Q1-E1-F9

Method BLASTX
NCBI GI g1657621
BLAST score 337
E value 9.0e-32
Match length 108
% identity 61

NCBI Description (U72505) G6p [Arabidopsis thaliana] >gi\_3068711 (AF049236)

putative acyl-coA dehydrogenase [Arabidopsis thaliana]

Seq. No. 37260

Seg. ID LIB3072-054-Q1-E1-H3

Method BLASTN
NCBI GI g256428
BLAST score 292
E value 1.0e-163
Match length 353
% identity 96

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37261

Seq. ID LIB3072-054-Q1-E1-H4

Method BLASTN
NCBI GI g927574
BLAST score 44
E value 8.0e-16
Match length 48
% identity 98

NCBI Description Glycine max williams alpha galactosidase mRNA, complete





cds. >gi 2086979 gb I36466 I36466 Sequence 8 from patent US

37262 Seq. No. Seq. ID LIB3072-055-Q1-K1-A6 Method BLASTN NCBI GI g288618 BLAST score 198 1.0e-107 E value Match length 285 92 % identity NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II 37263 Seq. No. Seq. ID LIB3072-055-Q1-K1-B11 BLASTN Method NCBI GI g256428 BLAST score 124 1.0e-63 E value Match length 218 89 % identity NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and Forrest, mRNA, 1259 nt] Seq. No. 37264 Seq. ID LIB3072-055-Q1-K1-C11 Method BLASTN NCBI GI g288618 339 BLAST score 0.0e+00E value 369 Match length 98 % identity NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II Seq. No. 37265 Seq. ID LIB3072-055-Q1-K1-C12 Method BLASTN NCBI GI g288618 BLAST score 38 E value 4.0e-12 Match length 130 87 % identity NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II Seq. No. 37266 LIB3072-055-Q1-K1-F5 Seq. ID Method BLASTN NCBI GI g256428 BLAST score 263 E value 1.0e-146 Match length 356 94 % identity NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and Forrest, mRNA, 1259 nt]

Seq. No. 37267

Seq. ID LIB3072-055-Q1-K1-G4

Method BLASTN



```
NCBI GI
                  q169928
BLAST score
                  83
E value
                  3.0e-39
Match length
                  163
                  88
% identity
NCBI Description
                  Glycine max alpha'-type beta conglycinin storage protein
                  gene, complete cds, clone ch4A
Seq. No.
                  37268
Seq. ID
                  LIB3072-055-Q1-K1-G7
Method
                  BLASTN
NCBI GI
                  q256428
BLAST score
                  228
E value
                  1.0e-125
                  312
Match length
                  95
% identity
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                  Forrest, mRNA, 1259 nt]
                  37269
Seq. No.
                  LIB3072-055-Q1-K1-H8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g18571
BLAST score
                  156
                  1.0e-82
E value
                  184
Match length
% identity
                  96
NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II
                  37270
Seq. No.
Seq. ID
                  LIB3072-056-Q1-K1-C3
Method
                  BLASTN
NCBI GI
                  q256428
BLAST score
                  194
E value
                  1.0e-105
Match length
                  359
% identity
                  89
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                  Forrest, mRNA, 1259 nt]
Seq. No.
                  37271
Seq. ID
                  LIB3072-056-Q1-K1-C4
Method
                  BLASTN
NCBI GI
                  g18571
BLAST score
                  218
                  1.0e-119
E value
Match length
                  298
% identity
                  93
NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II
                  37272
Seq. No.
Seq. ID
                  LIB3072-056-Q1-K1-D6
```

BLASTN Method g169944 NCBI GI BLAST score 145 6.0e-76 E value Match length 269

% identity 90

NCBI Description Soybean protease inhibitor C-II mRNA, complete cds

Seq. No. 37273

Seg. ID LIB3072-056-Q1-K1-F5

Method BLASTX
NCBI GI g585963
BLAST score 211
E value 5.0e-17
Match length 64
% identity 66

NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No. 37274

Seq. ID LIB3072-056-Q1-K1-G12

Method BLASTN
NCBI GI g288618
BLAST score 368
E value 0.0e+00
Match length 413
% identity 97

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No. 37275

Seq. ID LIB3072-056-Q1-K1-H10

Method BLASTN
NCBI GI g18571
BLAST score 44
E value 1.0e-15
Match length 239
% identity 80

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37276

Seq. ID LIB3072-057-Q1-K1-A1

Method BLASTN
NCBI GI g18571
BLAST score 371
E value 0.0e+00
Match length 400
% identity 98

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37277

Seq. ID LIB3072-057-Q1-K1-B8

Method BLASTX
NCBI GI g117765
BLAST score 243
E value 3.0e-21
Match length 64
% identity 72

NCBI Description CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC13III)

>gi\_21439\_emb\_CAA44055\_ (X62124) cytochrome c1 [Solanum

tuberosum]

Seq. No. 37278

Seq. ID LIB3072-057-Q1-K1-D8



Method BLASTN
NCBI GI g18571
BLAST score 82
E value 2.0e-38
Match length 265

Match length 265 % identity 83

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37279

Seq. ID LIB3072-057-Q1-K1-E3

Method BLASTN
NCBI GI g18571
BLAST score 369
E value 0.0e+00
Match length 420
% identity 97

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37280

Seq. ID LIB3072-057-Q1-K1-F8

Method BLASTN
NCBI GI g2879810
BLAST score 72
E value 2.0e-32
Match length 171
% identity 87

NCBI Description Lupinus luteus mRNA for ribosomal protein L30

Seq. No. 37281

Seq. ID LIB3072-057-Q1-K1-G8

Method BLASTN
NCBI GI g18571
BLAST score 68
E value 6.0e-30
Match length 263
% identity 83

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37282

Seq. ID LIB3072-057-Q1-K1-H3

Method BLASTN
NCBI GI g18571
BLAST score 72
E value 2.0e-32
Match length 143
% identity 91

NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II

Seq. No. 37283

Seq. ID LIB3072-057-Q1-K1-H4

Method BLASTX
NCBI GI g3914535
BLAST score 176
E value 5.0e-13
Match length 64
% identity 58

NCBI Description 60S RIBOSOMAL PROTEIN L13A >gi\_2791948\_emb\_CAA11283\_

Method

BLASTX





## (AJ223363) ribosomal protein L13a [Lupinus luteus]

```
37284
Seq. No.
                  LIB3072-058-Q1-K1-C10
Seq. ID
                  BLASTN
Method
NCBI GI
                  q288618
                  358
BLAST score
                  0.0e+00
E value
                  389
Match length
% identity
                  98
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                  37285
Seq. No.
                  LIB3072-058-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3492806
BLAST score
                   356
                   5.0e-34
E value
Match length
                   101
                   65
% identity
                   (AJ225045) adventitious rooting related oxygenase [Malus
NCBI Description
                   domestica]
                   37286
Seq. No.
Seq. ID
                   LIB3072-058-Q1-K1-D9
Method
                   BLASTN
NCBI GI
                   g256428
BLAST score
                   377
                   0.0e+00
E value
                   410
Match length
                   99
% identity
                   KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                   Forrest, mRNA, 1259 nt]
Seq. No.
                   37287
                   LIB3072-058-Q1-K1-G9
Seq. ID
Method
                   BLASTN
                   q288618
NCBI GI
BLAST score
                   287
                   1.0e-160
E value
                   350
Match length
                   96
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                   37288
Seq. No.
                   LIB3072-059-Q1-K1-A2
Seq. ID
                   BLASTN
Method
                   g288618
NCBI GI
                   144
BLAST score
                   3.0e-75
E value
                   276
Match length
                   88
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                   37289
Seq. No.
Seq. ID
                   LIB3072-059-Q1-K1-A7
```



NCBI GI g4455235 BLAST score 157 E value 7.0e-11 Match length 63 % identity 48

NCBI Description (AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA

SUBUNIT-like [Arabidopsis thaliana]

Seq. No. 37290

Seq. ID LIB3072-059-Q1-K1-B2

Method BLASTX
NCBI GI g2129842
BLAST score 232
E value 1.0e-19
Match length 73
% identity 56

NCBI Description SE60 protein - soybean >gi\_509769\_emb\_CAA79164\_ (Z18359)

seed-specific low molecular weight sulfur-rich protein

[Glycine max]

Seq. No. 37291

Seq. ID LIB3072-059-Q1-K1-C3

Method BLASTX
NCBI GI 94191788
BLAST score 285
E value 1.0e-25
Match length 119
% identity 51

NCBI Description (AC005917) putative 1-aminocyclopropane-1-carboxylate

oxidase [Arabidopsis thaliana]

Seq. No. 37292

Seq. ID LIB3072-059-Q1-K1-C9

Method BLASTN
NCBI GI g256428
BLAST score 350
E value 0.0e+00
Match length 368
% identity 99

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37293

Seq. ID LIB3072-059-Q1-K1-D4

Method BLASTN
NCBI GI g288618
BLAST score 355
E value 0.0e+00
Match length 382
% identity 98

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No. 37294

Seq. ID LIB3072-059-Q1-K1-E5

Method BLASTN NCBI GI g34518 BLAST score 62

```
E value 1.0e-26
Match length 194
% identity 83
```

NCBI Description Human mRNA for MDNCF (monocyte-derived neutrophil

chemotactic factor)

Seq. No. 37295

Seq. ID LIB3072-059-Q1-K1-E6

Method BLASTX
NCBI GI g4103342
BLAST score 436
E value 3.0e-43
Match length 120
% identity 75

NCBI Description (AF022377) agamous-like putative transcription factor

[Cucumis sativus]

Seq. No. 37296

Seq. ID LIB3072-059-Q1-K1-F10

Method BLASTX
NCBI GI g3643595
BLAST score 214
E value 4.0e-17
Match length 90
% identity 47

NCBI Description (AC005395) putative oleosin protein [Arabidopsis thaliana]

Seq. No. 37297

Seq. ID LIB3072-059-Q1-K1-F8

Method BLASTN
NCBI GI g256428
BLAST score 100
E value 5.0e-49
Match length 236
% identity 86

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 37298

Seq. ID LIB3072-060-Q1-K1-C7

Method BLASTN
NCBI GI g2055227
BLAST score 259
E value 1.0e-144
Match length 330
% identity 95

NCBI Description Glycine max mRNA for SRC1, complete cds

Seq. No.

37299

Seq. ID LIB3072-060-Q1-K1-E3

Method BLASTN
NCBI GI g288618
BLAST score 237
E value 1.0e-131
Match length 293
% identity 95

NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II



```
Seq. No.
                  37300
                  LIB3072-060-Q1-K1-F10
Seq. ID
Method
                  BLASTN
                  g288618
NCBI GI
                  299
BLAST score
E value
                  1.0e-167
                  399
Match length
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                  37301
Seq. No.
Seq. ID
                  LIB3072-061-Q1-K1-C10
                  BLASTN
Method
                  a288618
NCBI GI
                  318
BLAST score
                  1.0e-179
E value
Match length
                  342
% identity
                  98
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                  37302
Seq. No.
                  LIB3072-061-Q1-K1-C6
Seq. ID
Method
                  BLASTN
                  q288618
NCBI GI
                  311
BLAST score
                  1.0e-175
E value
                  351
Match length
                   97
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                   37303
Seq. No.
                  LIB3072-061-Q1-K1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                   q256428
BLAST score
                   297
                   1.0e-166
E value
Match length
                   323
                   98
% identity
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                   Forrest, mRNA, 1259 nt]
                   37304
Seq. No.
                   LIB3072-061-Q1-K1-F2
Seq. ID
                   BLASTN
Method
                   g256428
NCBI GI
                   330
BLAST score
                   0.0e+00
E value
                   352
Match length
                   99
% identity
                  KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                   Forrest, mRNA, 1259 nt]
                   37305
Seq. No.
Seq. ID
                   LIB3072-061-Q1-K1-F3
                   BLASTX
Method
NCBI GI
                   g124224
```



```
BLAST score
E value
                  2.0e-18
                  96
Match length
                  51
% identity
                  INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi_100345_pir__S21060 translation initiation factor eIF-5A
                  - common tobacco >gi 19887 emb CAA45105 (X63543)
                  eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
                  37306
Seq. No.
                  LIB3073-001-Q1-K1-A6
Seq. ID
Method
                  BLASTX
                  g2739375
NCBI GI
BLAST score
                  141
                  8.0e-09
E value
                  46
Match length
                  63
% identity
                  (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                  37307
Seq. No.
                  LIB3073-001-Q1-K1-B11
Seq. ID
                  BLASTN
Method
                  g1055367
NCBI GI
BLAST score
                  73
                  7.0e-33
E value
                  321
Match length
% identity
                  81
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   37308
Seq. No.
                   LIB3073-001-Q1-K1-D1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q169974
                   162
BLAST score
E value
                   4.0e-86
Match length
                   173
                   99
% identity
NCBI Description Glycine max vspA gene, complete cds
                   37309
Seq. No.
                   LIB3073-001-Q1-K1-D7
Seq. ID
                   BLASTN
Method
                   g170089
NCBI GI
BLAST score
                   74
                   1.0e-33
E value
                   213
Match length
                   84
% identity
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
                   37310
Seq. No.
                   LIB3073-001-Q1-K1-F11
Seq. ID
```

BLASTN Method g169974 NCBI GI 158 BLAST score 8.0e-84 E value Match length 221



```
% identity
NCBI Description Glycine max vspA gene, complete cds
                  37311
Seq. No.
                  LIB3073-001-Q1-K1-F7
Seq. ID
                  BLASTN
Method
                  g18741
NCBI GI
                  148
BLAST score
                  7.0e-78
E value
                  219
Match length
                  93
% identity
                  Glycine max gene encoding ribulose-1,5-bisphosphate
NCBI Description
                  carboxylase small subunit
                  37312
Seq. No.
                  LIB3073-001-Q1-K1-H6
Seq. ID
                  BLASTN
Method
                  g170057
NCBI GI
                  186
BLAST score
                  1.0e-100
E value
                  222
Match length
                  96
% identity
                  Soybean ribulose 1,5-bisphosphate carboxylase small subunit
NCBI Description
                  (SRS4) gene, complete cds
                  37313
Seq. No.
                  LIB3073-002-Q1-K1-A10
Seq. ID
                  BLASTX
Method
                  g1173027
NCBI GI
BLAST score
                  146
                  1.0e-09
E value
                  51
Match length
                  61
% identity
                  60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal
NCBI Description
                  protein L31 [Nicotiana glutinosa]
                  37314
Seq. No.
                  LIB3073-002-Q1-K1-B5
Seq. ID
                  BLASTN
Method
NCBI GI
                   q169974
                   131
BLAST score
                   1.0e-67
E value
                   290
Match length
                   88
% identity
NCBI Description Glycine max vspA gene, complete cds
                   37315
Seq. No.
                   LIB3073-002-Q1-K1-B8
Seq. ID
Method
                   BLASTN
                   q456567
NCBI GI
```

Method BLASTN
NCBI GI 9456567
BLAST score 36
E value 6.0e-11
Match length 52
% identity 92

NCBI Description Pisum sativum ubiquitin conjugating enzyme (UBC4), complete

:ds

NCBI GI

BLAST score

g296408

63



```
Seq. No.
                  LIB3073-002-Q1-K1-C2
Seq. ID
                  BLASTN
Method
                  g1055367
NCBI GI
BLAST score
                  78
                  6.0e-36
E value
                  238
Match length
                  83
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
Seq. No.
                  37317
                  LIB3073-002-Q1-K1-C5
Seq. ID
                  BLASTN
Method
                  g18730
NCBI GI
                  37
BLAST score
                  1.0e-11
E value
                   57
Match length
% identity
                   91
                  Soybean 4.5 - 5S rRNA intergenic region
NCBI Description
Seq. No.
                   37318
                   LIB3073-002-Q1-K1-D2
Seq. ID
                   BLASTN
Method
                   g343349
NCBI GI
                   42
BLAST score
                   1.0e-14
E value
Match length
                   90
                   87
% identity
                  Glysine max mitochondrial DNA sequence, transcription
NCBI Description
                   initiation motif
Seq. No.
                   37319
Seq. ID
                   LIB3073-002-Q1-K1-D3
                   BLASTX
Method
                   g2252634
NCBI GI
BLAST score
                   233
                   8.0e-20
E value
                   76
Match length
                   49
% identity
                  (U95973) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   37320
Seq. No.
Seq. ID
                   LIB3073-002-Q1-K1-D7
                   BLASTN
Method
                   g18644
NCBI GI
BLAST score
                   89
                   2.0e-42
E value
                   189
Match length
                   87
% identity
NCBI Description Soybean mRNA for HMG-1 like protein
Seq. No.
                   37321
Seq. ID
                   LIB3073-002-Q1-K1-E3
                   BLASTN
Method
```

- <u>\*</u>



E value Match length 84 % identity

NCBI Description G.max ADR12 mRNA

37322 Seq. No.

LIB3073-002-Q1-K1-E6 Seq. ID

BLASTN Method g296408 NCBI GI 36 BLAST score 7.0e-11 E value 60 Match length % identity 90

NCBI Description G.max ADR12 mRNA

37323 Seq. No.

LIB3073-002-Q1-K1-F5 Seq. ID

BLASTN Method g1055367 NCBI GI BLAST score 185 1.0e-100 E value 257 Match length 93 % identity

Glycine max ribulose-1,5-bisphosphate carboxylase small NCBI Description

subunit mRNA, complete cds

37324 Seq. No.

LIB3073-002-Q1-K1-G3 Seq. ID

BLASTN Method q473604 NCBI GI BLAST score 65 4.0e-28 E value 117 Match length % identity 89

NCBI Description Zea mays W-22 histone H2B mRNA, complete cds

Seq. No.

37325 LIB3073-002-Q1-K1-H1 Seq. ID

Method BLASTN NCBI GI q169974 BLAST score 173 1.0e-92 E value 265 Match length 91 % identity

NCBI Description Glycine max vspA gene, complete cds

Seq. No.

Seq. ID LIB3073-003-Q1-K1-A2

37326

Method BLASTN NCBI GI g1055367 BLAST score 63 6.0e-27 E value 174 Match length 85 % identity

Glycine max ribulose-1,5-bisphosphate carboxylase small NCBI Description

subunit mRNA, complete cds



Seq. No. LIB3073-003-Q1-K1-A8 Seq. ID BLASTN Method

g169974 NCBI GI BLAST score 116 1.0e-58 E value 288 Match length 85 % identity

NCBI Description Glycine max vspA gene, complete cds

37328 Seq. No.

LIB3073-003-Q1-K1-B2 Seq. ID

BLASTN Method g169974 NCBI GI 98 BLAST score 7.0e-48E value 302 Match length 83 % identity

Glycine max vspA gene, complete cds NCBI Description

37329 Seq. No.

Seq. ID LIB3073-003-Q1-K1-C2

Method BLASTX g131004 NCBI GI 216 BLAST score 1.0e-17 E value 84 Match length % identity 51

REPETITIVE PROLINE-RICH CELL WALL PROTEIN 3 PRECURSOR NCBI Description

>gi\_99948\_pir\_\_B35532 proline-rich protein 2 precursor soybean >gi 170068 (J05209) cell wall protein (SbPRP3)

precursor [Glycine max]

37330 Seq. No.

LIB3073-003-Q1-K1-E12 Seq. ID

Method BLASTX g417103 NCBI GI 276 BLAST score 2.0e-24 E value 118 Match length 56 % identity

HISTONE H3.2, MINOR >gi 282871 pir S24346 histone NCBI Description

H3.3-like protein - Arabidopsis thaliana

>gi 16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 404825 emb CAA42958 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 488563 (U09458) histone H3.2 [Medicago sativa]  $>gi_488567$  ( $\overline{U}09460$ ) histone H3.2 [Medicago sativa] >gi 488569 (U09461) histone H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2 [Medicago sativa] >gi 488577 (U09465) histone H3.2

[Medicago sativa] >gi 510911 emb CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi 1435157 emb CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]

>gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi 3273350\_dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >qi 3885890 (AF093633) histone H3 [Oryza sativa] >gi 4038469 gb AAC97380 (AF109910) histone H3 [Porteresia





coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone
H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_
(AL035708) Histon H3 [Arabidopsis thaliana]

```
Seq. No.
Seq. ID
                   LIB3073-003-Q1-K1-G1
Method
                   BLASTX
NCBI GI
                   g133913
BLAST score
                   117
                   7.0e-10
E value
Match length
                   69
% identity
                   52
                   CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 >gi 70858_pir R3PM2
NCBI Description
                   ribosomal protein S2 - garden pea chloroplast >gi_12138_emb_CAA27546_ (X03912) ORF (aa 1-236) with
                   homology to ribosomal protein S2 [Pisum sativum]
Seq. No.
                   37332
                   LIB3073-003-Q1-K1-G12
Seq. ID
                   BLASTX
Method
                   q4539400
NCBI GI
                   208
BLAST score
E value
                   2.0e-16
Match length
                   50
                   74
% identity
                   (AL035526) putative protein [Arabidopsis thaliana]
NCBI Description
                   37333
Seq. No.
                   LIB3073-003-Q1-K1-G4
Seq. ID
Method
                   BLASTN
                   g1055367
NCBI GI
BLAST score
                   299
E value
                   1.0e-167
Match length
                   378
                    95
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
Seq. No.
                   37334
                   LIB3073-003-Q1-K1-H2
Seq. ID
                   BLASTN
Method
                   g169974
NCBI GI
BLAST score
                    167
                    5.0e-89
E value
                    343
Match length
                   87
% identity
NCBI Description Glycine max vspA gene, complete cds
                    37335
Seq. No.
                    LIB3073-004-Q1-K1-A3
Seq. ID
                   BLASTN
Method
                    q1055367
NCBI GI
BLAST score
                    124
                    2.0e-63
E value
                    276
Match length
```

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

86

% identity



76

Match length

% identity

## subunit mRNA, complete cds

```
37336
Seq. No.
                  LIB3073-004-Q1-K1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2815245
BLAST score
                  76
                  1.0e-34
E value
                  236
Match length
                  83
% identity
NCBI Description C.arietinum mRNA for class I type 2 metallothionein (clone:
                  CanMT-2)
                  37337
Seq. No.
                  LIB3073-004-Q1-K1-C2
Seq. ID
                  BLASTX
Method
                  g4538959
NCBI GI
BLAST score
                  442
                  6.0e-44
E value
                  94
Match length
                  83
% identity
                  (AL049488) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  37338
                  LIB3073-004-Q1-K1-C3
Seq. ID
                  BLASTX
Method
                  q4115914
NCBI GI
                  170
BLAST score
E value
                  3.0e-12
                  80
Match length
                  45
% identity
                  (AF118222) contains similarity to Iron/Ascorbate family of
NCBI Description
                  oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85,
                  N=1) [Arabidopsis thaliana] >gi_4539410_emb_CAB40043.1_
                   (AL049524) putative Fe(II)/ascorbate oxidase [Arabidopsis
                  thaliana]
                  37339
Seq. No.
                  LIB3073-004-Q1-K1-D10
Seq. ID
                  BLASTN
Method
                  g169974
NCBI GI
                   245
BLAST score
                   1.0e-135
E value
                   377
Match length
                   91
% identity
NCBI Description Glycine max vspA gene, complete cds
                   37340
Seq. No.
                  LIB3073-004-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                   g100200
NCBI GI
                   196
BLAST score
                   1.0e-15
E value
```

NCBI Description chlorophyll a/b-binding protein type I precursor - tomato



```
Seq. No.
                  LIB3073-004-Q1-K1-F5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170057
                  43
BLAST score
                  3.0e-15
E value
Match length
                  51
                  96
% identity
                  Soybean ribulose 1,5-bisphosphate carboxylase small subunit
NCBI Description
                   (SRS4) gene, complete cds
                  37342
Seq. No.
Seq. ID
                  LIB3073-005-Q1-K1-D8
Method
                  BLASTN
                  q836895
NCBI GI
BLAST score
                   41
                   3.0e-14
E value
                   77
Match length
                   88
% identity
NCBI Description Saccharomyces cerevisiae CSP2 gene, complete cds
                   37343
Seq. No.
                   LIB3073-005-Q1-K1-F6
Seq. ID
Method
                   BLASTN
                   q170091
NCBI GI
BLAST score
                   142
                   3.0e-74
E value
                   258
Match length
                   89
% identity
NCBI Description Glycine max vegetative storage protein (vspB) gene,
                   complete cds
                   37344
Seq. No.
Seq. ID
                   LIB3073-005-Q1-K1-G9
Method
                   BLASTN
NCBI GI
                   g170091
BLAST score
                   297
                   1.0e-166
E value
                   393
Match length
% identity
                   94
NCBI Description Glycine max vegetative storage protein (vspB) gene,
                   complete cds
Seq. No.
                   37345
                   LIB3073-006-Q1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q132113
BLAST score
                   146
                   4.0e-15
E value
Match length
                   106
                   49
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 4 PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 4) >gi_68054_pir__RKSYS4
                   ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.1.1.39) small chain
                   precursor SRS4 - soybean >gi_170058 (M16889) ribulose
                   1,5-bisphosphate carboxylase [Glycine max]
```

>gi\_225579\_prf\_\_1306410A ribulose bisphosphate carboxylase



## S [Glycine max]

```
37346
Seq. No.
                  LIB3073-006-Q1-K1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g541943
BLAST score
                  164
                  1.0e-11
E value
                  66
Match length
                  53
% identity
                  metallothionein - soybean >gi_228682_prf__1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
                  37347
Seq. No.
                  LIB3073-006-Q1-K1-C10
Seq. ID
                  BLASTX
Method
                  q131397
NCBI GI
BLAST score
                  157
                  1.0e-10
E value
Match length
                  87
% identity
                  52
                  OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
NCBI Description
                  SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                  >gi_81480_pir__S00008 photosystem II oxygen-evolving
                  complex protein 3 precursor - spinach
                  >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the
                  photosynthetic oxygen- evolving protein (OEC) [Spinacia
                   oleracea] >gi_225597_prf__1307179B luminal protein 16kD
                   [Spinacia oleracea]
                   37348
Seq. No.
                   LIB3073-006-Q1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4567207
BLAST score
                   218
                   9.0e-18
E value
                   77
Match length
                   51
% identity
                  (AC007168) unknown protein [Arabidopsis thaliana]
NCBI Description
                   37349
Seq. No.
                   LIB3073-007-Q1-K1-C3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g11576
BLAST score
                   145
                   7.0e-76
E value
Match length
                   309
                   87
% identity
                   Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,
NCBI Description
                   NADH dehydrogenase and ORF
                   37350
Seq. No.
                   LIB3073-007-Q1-K1-D5
Seq. ID
                   BLASTN
Method
```

g169897

7.0e-24

58

NCBI GI

E value

BLAST score



Match length 130 % identity 86

NCBI Description G.max 28 kDa protein, complete cds

Seq. No.

37351

Seq. ID

LIB3073-008-Q1-K1-C1

Method NCBI GI BLAST score BLASTN g1055367

BLAST score 395 E value 0.0e+00 Match length 411 % identity 99

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No.

37352

Seq. ID

LIB3073-008-Q1-K1-G1

Method BLASTX
NCBI GI g3243234
BLAST score 200
E value 9.0e-16
Match length 74
% identity 59

NCBI Description (AF071477) isoflavone reductase related protein [Pyrus

communis]

Seq. No.

37353

Seq. ID

LIB3073-008-Q1-K1-G8

Method BLASTN
NCBI GI g1885374
BLAST score 50
E value 2.0e-19
Match length 50
% identity 100

NCBI Description

Glycine soja small subunit ribosomal RNA gene, partial sequence, internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence,

and large subunit ribosomal RNA gene, partial se

Seq. No.

37354

Seq. ID

LIB3073-008-Q1-K1-H5

Method BLASTN
NCBI GI g1079735
BLAST score 120
E value 3.0e-61
Match length 188
% identity 91

NCBI Description Glycine soja ribulose 1,5-bisphosphate carboxylase small

subunit precursor (rbcS) gene, nuclear gene encoding

chloroplast protein, complete cds

Seq. No.

37355

Seq. ID

LIB3073-009-Q1-K1-A10

Method BLASTX
NCBI GI g2500380
BLAST score 180
E value 1.0e-13



Match length 57 % identity 61

% identity 61
NCBI Description 60S RIBO

60S RIBOSOMAL PROTEIN L44 >gi\_2119128\_pir\_\_ JC4923 ribosomal protein RL44 - upland cotton >gi\_1553129 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi\_1553131

(U64678) ribosomal protein L44 isoform b [Gossypium

hirsutum]

Seq. No. 37356

Seq. ID LIB3073-009-Q1-K1-H11

Method BLASTN
NCBI GI g1055367
BLAST score 206
E value 1.0e-112
Match length 270
% identity 94

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 37357

Seq. ID LIB3073-010-Q1-K1-A6

Method BLASTN
NCBI GI g1055367
BLAST score 240
E value 1.0e-132
Match length 363
% identity 92

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 37358

Seq. ID LIB3073-010-Q1-K1-B1

Method BLASTX
NCBI GI g567893
BLAST score 205
E value 3.0e-16
Match length 97
% identity 24

NCBI Description (L37382) beta-galactosidase-complementation protein

[Cloning vector]

Seq. No. 37359

Seq. ID LIB3073-010-Q1-K1-B8

Method BLASTN
NCBI GI g170091
BLAST score 352
E value 0.0e+00
Match length 392
% identity 97

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 37360

Seq. ID LIB3073-010-Q1-K1-C7

Method BLASTN
NCBI GI g170073
BLAST score 49

E value 1.0e-18
Match length 169
% identity 82

NCBI Description Soybean calmodulin (SCaM-3) mRNA, complete cds

Seq. No. 37361

Seq. ID LIB3073-010-Q1-K1-D9

Method BLASTX
NCBI GI g2879811
BLAST score 267
E value 2.0e-23
Match length 100
% identity 58

NCBI Description (AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No. 37362

Seq. ID LIB3073-010-Q1-K1-E12

Method BLASTX
NCBI GI g508304
BLAST score 150
E value 1.0e-09
Match length 72
% identity 51

NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 37363

Seq. ID LIB3073-010-Q1-K1-H7

Method BLASTX
NCBI GI g121080
BLAST score 144
E value 3.0e-09
Match length 80
% identity 45

NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR

>gi\_1070638\_pir\_\_GCPMH glycine cleavage system protein H precursor - garden pea >gi\_20737\_emb\_CAA45978\_ (X64726) H protein [Pisum sativum] >gi\_169093 (J05164) H-protein of glycine decarboxylase precursor (EC 2.1.2.10) [Pisum

sativum] >gi 287815 emb CAA37704 (X53656) H-protein [Pisum

sativum]

Seq. No. 37364

Seq. ID LIB3073-011-Q1-K1-C9

Method BLASTN
NCBI GI g170089
BLAST score 125
E value 6.0e-64
Match length 325
% identity 85

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No. 37365

Seq. ID LIB3073-011-Q1-K1-D10

Method BLASTX
NCBI GI g2879811
BLAST score 143
E value 3.0e-09

Match length 56 % identity

(AJ223316) ribosomal protein L30 [Lupinus luteus] NCBI Description

Seq. No.

37366

Seq. ID

LIB3073-011-Q1-K1-H9

Method NCBI GI BLASTN q2055227

BLAST score E value

255

Match length % identity

1.0e-141 324 99

NCBI Description Glycine max mRNA for SRC1, complete cds

Seq. No.

37367

Seq. ID

LIB3073-012-Q1-K1-B12

Method NCBI GI BLASTN q2995809

BLAST score

36

E value Match length 4.0e-11

% identity

52 92

NCBI Description

Trifolium albopurpureum 18S ribosomal RNA gene, partial

sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence;

and 26S ribosomal RNA gene, partial sequence

Seq. No.

37368

Seq. ID

LIB3073-012-Q1-K1-H11

BLASTX Method g1632831 NCBI GI 150 BLAST score E value

7.0e-10 76 Match length 43 % identity

(Z49698) orf [Ricinus communis] NCBI Description

Seq. No.

37369

Seq. ID

LIB3073-013-Q1-K1-A1

BLASTX Method q4185505 NCBI GI 161 BLAST score 6.0e-11 E value Match length 38 % identity

NCBI Description

(AF101038) nonspecific lipid-transfer protein precursor

[Brassica napus]

Seq. No.

37370

Seq. ID

LIB3073-013-Q1-K1-A11

Method BLASTX q1916809 NCBI GI BLAST score 279 E value 9.0e-32 118 Match length % identity 57

NCBI Description (U81163) auxin-binding protein [Prunus persica]



```
37371
Seq. No.
                   LIB3073-013-Q1-K1-D5
Seq. ID
                   BLASTX
Method
                   g134145
NCBI GI
                   302
BLAST score
                   2.0e-27
E value
                   123
Match length
                   53
% identity
                   STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE
NCBI Description
                   PROTEIN A) >gi_99886_pir__S08511 28K protein - soybean
                   >gi_169898 (M37530) 28 kDa protein [Glycine max] >gi_169975
                   (M76981) vegetative storage protein [Glycine max]
                   >gi_226867_prf__1609232B 28kD glycoprotein [Glycine max]
>gi_444325_prf__1906374A vegetative storage protein
                   [Glycine max]
                   37372
Seq. No.
                   LIB3073-013-Q1-K1-G10
Seq. ID
                   BLASTN
Method
                   g170067
NCBI GI
                   96
BLAST score
                   4.0e-47
E value
                   120
Match length
                   95
% identity
                   Soybean (G.max) proline-rich cell wall protein (SbPRP3)
NCBI Description
                   gene, complete cds
                   37373
Seq. No.
                   LIB3073-014-Q1-K1-B4
Seq. ID
                   BLASTN
Method
                   q1055367
NCBI GI
                    246
BLAST score
                    1.0e-136
E value
Match length
                    276
                    97
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                    subunit mRNA, complete cds
                    37374
Seq. No.
                    LIB3073-015-Q1-K1-A1
Seq. ID
                    BLASTN
Method
                    q38422
NCBI GI
                    36
BLAST score
                    5.0e-11
E value
                    128
Match length
% identity
NCBI Description H.sapiens mRNA for ribosomal protein S18
                    37375
Seq. No.
Seq. ID
                    LIB3073-015-Q1-K1-A2
                    BLASTN
Method
                    q1794146
NCBI GI
                    46
BLAST score
```

1.0e-16

66

92

E value Match length

% identity

```
NCBI Description Carrot mRNA for root specific gene, complete cds
                  37376
Seq. No.
                  LIB3073-015-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                  g131385
NCBI GI
BLAST score
                  132
                  8.0e-09
E value
                  94
Match length
                  43
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN)
                  37377
Seq. No.
                  LIB3073-015-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1945611
                  236
BLAST score
                  8.0e-20
E value
                  130
Match length
% identity
                  (AB003103) 26S proteasome subunit p55 [Homo sapiens]
NCBI Description
```

NCBI Description (AB003103) 26S proteasome subunit p55 [Homo sapiens]
>gi\_4506221\_ref\_NP\_002807.1\_pPSMD12\_ proteasome (prosome,
macropain) 26S subunit, non-ATPase,

Seq. No. 37378

Seq. ID LIB3073-015-Q1-K1-H12

Method BLASTN
NCBI GI g506628
BLAST score 84
E value 2.0e-39
Match length 120
% identity 93

NCBI Description Glycine max cv. Dare photosystem II type I chlorophyll

a/b-binding protein (lhcb1\*7) gene, complete cds

Seq. No. 37379

Seq. ID LIB3073-015-Q1-K1-H4

Method BLASTN
NCBI GI g598848
BLAST score 41
E value 5.0e-14
Match length 65
% identity 91

NCBI Description Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No. 37380

Seq. ID LIB3073-016-Q1-K1-C1

Method BLASTN
NCBI GI g170087
BLAST score 106
E value 1.0e-52
Match length 174
% identity 90

NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)



```
Seq. No.
Seq. ID
                  LIB3073-016-Q1-K1-G6
                  BLASTN
Method
                  g170067
NCBI GI
                  55
BLAST score
                  4.0e-22
E value
                  59
Match length
                  98
% identity
                  Soybean (G.max) proline-rich cell wall protein (SbPRP3)
NCBI Description
                  gene, complete cds
                  37382
Seq. No.
                  LIB3073-017-Q1-K1-A3
Seq. ID
Method
                  BLASTN
                  g169364
NCBI GI
                  80
BLAST score
                  6.0e-37
E value
                  191
Match length
                  86
% identity
                  Phaseolus vulgaris 5.8 Kb basic protein (PR4) gene,
NCBI Description
                  complete cds. >gi_217988 dbj_D12914 PHVPVPR4 Phaseolus
                  vulgaris PvPR4 mRNA for 5.8 kb basic protein, complete cds
                   37383
Seq. No.
                  LIB3073-017-Q1-K1-B11
Seq. ID
                  BLASTN
Method
                   g2565428
NCBI GI
                   38
BLAST score
                   4.0e-12
E value
                   101
Match length
                   86
% identity
                   Onobrychis viciifolia glycine-rich protein mRNA, complete
NCBI Description
                   cds
                   37384
Seq. No.
                   LIB3073-017-Q1-K1-B5
Seq. ID
                   BLASTN
Method
                   q1079735
NCBI GI
BLAST score
                   109
                   1.0e-54
E value
                   217
Match length
                   88
% identity
                   Glycine soja ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit precursor (rbcS) gene, nuclear gene encoding
                   chloroplast protein, complete cds
                   37385
Seq. No.
                   LIB3073-017-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   g1169186
NCBI GI
BLAST score
                   215
                   2.0e-17
E value
```

Match length 63 % identity 59

NCBI Description THIOL PROTEASE SEN102 PRECURSOR >gi\_1085732\_pir\_\_S36421

cysteine proteinase - Hemerocallis sp

>gi 1364024 pir S57777 cysteine protease precursor -



Hemerocallis x hybrida >gi\_396568\_emb\_CAA52425\_ (X74406)
thiol-protease [Hemerocallis sp.]

 Seq. No.
 37386

 Seq. ID
 LIB3073-017-Q1-K1-C9

 Method
 BLASTN

 MEDIT GT
 170053

NCBI GI g170053
BLAST score 98
E value 7.0e-48
Match length 179
% identity 89

NCBI Description Soybean ribosomal protein S11 mRNA, 3' end

Seq. No. 37387

Seq. ID LIB3073-017-Q1-K1-D8

Method BLASTN
NCBI GI g1055367
BLAST score 270
E value 1.0e-150
Match length 370
% identity 93

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 37388

Seq. ID LIB3073-017-Q1-K1-E11

Method BLASTN
NCBI GI g170091
BLAST score 184
E value 4.0e-99
Match length 364
% identity 89

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 37389

Seq. ID LIB3073-017-Q1-K1-F3

Method BLASTN
NCBI GI g1055367
BLAST score 137
E value 4.0e-71
Match length 177
% identity 94

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 37390

Seq. ID LIB3073-017-Q1-K1-F9

Method BLASTX
NCBI GI g3080415
BLAST score 205
E value 1.0e-16
Match length 45
% identity 78

NCBI Description (AL022604) cysteine proteinase - like protein [Arabidopsis

thaliana]

NCBI GI

BLAST score

g170091 215



```
Seq. No.
                  LIB3073-018-Q1-K1-D9
Seq. ID
                  BLASTN
Method
                  g169974
NCBI GI
                  145
BLAST score
                  7.0e-76
E value
                  233
Match length
                  94
% identity
NCBI Description Glycine max vspA gene, complete cds
                  37392
Seq. No.
                  LIB3073-018-Q1-K1-G7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g473604
                  73
BLAST score
                  8.0e-33
E value
Match length
                  133
% identity
                  89
NCBI Description Zea mays W-22 histone H2B mRNA, complete cds
Seq. No.
                   37393
Seq. ID
                  LIB3073-018-Q1-K1-H3
Method
                  BLASTN
                   g170067
NCBI GI
BLAST score
                   148
                   1.0e-77
E value
Match length
                   340
% identity
                   86
                  Soybean (G.max) proline-rich cell wall protein (SbPRP3)
NCBI Description
                   gene, complete cds
Seq. No.
                   37394
                   LIB3073-019-Q1-K1-A11
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1055367
                   185
BLAST score
                   1.0e-99
E value
                   289
Match length
% identity
                   91
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   37395
Seq. No.
Seq. ID
                   LIB3073-019-Q1-K1-C5
                   BLASTN
Method
                   g2879810
NCBI GI
                   62
BLAST score
                   2.0e-26
E value
                   139
Match length
                   85
% identity
NCBI Description Lupinus luteus mRNA for ribosomal protein L30
                   37396
Seq. No.
                   LIB3073-019-Q1-K1-G1
Seq. ID
Method
                   BLASTN
```

```
1.0e-117
E value
Match length
                  341
% identity
                  91
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
Seq. No.
                  37397
Seq. ID
                  LIB3073-020-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  g231660
BLAST score
                  176
E value
                  9.0e-13
Match length
                  89
                  48
% identity
NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
                  37398
Seq. No.
Seq. ID
                  LIB3073-020-Q1-K1-F1
Method
                  BLASTN
                  q170067
NCBI GI
BLAST score
                  154
                   3.0e-81
E value
Match length
                  329
% identity
                  87
NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP3)
                  gene, complete cds
                   37399
Seq. No.
Seq. ID
                  LIB3073-020-Q1-K1-H2
Method
                  BLASTN
NCBI GI
                  g170067
                  108
BLAST score
E value
                   6.0e-54
Match length
                   224
% identity
                  87
                  Soybean (G.max) proline-rich cell wall protein (SbPRP3)
NCBI Description
                   gene, complete cds
Seq. No.
                   37400
                  LIB3073-021-Q1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                   237
                   1.0e-130
E value
                  383
Match length
                   91
% identity
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   37401
Seq. ID
                  LIB3073-022-Q1-K1-A10
                  BLASTN
Method
NCBI GI
                  g169974
BLAST score
                   268
                  1.0e-149
E value
Match length
                   396
                   92
% identity
NCBI Description Glycine max vspA gene, complete cds
```



```
Seq. No.
                  37402
Seq. ID
                  LIB3073-023-Q1-K1-A11
Method
                  BLASTN
                  g18741
NCBI GI
                  44
BLAST score
E value
                  6.0e-16
                  140
Match length
                  83
% identity
                  Glycine max gene encoding ribulose-1,5-bisphosphate
NCBI Description
                  carboxylase small subunit
Seq. No.
                  37403
Seq. ID
                  LIB3073-023-Q1-K1-B2
Method
                  BLASTN
                  g11576
NCBI GI
                  89
BLAST score
E value
                  2.0e-42
Match length
                  93
                  99
% identity
                  Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,
NCBI Description
                  NADH dehydrogenase and ORF
Seq. No.
                   37404
                  LIB3073-023-Q1-K1-B9
Seq. ID
Method
                  BLASTN
                   q18741
NCBI GI
                   166
BLAST score
E value
                   2.0e-88
                   344
Match length
% identity
                  Glycine max gene encoding ribulose-1,5-bisphosphate
NCBI Description
                   carboxylase small subunit
                   37405
Seq. No.
                   LIB3073-023-Q1-K1-H2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q18761
BLAST score
                   262
E value
                   1.0e-146
Match length
                   301
                   97
% identity
NCBI Description Soybean stem mRNA for 31 kD glycoprotein
                   37406
Seq. No.
                   LIB3073-024-Q1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1370287
                   249
BLAST score
E value
                   2.0e-41
Match length
                   111
                   79
% identity
NCBI Description (Z73553) core protein [Pisum sativum]
```

37407

BLASTN

LIB3073-024-Q1-K1-D1

Seq. No.

Seq. ID

Method



```
NCBI GI g169974
BLAST score 112
E value 3.0e-56
Match length 240
% identity 87
```

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 37408

Seq. ID LIB3073-024-Q1-K1-E7

Method BLASTX
NCBI GI g134145
BLAST score 106
E value 5.0e-11
Match length 103
% identity 52

NCBI Description STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE PROTEIN A) >gi 99886 pir S08511 28K protein - soybean

>gi\_169898 (M37530) 28 kDa protein [Glycine max] >gi\_169975

 $(M7\overline{6}981)$  vegetative storage protein [Glycine max]

>gi\_226867\_prf\_\_1609232B 28kD glycoprotein [Glycine max] >gi\_444325\_prf\_\_1906374A vegetative storage protein

[Glycine max]

Seq. No. 37409

Seq. ID LIB3073-025-Q1-K1-B1

Method BLASTX
NCBI GI g3914442
BLAST score 192
E value 6.0e-15
Match length 66
% identity 62

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)

>gi 1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No. 37410

Seg. ID LIB3073-025-Q1-K1-F3

Method BLASTN
NCBI GI g1055367
BLAST score 392
E value 0.0e+00
Match length 395
% identity 100

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 37411

Seq. ID LIB3073-025-Q1-K1-H12

Method BLASTN NCBI GI g2815245

BLAST score 87
E value 4.0e-41
Match length 250
% identity 84

NCBI Description C.arietinum mRNA for class I type 2 metallothionein (clone:

CanMT-2)



% identity

NCBI Description

```
Seq. No.
                   LIB3073-026-Q1-K1-B9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1055367
BLAST score
                   179
                   3.0e-96
E value
Match length
                   231
                   94
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
Seq. No.
                   37413
                   LIB3073-026-Q1-K1-D1
Seq. ID
Method
                   BLASTN
                   q2815245
NCBI GI
                   78
BLAST score
                   9.0e-36
E value
Match length
                   250
% identity
                   C.arietinum mRNA for class I type 2 metallothionein (clone:
NCBI Description
                   CanMT-2)
Seq. No.
                   37414
                   LIB3073-026-Q1-K1-E3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1055367
BLAST score
                   322
                   0.0e + 00
E value
Match length
                   362
                   97
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
Seq. No.
                   37415
Seq. ID
                   LIB3073-026-Q1-K1-E4
Method
                   BLASTX
NCBI GI
                   g132086
                   240
BLAST score
E value
                   1.0e-21
                   111
Match length
                   57
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT 1) >gi_68053_pir__RKSYS
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{EC} 4.\overline{1}.1.39) small chain
                   precursor SRS1 - soybean >gi_18742_emb_CAA23736_ (V00458)
                   rubpcase [Glycine max]
                   37416
Seq. No.
                   LIB3073-026-Q1-K1-H10
Seq. ID
                   BLASTN
Method
                   g984307
NCBI GI
                   132
BLAST score
                    4.0e-68
E value
                   250
Match length
```

Glycine max ribosomal protein S16 (rps16) gene, partial

cds, beta-carboxyltransferase (accD), photosystem I



component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precurso

37417 Seq. No. LIB3073-026-Q1-K1-H4 Seq. ID Method BLASTN g170091 NCBI GI BLAST score 62 2.0e-26 E value 170 Match length 85 % identity NCBI Description Glycine max vegetative storage protein (vspB) gene, complete cds 37418 Seq. No. LIB3074-003-Q1-K1-A11 Seq. ID Method BLASTX g3717987 NCBI GI BLAST score 141 E value 3.0e-09 Match length 64 59 % identity (AJ005899) G subunit of Vacuolar-type H+-ATPase [Nicotiana NCBI Description tabacum] 37419 Seq. No. LIB3074-003-Q1-K1-B9 Seq. ID Method BLASTN g18571 NCBI GI BLAST score 146 2.0e-76 E value Match length 302 87 % identity NCBI Description G.max D-II mRNA for proteinase isoinhibitor D-II Seq. No. 37420 Seq. ID LIB3074-003-Q1-K1-D4 Method BLASTX NCBI GI a531829 BLAST score 190 1.0e-14 E value 78 Match length % identity 54

NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector pSport1]

Seq. No. 37421

Seq. ID LIB3074-003-Q1-K1-G10

Method BLASTN
NCBI GI g169974
BLAST score 81
E value 1.0e-37
Match length 112
% identity 93

NCBI Description Glycine max vspA gene, complete cds



```
Seq. No.
                  LIB3074-004-Q1-K1-B11
Seq. ID
                  BLASTN
Method
                  g170089
NCBI GI
BLAST score
                  330
                  0.0e+00
E value
                  337
Match length
                  99
% identity
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
                  37423
Seq. No.
Seq. ID
                  LIB3074-004-Q1-K1-B8
Method
                  BLASTN
                  g170087
NCBI GI
                  221
BLAST score
                  1.0e-121
E value
Match length
                  241
% identity
                  98
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
Seq. No.
                  37424
Seq. ID
                  LIB3074-004-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  g2982289
BLAST score
                   450
                   6.0e-45
E value
Match length
                   91
% identity
                   95
                  (AF051229) 60S ribosomal protein L17 [Picea mariana]
NCBI Description
                   37425
Seq. No.
                   LIB3074-004-Q1-K1-E11
Seq. ID
Method
                   BLASTX
                   g3283409
NCBI GI
BLAST score
                   171
                   3.0e-12
E value
                   63
Match length
                   57
% identity
                   (AF068754) heat shock factor binding protein 1 HSBP1 [Homo
NCBI Description
                   sapiens] >gi_4557647_ref_NP_001528.1_pHSBP1_ heat shock
                   factor binding protein
                   37426
Seq. No.
Seq. ID
                   LIB3074-004-Q1-K1-E4
                   BLASTN
Method
                   q1055367
NCBI GI
BLAST score
                   266
                   1.0e-148
E value
                   326
Match length
                   95
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   37427
Seq. No.
Seq. ID
                   LIB3074-004-Q1-K1-F1
```

BLASTN

g456713

Method NCBI GI



```
BLAST score
E value
                   4.0e-42
Match length
                   120
                   27
% identity
NCBI Description Glycine max gene for ubiquitin, complete cds
Seq. No.
                   LIB3074-004-Q1-K1-F4
Seq. ID
Method
                   BLASTX
                   q3021348
NCBI GI
BLAST score
                   213
E value
                   4.0e-17
Match length
                   98
                   50
% identity
NCBI Description (AJ004961) ribosomal protein L18 [Cicer arietinum]
                   37429
Seq. No.
                   LIB3074-004-Q1-K1-F8
Seq. ID
Method
                   BLASTX
                   g2493694
NCBI GI
BLAST score
                   204
                   4.0e-16
E value
                   103
Match length
% identity
                    43
NCBI Description PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII
                   6.1 KD PROTEIN) >gi_1076268_pir__S53025 photosystem II protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein
                    of photosystem II [Spinacia oleracea]
Seq. No.
                    37430
                   LIB3074-004-Q1-K1-G1
Seq. ID
Method
                   BLASTX
                    q2677830
NCBI GI
BLAST score
                    182
                    2.0e-13
E value
Match length
                    38
% identity
                   (U93168) ribosomal protein L12 [Prunus armeniaca]
NCBI Description
Seq. No.
                    37431
                    LIB3074-004-Q1-K1-G12
Seq. ID
Method
                    BLASTN
NCBI GI
                    g2924257
BLAST score
                    58
E value
                    6.0e-24
Match length
                    118
                    87
% identity
                   Tobacco chloroplast genome DNA
NCBI Description
```

Seq. No. 37432

LIB3074-004-Q1-K1-G6 Seq. ID

Method BLASTX NCBI GI g3914472 BLAST score 218 E value 9.0e-18 Match length 94 54 % identity

5751

NCBI Description





```
PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)
NCBI Description
                   >gi_322764_pir__S32021 photosystem II 10K protein - common
                   tobacco > g\bar{i}_22\overline{66}9_emb_CAA49693_ (X70088) NtpII10 [Nicotiana
                   tabacum]
Seq. No.
                   37433
                  LIB3074-004-Q1-K1-H7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g310575
BLAST score
                   66
E value
                  8.0e-29
Match length
                   172
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
Seq. No.
                   37434
Seq. ID
                   LIB3074-009-Q1-E1-C11
Method
                   BLASTX
NCBI GI
                   g746510
BLAST score
                   263
                   6.0e-23
E value
                   95
Match length
% identity
                   52
                   (U23517) similar to ubiquitin conjugating enzyme
NCBI Description
                   [Caenorhabditis elegans]
Seq. No.
                   37435
Seq. ID
                   LIB3074-009-Q1-E1-C7
Method
                   BLASTN
NCBI GI
                   g531828
BLAST score
                   48
                   4.0e-18
E value
Match length
                   96
% identity
                   88
NCBI Description Cloning vector pSport1, complete cds
                   37436
Seq. No.
Seq. ID
                   LIB3074-009-Q1-E1-C8
Method
                   BLASTN
                   g169974
NCBI GI
BLAST score
                   106
                   8.0e-53
E value
                   190
Match length
% identity
                   90
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   37437
                   LIB3074-009-Q1-E1-D6
Seq. ID
                   BLASTX
Method
                   g2347088
NCBI GI
                   140
BLAST score
                   5.0e-09
E value
                   47
Match length
                   57
% identity
                   (U72765) non-specific lipid transfer protein PvLTP-24
```

[Phaseolus vulgaris]



```
Seq. No.
                  LIB3074-009-Q1-E1-G5
Seq. ID
                  BLASTN
Method
                  q984889
NCBI GI
                  54
BLAST score
                  2.0e-21
E value
                   206
Match length
% identity
                   82
NCBI Description Plasmid pBSL119 cloning vector, complete sequence
Seq. No.
                   37439
Seq. ID
                   LIB3074-009-Q1-E1-G7
Method
                  BLASTN
NCBI GI
                   g169974
BLAST score
                   288
                   1.0e-161
E value
Match length
                   396
% identity
                   93
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   37440
Seq. ID
                   LIB3074-009-Q1-E1-H12
Method
                   BLASTX
NCBI GI
                   g2495889
BLAST score
                   141
                   9.0e-09
E value
Match length
                   62
                   42
% identity
                   HYPOTHETICAL PROTEIN MJ0284 >gi_2128214_pir__E64335
NCBI Description
                   hypothetical protein MJ0284 - Methanococcus jannaschii
                   >gi 1499066 (U67483) conserved hypothetical protein
                   [Methanococcus jannaschii]
                   37441
Seq. No.
                   LIB3074-010-Q1-E1-E12
Seq. ID
Method
                   BLASTN
                   q11576
NCBI GI
                   41
BLAST score
                   5.0e-14
E value
                   177
Match length
% identity
                   Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,
NCBI Description
                   NADH dehydrogenase and ORF
                   37442
Seq. No.
Seq. ID
                   LIB3074-010-Q1-E1-F2
Method
                   BLASTN
                   g169974
NCBI GI
BLAST score
                   162
                   6.0e-86
E value
                   304
Match length
                   94
% identity
NCBI Description Glycine max vspA gene, complete cds
```

37443

BLASTN

LIB3074-010-Q1-E1-G1

Seq. No. Seq. ID

Method



NCBI GI g169974
BLAST score 101
E value 7.0e-50
Match length 177
% identity 89

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 37444

Seq. ID LIB3074-010-Q1-E1-G12

Method BLASTN
NCBI GI g169974
BLAST score 90
E value 3.0e-43
Match length 214
% identity 86

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 37445

Seq. ID LIB3074-010-Q1-E1-G3

Method BLASTX
NCBI GI g3914136
BLAST score 111
E value 9.0e-11
Match length 94
% identity 48

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)

>gi 2632171 emb CAA05771\_ (AJ002958) lipid transfer protein

[Cicer arietinum]

Seq. No. 37446

Seq. ID LIB3074-010-Q1-E1-G7

Method BLASTX
NCBI GI g400198
BLAST score 158
E value 1.0e-10
Match length 105
% identity 37

NCBI Description PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)

(LIGHT-REGULATED UNKNOWN 11 KD PROTEIN)

>gi\_99604\_pir\_\_S21023 hypothetical protein - upland cotton
>gi\_1361978\_pir\_\_A57500 photosystem II protein psbT upland cotton >gi\_18512\_emb\_CAA38027\_ (X54092) unknown

reading frame [Gossypium hirsutum]

Seq. No. 37447

Seq. ID LIB3074-010-Q1-E1-H12

Method BLASTX
NCBI GI g100602
BLAST score 174
E value 6.0e-13
Match length 76
% identity 45

NCBI Description infection-related protein - barley

Seq. No. 37448

Seq. ID LIB3074-011-Q1-E1-F12

Method BLASTN



```
q1053215
  NCBI GI
                    125
  BLAST score
                    2.0e-64
  E value
                    125
  Match length
                    100
  % identity
                    Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
  NCBI Description
                    nuclear gene encoding chloroplast protein, complete cds
  Seq. No.
                    LIB3074-011-Q1-E1-H1
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                    g2826900
  BLAST score
                     386
                     1.0e-37
  E value
  Match length
                     101
                     75
  % identity
                     (AB004461) DNA polymerase alpha catalytic subunit [Oryza
  NCBI Description
  Seq. No.
                     37450
  Seq. ID
                     LIB3074-012-Q1-E1-C6
  Method
                     BLASTX
  NCBI GI
                     q2055228
  BLAST score
                     201
  E value
                     7.0e-16
                     79
  Match length
  % identity
  NCBI Description
                     (AB000129) SRC1 [Glycine max]
  Seq. No.
                     37451
                     LIB3074-012-Q1-E1-C8
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     g11576
                     57
  BLAST score
  E value
                     2.0e-23
  Match length
                     249
  % identity
                     Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,
  NCBI Description
                     NADH dehydrogenase and ORF
  Seq. No.
                     37452
                     LIB3074-012-Q1-E1-D8
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g3980238
  BLAST score
                     169
                     7.0e-12
  E value
                     53
  Match length
  % identity
                     62
                    (Z21677) ribosomal protein L18 [Thermotoga maritima]
  NCBI Description
                     37453
  Seq. No.
Seq. ID
                     LIB3074-012-Q1-E1-F8
                     BLASTN
  Method
  NCBI GI
                     g170091
  BLAST score
                     212
  E value
                     1.0e-116
```

Match length



% identity 89

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 37454

Seq. ID LIB3074-012-Q1-E1-G8

Method BLASTX
NCBI GI g3334113
BLAST score 376
E value 3.0e-36
Match length 87
% identity 80

NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)

acyl-CoA-binding protein [Gossypium hirsutum]

Seq. No. 37455

Seq. ID LIB3074-012-Q1-E1-H9

Method BLASTX
NCBI GI g3168840
BLAST score 257
E value 2.0e-22
Match length 67
% identity 70

NCBI Description (U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No. 37456

Seq. ID LIB3074-017-Q1-E1-A11

Method BLASTX
NCBI GI g3461836
BLAST score 172
E value 1.0e-12
Match length 66
% identity 56

NCBI Description (AC005315) putative protein kinase [Arabidopsis thaliana]

>gi 3927841 (AC005727) putative protein kinase [Arabidopsis

thaliana]

Seq. No. 37457

Seq. ID LIB3074-017-Q1-E1-A2

Method BLASTN
NCBI GI g169974
BLAST score 245
E value 1.0e-135
Match length 357
% identity 92

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 37458

Seq. ID LIB3074-017-Q1-E1-B2

Method BLASTX
NCBI GI g3892056
BLAST score 173
E value 2.0e-12
Match length 86
% identity 47

NCBI Description (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]



```
Seq. No.
                  LIB3074-017-Q1-E1-B5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g170091
BLAST score
                  60
                  3.0e-25
E value
Match length
                  208
                  82
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
Seq. No.
                   37460
Seq. ID
                  LIB3074-017-Q1-E1-E7
                  BLASTX
Method
                   q2499966
NCBI GI
                   144
BLAST score
                   6.0e-12
E value
Match length
% identity
                   60
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E
NCBI Description
                   A) >gi_632722_bbs_151001 (S72356) photosystem I subunit
                   PSI-E Nicotiana sylvestris, leaves, Peptide Chloroplast,
                   141 aa] [Nicotiana sylvestris]
                   37461
Seq. No.
                   LIB3074-017-Q1-E1-F1
Seq. ID
                   BLASTX
Method
                   q2431767
NCBI GI
BLAST score
                   106
                   7.0e-09
E value
                   86
Match length
                   52
% identity
                   (U62751) acidic ribosomal protein P3a [Zea mays]
NCBI Description
                   37462
Seq. No.
                   LIB3074-017-Q1-E1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4098517
BLAST score
                   260
                   6.0e-23
E value
                   85
Match length
                   65
% identity
                   (U79114) auxin-binding protein ABP19 [Prunus persica]
NCBI Description
                   37463
Seq. No.
                   LIB3074-017-Q1-E1-G2
Seq. ID
Method
                   BLASTN
                   g1055367
NCBI GI
                   179
BLAST score
                   4.0e-96
E value
                   323
Match length
                   89
 % identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
```

LIB3074-017-Q1-E1-H1

Seq. No.

Seq. ID

```
BLASTX
Method
NCBI GI
                  q541943
                  280
BLAST score
                  5.0e-25
E value
                  73
Match length
                  68
% identity
NCBI Description metallothionein - soybean >gi_228682_prf__1808316A
                  metallothionein-like protein [Glycine max]
                   37465
Seq. No.
                  LIB3074-017-Q1-E1-H2
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1055367
                   334
BLAST score
                   0.0e + 00
E value
                   413
Match length
% identity
NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small
                   subunit mRNA, complete cds
                   37466
Seq. No.
                   LIB3074-017-Q1-E1-H7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g541943
                   167
BLAST score
                   7.0e-12
E value
                   50
Match length
% identity
NCBI Description metallothionein - soybean >gi_228682 prf_ 1808316A
                   metallothionein-like protein [Glycine max]
                   37467
Seq. No.
                   LIB3074-018-Q1-E1-C9
Seq. ID
Method
                   BLASTN
                   g303900
NCBI GI
BLAST score
                   218
                   1.0e-119
E value
Match length
                   295
                   31
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
                   37468
Seq. No.
                   LIB3074-018-Q1-E1-F4
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1262439
                   391
BLAST score
                   0.0e + 00
E value
                   391
Match length
 % identity
                   Glycine max lipoxygenase (vlxC) mRNA, complete cds
 NCBI Description
                   37469
 Seq. No.
                   LIB3074-019-Q1-E1-A5
```

Seq. ID

BLASTN Method NCBI GI g169897 BLAST score 36 5.0e-11 E value



```
Match length
                  81
% identity
NCBI Description G.max 28 kDa protein, complete cds
                  37470
Seq. No.
                  LIB3074-019-Q1-E1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                  102
E value
                  2.0e-50
                  190
Match length
% identity
                  89
NCBI Description Glycine max vspA gene, complete cds
                  37471
Seq. No.
                  LIB3074-019-Q1-E1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g602358
BLAST score
                  37
                  1.0e-11
E value
                  79
Match length
                  87
% identity
NCBI Description P.sativum mRNA for type II chlorophyll a/b binding protein
Seq. No.
                  37472
                  LIB3074-020-Q1-E1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076696
BLAST score
                  103
                   5.0e-13
E value
Match length
                  120
% identity
                   42
NCBI Description cyprosin - cardoon >gi_556819 emb_CAA57510_ (X81984)
                  cyprosin [Cynara cardunculus]
Seq. No.
                   37473
                  LIB3074-020-Q1-E1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3319341
                   255
BLAST score
                   1.0e-22
E value
                   57
Match length
                   72
% identity
                   (AF077407) similar to Medicago sativa nucleic acid binding
NCBI Description
                   protein Alfin-1 (GB:L07291) [Arabidopsis thaliana]
```

Seq. No. 37474

Seq. ID LIB3074-020-Q1-E1-G3

Method BLASTN
NCBI GI g170067
BLAST score 52
E value 2.0e-20
Match length 112
% identity 87

NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP3)

gene, complete cds

```
37475
Seq. No.
                  LIB3074-021-Q1-E1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1236950
BLAST score
                  50
                  2.0e-19
E value
Match length
                  142
% identity
                  85
                  Glycine max nucleoside diphosphate kinase mRNA, complete
NCBI Description
                  37476
Seq. No.
                  LIB3074-022-Q1-E1-A1
                  BLASTN
                  q18551
                  398
                  0.0e+00
```

Seq. ID Method NCBI GI BLAST score E value Match length

413 % identity

NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

Seq. No. 37477 Seq. ID LIB3074-022-Q1-E1-A2 Method BLASTN NCBI GI g18551 BLAST score 151

2.0e-79 E value 259 Match length 90 % identity

Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding NCBI Description

protein

37478 Seq. No.

LIB3074-022-Q1-E1-A3 Seq. ID

Method BLASTN NCBI GI g18551 BLAST score 111 1.0e-55 E value Match length 255 % identity 86

NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

Seq. No. 37479

Seq. ID LIB3074-022-Q1-E1-A5

Method BLASTX NCBI GI g441457 BLAST score 144 E value 5.0e-11 Match length 63 % identity 62

NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon

esculentum]

Seq. No. 37480

Seq. ID LIB3074-022-Q1-E1-B5

BLAST score

E value

61

5.0e-26



```
Method
                  BLASTN
                  q397556
NCBI GI
                  117
BLAST score
                  4.0e-59
E value
Match length
                  201
% identity
                  90
NCBI Description N.tabacum psaH gene for photosystem I psaH protein
Seq. No.
                  37481
Seq. ID
                  LIB3074-022-Q1-E1-C5
Method
                  BLASTX
NCBI GI
                  q4098517
BLAST score
                  126
                  2.0e-09
E value
Match length
                  98
                   44
% identity
                  (U79114) auxin-binding protein ABP19 [Prunus persica]
NCBI Description
Seq. No.
Seq. ID
                  LIB3074-022-Q1-E1-D10
Method
                  BLASTN
NCBI GI
                   g3900979
BLAST score
                   33
E value
                   4.0e-09
Match length
                  77
                   86
% identity
                  Eichhornia crassipes mRNA for metallothionein-like protein,
NCBI Description
                   37483
Seq. No.
                   LIB3074-022-Q1-E1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4006858
BLAST score
                   179
E value
                   3.0e-13
Match length
                   92
% identity
                   43
                   (Z99707) cold acclimation protein homolog [Arabidopsis
NCBI Description
                   thaliana]
                   37484
Seq. No.
                   LIB3074-022-Q1-E1-G2
Seq. ID
                   BLASTN
Method
                   g1055367
NCBI GI
                   80
BLAST score
E value
                   3.0e-37
                   252
Match length
                   84
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   37485
Seq. No.
Seq. ID
                   LIB3074-023-Q1-E1-F11
                   BLASTN
Method
                   g2995842
NCBI GI
```



Match length % identity Trifolium stoloniferum 18S ribosomal RNA gene, partial NCBI Description sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence 37486 Seq. No. LIB3074-024-Q1-E1-F3 Seq. ID Method BLASTN q11576 NCBI GI BLAST score 82 E value 1.0e-38 Match length 146 % identity Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val, NCBI Description NADH dehydrogenase and ORF 37487 Seq. No. LIB3074-025-Q1-E1-A2 Seq. ID Method BLASTN g18551 NCBI GI BLAST score 129 E value 2.0e-66 Match length 232 % identity 95 Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding NCBI Description protein 37488 Seq. No. LIB3074-025-Q1-E1-B7 Seq. ID Method BLASTN NCBI GI g170091 254 BLAST score E value 1.0e-141 Match length 330 % identity 95 Glycine max vegetative storage protein (vspB) gene, NCBI Description complete cds 37489 Seq. No. LIB3074-025-Q1-E1-G1 Seq. ID BLASTN Method NCBI GI g11576 123 BLAST score

1.0e-62 E value 261 Match length 89 % identity

Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val, NCBI Description

NADH dehydrogenase and ORF

Seq. No.

37490

Seq. ID

LIB3074-025-Q1-E1-G10

BLASTX Method g2851508 NCBI GI BLAST score 231 1.0e-19 E value



Match length 66 % identity 61

NCBI Description 60S RIBOSOMAL PROTEIN L21 >gi\_2160162 (AC000132) Similar to

ribosomal protein L21 (gb L38826). ESTs

gb\_AA395597,gb\_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi\_3482935 (AC003970) Putative ribosomal protein

L21 [Arabidopsis thaliana]

Seq. No. 37491

Seq. ID LIB3074-025-Q1-E1-H8

Method BLASTN
NCBI GI g18551
BLAST score 203
E value 1.0e-110
Match length 255
% identity 95

NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

Seq. No. 37492

Seq. ID LIB3074-026-Q1-E1-A6

Method BLASTN
NCBI GI g170091
BLAST score 247
E value 1.0e-136
Match length 391
% identity 91

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 37493

Seq. ID LIB3074-026-Q1-E1-B1

Method BLASTN
NCBI GI g3021374
BLAST score 56
E value 7.0e-23
Match length 148
% identity 84

NCBI Description Glycine max mRNA for profilin, PRO1

Seq. No. 37494

Seq. ID LIB3074-026-Q1-E1-B2

Method BLASTX
NCBI GI g3237190
BLAST score 149
E value 1.0e-09
Match length 86
% identity 41

NCBI Description (AB014760) cystein proteinase inhibitor [Cucumis sativus]

Seq. No. 37495

Seq. ID LIB3074-026-Q1-E1-B3

Method BLASTN
NCBI GI g1236950
BLAST score 47

E value 2.0e-17 Match length 175



38

153

92

4.0e-12

BLAST score

% identity

E value Match length

% identity Glycine max nucleoside diphosphate kinase mRNA, complete NCBI Description cds 37496 Seq. No. Seq. ID LIB3074-026-Q1-E1-B6 Method BLASTN NCBI GI g343648 BLAST score 36 E value 7.0e-11 Match length 48 % identity 94 Vigna unquiculata chloroplast ribosomal protein (L16 and NCBI Description L14) genes, 3' and 5' end respectively Seq. No. 37497 Seq. ID LIB3074-026-Q1-E1-C1 Method BLASTX NCBI GI g3643607 BLAST score 299 E value 2.0e-27 Match length 84 % identity 39 NCBI Description (AC005395) unknown protein [Arabidopsis thaliana] Seq. No. 37498 Seq. ID LIB3074-026-Q1-E1-C7 Method BLASTX NCBI GI g543868 BLAST score 233 6.0e-20 E value Match length 67 % identity 64 ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL NCBI Description >gi 1076683 pir B47493 H+-transporting ATP synthase (EC 3.6.1.34) epsilon chain - sweet potato >gi\_303625\_dbj\_BAA03527\_ (D14700) F1-ATPase epsilon-subunit [Ipomoea batatas] 37499 Seq. No. Seq. ID LIB3074-026-Q1-E1-C9 Method BLASTN NCBI GI g169974 BLAST score 165 1.0e-87 E value 389 Match length 86 % identity NCBI Description Glycine max vspA gene, complete cds 37500 Seq. No. Seq. ID LIB3074-026-Q1-E1-E5 Method BLASTN NCBI GI g1053044



NCBI Description Glycine max histone H3 gene, partial cds, clone S1

Seq. No. 37501

Seq. ID LIB3074-026-Q1-E1-G1

Method BLASTX
NCBI GI g4539316
BLAST score 157
E value 1.0e-10
Match length 87
% identity 51

NCBI Description (AL035679) putative fructose-bisphosphate aldolase

[Arabidopsis thaliana]

Seq. No. 37502

Seq. ID LIB3074-028-Q1-K1-A3

Method BLASTX
NCBI GI g541943
BLAST score 126
E value 7.0e-13
Match length 63
% identity 67

NCBI Description metallothionein - soybean >gi\_228682\_prf\_\_1808316A

metallothionein-like protein [Glycine max]

Seq. No. 37503

Seq. ID LIB3074-028-Q1-K1-C7

Method BLASTX
NCBI GI g729479
BLAST score 147
E value 2.0e-09
Match length 113
% identity 31

NCBI Description FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi\_551131

(U14956) ferredoxin NADP+ reductase precursor [Vicia faba]

Seq. No. 37504

Seq. ID LIB3074-028-Q1-K1-D3

Method BLASTN
NCBI GI g728715
BLAST score 62
E value 3.0e-26
Match length 152
% identity 86

NCBI Description S.oleracea mRNA for 6.1 kDa polypeptide of photosystem II

Seq. No. 37505

Seq. ID LIB3074-028-Q1-K1-E10

Method BLASTX
NCBI GI g134145
BLAST score 222
E value 3.0e-18
Match length 72
% identity 64

NCBI Description STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE

PROTEIN A) >gi\_99886\_pir\_\_S08511 28K protein - soybean >gi 169898 (M37530) 28 kDa protein [Glycine max] >gi\_169975

(M76981) vegetative storage protein [Glycine max]



>gi\_226867\_prf\_\_1609232B 28kD glycoprotein [Glycine max]
>gi\_444325\_prf\_\_1906374A vegetative storage protein
[Glycine max]

Seq. No. 37506

Seq. ID LIB3074-028-Q1-K1-F12

Method BLASTX
NCBI GI g115797
BLAST score 364
E value 9.0e-35
Match length 99
% identity 70

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-215) (LHCP) >gi 100026 pir S16592 chlorophyll

a/b-binding protein - garden pea >gi\_20658\_emb\_CAA40365\_ (X57082) chlorophyll a/b-binding protein [Pisum sativum]

Seq. No. 37507

Seq. ID LIB3074-028-Q1-K1-F5

Method BLASTX
NCBI GI g3287270
BLAST score 203
E value 5.0e-16
Match length 111
% identity 26

NCBI Description (Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No. 37508

Seq. ID LIB3074-028-Q1-K1-H4

Method BLASTN
NCBI GI g18551
BLAST score 261
E value 1.0e-145
Match length 309
% identity 96

NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

Seq. No. 37509

Seq. ID LIB3074-028-Q1-K1-H5

Method BLASTX
NCBI GI g2959358
BLAST score 286
E value 1.0e-25
Match length 85
% identity 67

NCBI Description (X96758) clathrin coat assembly protein AP17 [Zea mays]

Seq. No.

Seq. ID LIB3074-029-Q1-K1-B4

37510

Method BLASTN
NCBI GI g169974
BLAST score 241
E value 1.0e-133
Match length 349
% identity 92

NCBI Description Glycine max vspA gene, complete cds

Seq. No.

Seq. ID

37516

LIB3074-030-Q1-K1-D3



```
Seq. No.
                    37511
  Seq. ID
                    LIB3074-029-Q1-K1-B5
  Method
                    BLASTN
NCBI GI
                    g170091
  BLAST score
                     90
  E value
                    3.0e-43
                    234
  Match length
  % identity
                    85
  NCBI Description
                    Glycine max vegetative storage protein (vspB) gene,
                    complete cds
  Seq. No.
                    37512
  Seq. ID
                    LIB3074-029-Q1-K1-F10
  Method
                    BLASTN
  NCBI GI
                    g1055367
  BLAST score
                    372
  E value
                    0.0e+00
  Match length
                    388
                    99
  % identity
  NCBI Description
                    Glycine max ribulose-1,5-bisphosphate carboxylase small
                    subunit mRNA, complete cds
  Seq. No.
                    37513
  Seq. ID
                    LIB3074-029-Q1-K1-F4
  Method
                    BLASTN
  NCBI GI
                    g2564044
  BLAST score
                    39
  E value
                    2.0e-12
  Match length
                    59
                    92
  % identity
  NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                    K19P17, complete sequence [Arabidopsis thaliana]
  Seq. No.
                    37514
  Seq. ID
                    LIB3074-030-Q1-K1-B2
  Method
                    BLASTN
                    g1277167
  NCBI GI
  BLAST score
                    52
  E value
                    1.0e-20
  Match length
                    160
  % identity
                    84
  NCBI Description Glycine max cysteine proteinase inhibitor mRNA, partial cds
  Seq. No.
                    37515
  Seq. ID
                    LIB3074-030-Q1-K1-B5
  Method
                    BLASTX
  NCBI GI
                    g3334113
  BLAST score
                    145
  E value
                    2.0e-09
  Match length
                    75
  % identity
                    41
  NCBI Description
                    ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
                    acyl-CoA-binding protein [Gossypium hirsutum]
```



```
Method
                   BLASTN
NCBI GI
                  g18741
BLAST score
                   46
                   5.0e-17
E value
Match length
                  182
                  81
% identity
NCBI Description
                  Glycine max gene encoding ribulose-1,5-bisphosphate
                  carboxylase small subunit
Seq. No.
                  37517
                  LIB3074-030-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4218120
BLAST score
                  107
                  5.0e-09
E value
Match length
                  72
% identity
                  53
NCBI Description
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  37518
Seq. ID
                  LIB3074-030-Q1-K2-C2
Method
                  BLASTX
NCBI GI
                  g2494174
BLAST score
                  302
E value
                  2.0e-27
Match length
                  95
% identity
                  62
NCBI Description
                  GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi 497979 (U10034)
                  glutamate decarboxylase [Arabidopsis Thaliana]
Seq. No.
                  37519
Seq. ID
                  LIB3074-030-Q1-K2-C5
Method
                  BLASTX
                  g4510363
NCBI GI
BLAST score
                  368
E value
                  3.0e-35
Match length
                  99
% identity
                  69
NCBI Description
                  (AC007017) putative DNA-binding protein [Arabidopsis
                  thaliana]
                  37520
Seq. No.
Seq. ID
                  LIB3074-030-Q1-K2-C8
Method
                  BLASTN
NCBI GI
                  g3135607
BLAST score
                  46
E value
                  6.0e-17
Match length
                  158
% identity
                  82
NCBI Description Cloning vector p34S-Tp, complete sequence
```

Seq. No. 37521

LIB3074-030-Q1-K2-D7 Seq. ID

Method BLASTN NCBI GI q170067 BLAST score 46



E value 9.0e-17
Match length 201
% identity 85

NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP3)

gene, complete cds \*

Seq. No. 37522

Seq. ID LIB3074-030-Q1-K2-E2

Method BLASTX
NCBI GI g4218120
BLAST score 179
E value 3.0e-13
Match length 53
% identity 62

NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis

thaliana]

Seq. No. 37523

Seq. ID LIB3074-030-Q1-K2-G2

Method BLASTX
NCBI GI g2407273
BLAST score 183
E value 1.0e-13
Match length 71
% identity 52

NCBI Description (AF017359) lipid transfer protein LPT II [Oryza sativa]

Seq. No. 37524

Seq. ID LIB3074-031-Q1-K1-A1

Method BLASTN
NCBI GI g18741
BLAST score 47
E value 6.0e-18
Match length 111
% identity 86

NCBI Description Glycine max gene encoding ribulose-1,5-bisphosphate

carboxylase small subunit

Seq. No. 37525

Seq. ID LIB3074-031-Q1-K1-H3

Method BLASTX
NCBI GI g322750
BLAST score 441
E value 6.0e-44
Match length 95
% identity 93

NCBI Description ubiquitin / ribosomal protein CEP52 - wood tobacco

>gi\_170217 (M74100) ubiquitin fusion protein [Nicotiana

sylvestris]

Seq. No. 37526

Seq. ID LIB3074-031-Q1-K2-A12

Method BLASTN
NCBI GI g18741
BLAST score 198
E value 1.0e-107
Match length 359



% identity 93

NCBI Description Glycine max gene encoding ribulose-1,5-bisphosphate

carboxylase small subunit

Seq. No. 37527

Seq. ID LIB3074-031-Q1-K2-B2

Method BLASTX
NCBI GI g4510379
BLAST score 257
E value 3.0e-22
Match length 82
% identity 59

NCBI Description (AC007017) hypothetical protein [Arabidopsis thaliana]

Seq. No. 37528

Seq. ID LIB3074-031-Q1-K2-C9

method BLASTN NCBL GI G1055367

NCBI GI g1055367 BLAST score 42 E value 7.0e-15 Match length 110 % identity 85

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 37529

Seq. ID LIB3074-031-Q1-K2-G1

Method BLASTN
NCBI GI g169897
BLAST score 102
E value 3.0e-50
Match length 172
% identity 95

NCBI Description G.max 28 kDa protein, complete cds

Seq. No. 37530

Seq. ID LIB3074-033-Q1-K1-A10

Method BLASTX
NCBI GI g2347088
BLAST score 146
E value 1.0e-09
Match length 61
% identity 49

NCBI Description (U72765) non-specific lipid transfer protein PvLTP-24

[Phaseolus vulgaris]

Seq. No. 37531

Seq. ID LIB3074-033-Q1-K1-C10

Method BLASTX
NCBI GI g2347088
BLAST score 157
E value 5.0e-11
Match length 47
% identity 66

NCBI Description (U72765) non-specific lipid transfer protein PvLTP-24

[Phaseolus vulgaris]

```
Seq. No.
                  LIB3074-033-Q1-K1-E5
Seq. ID
                  BLASTN
Method
                  g531828
NCBI GI
                  35
BLAST score
E value
                  2.0e-10
                  123
Match length
                  82
% identity
NCBI Description Cloning vector pSport1, complete cds
                  37533
Seq. No.
                  LIB3074-034-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q127289
BLAST score
                   200
                   2.0e-17
E value
Match length
                   123
% identity
                   44
                  MITOCHONDRIAL PROCESSING PEPTIDASE BETA SUBUNIT PRECURSOR
NCBI Description
                   (BETA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE
                   PROTEIN I) >gi 482261 pir A29881 mitochondrial processing
                   peptidase (EC 3.4.99.41) beta chain precursor - Neurospora
                   crassa >gi 168858 (M20928) processing enhancing protein
                   precursor [Neurospora crassa]
Seq. No.
                   37534
                   LIB3074-034-Q1-K1-C12
Seq. ID
Method
                   BLASTX
                   g730010
NCBI GI
BLAST score
                   143
                   2.0e-09
E value
                   62
Match length
% identity
                   53
                  MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                   37535
Seq. No.
                   LIB3074-034-Q1-K1-D10
Seq. ID
                   BLASTX
Method
                   g2956754
NCBI GI
                   161
BLAST score
                   2.0e-11
E value
                   54
Match length
% identity
                   61
                   (AL022104) 6-phosphofructokinase [Schizosaccharomyces
NCBI Description
                   pombe]
                   37536
Seq. No.
Seq. ID
                   LIB3074-035-Q1-K1-A6
```

Method BLASTN NCBI GI g1420884

BLAST score 49
E value 9.0e-19
Match length 89
% identity 89

NCBI Description Phaseolus vulgaris proline-rich 14 kDa protein mRNA,

complete cds



```
Seq. No.
                  LIB3074-035-Q1-K1-A9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1055367
                  48
BLAST score
                  3.0e-18
E value
                  136
Match length
                  84
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
                  37538
Seq. No.
                  LIB3074-035-Q1-K1-E1
Seq. ID
                  BLASTN
Method
                  g531828
NCBI GI
                  39
BLAST score
                  4.0e-13
E value
                  79
Match length
                  87
% identity
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  37539
                  LIB3074-035-Q1-K1-F9
Seq. ID
Method
                  BLASTN
                  q169974
NCBI GI
                  107
BLAST score
                   2.0e-53
E value
Match length
                  155
                   92
% identity
NCBI Description Glycine max vspA gene, complete cds
                   37540
Seq. No.
                   LIB3074-036-Q1-K1-A6
Seq. ID
                  BLASTN
Method
                   q456567
NCBI GI
                   93
BLAST score
                   8.0e-45
E value
                   200
Match length
                   89
% identity
                  Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
NCBI Description
                   cds
                   37541
Seq. No.
Seq. ID
                   LIB3074-036-Q1-K1-C10
                   BLASTN
Method
                   g169974
NCBI GI
BLAST score
                   74
                   2.0e-33
E value
                   201
Match length
                   85
% identity
```

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 37542

LIB3074-036-Q1-K1-F8 Seq. ID

BLASTN Method NCBI GI q169974 191 BLAST score



```
1.0e-103
E value
                  311
Match length
% identity
NCBI Description Glycine max vspA gene, complete cds
                  37543
Seq. No.
                  LIB3074-036-Q1-K1-H11
Seq. ID
                  BLASTN
Method
                  g2055227
NCBI GI
                  43
BLAST score
                  7.0e-15
E value
                  81
Match length
                  95
% identity
NCBI Description Glycine max mRNA for SRC1, complete cds
                   37544
Seq. No.
                  LIB3074-037-Q1-K1-A11
Seq. ID
                  BLASTX
Method
                  g2558539
NCBI GI
                  187
BLAST score
                   2.0e-14
E value
Match length
                   70
% identity
                   56
                   (Z29958) ubiquitin-ribosomal protein fusion protein [Gallus
NCBI Description
                   gallus]
                   37545
Seq. No.
                   LIB3074-037-Q1-K1-A12
Seq. ID
                   BLASTX
Method
                   g322750
NCBI GI
                   342
BLAST score
                   2.0e-32
E value
Match length
                   112
                   64
% identity
                   ubiquitin / ribosomal protein CEP52 - wood tobacco
NCBI Description
                   >gi 170217 (M74100) ubiquitin fusion protein [Nicotiana
                   sylvestris]
                   37546
Seq. No.
                   LIB3074-037-Q1-K1-A4
Seq. ID
                   BLASTN
Method
                   g170067
NCBI GI
                   109
BLAST score
                   2.0e-54
E value
                   288
Match length
                   91
% identity
NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP3)
                   gene, complete cds
                   37547
Seq. No.
Seq. ID
                   LIB3074-037-Q1-K1-A5
                   BLASTX
Method
NCBI GI
                   g2104959
BLAST score
                   180
```

2.0e-13

71

55

E value

Match length % identity

Seq. ID

Method



```
(U96925) immunophilin [Vicia faba]
NCBI Description
                  37548
Seq. No.
                  LIB3074-037-Q1-K1-B7
Seq. ID
                  BLASTN
Method
                  g343041
NCBI GI
BLAST score
                  39
                  1.0e-12
E value
                  126
Match length
% identity
                  88
NCBI Description Pisum sativum chloroplast Val-tRNA gene
                  37549
Seq. No.
                  LIB3074-037-Q1-K1-C1
Seq. ID
                  BLASTN
Method
                  g170089
NCBI GI
                  214
BLAST score
                   1.0e-117
E value
                  398
Match length
                   89
% identity
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
                   37550
Seq. No.
                   LIB3074-037-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   q169900
NCBI GI
                   127
BLAST score
                   5.0e-10
E value
                   74
Match length
                   54
% identity
NCBI Description (M37529) 31 kDa protein [Glycine max]
Seq. No.
                   37551
                   LIB3074-037-Q1-K1-D1
Seq. ID
                   BLASTN
Method
                   g1055367
NCBI GI
                   204
BLAST score
                   1.0e-111
E value
                   298
Match length
                   94
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   37552
Seq. No.
                   LIB3074-037-Q1-K1-D10
Seq. ID
                   BLASTN
Method
                   g1055367
NCBI GI
BLAST score
                   180
                   8.0e-97
E value
                   268
Match length
                   92
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   37553
Seq. No.
```

LIB3074-037-Q1-K1-H1

BLASTN

```
NCBI GI g1055367
BLAST score 82
E value 2.0e-38
Match length 154
% identity 88
NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds
```

 Seq. No.
 37554

 Seq. ID
 LIB3074-037-Q1-K1-H8

 Method
 BLASTN

NCBI GI g18741
BLAST score 177
E value 7.0e-95
Match length 257
% identity 96

NCBI Description Glycine max gene encoding ribulose-1,5-bisphosphate

carboxylase small subunit

 Seq. No.
 37555

 Seq. ID
 LIB3074-038-Q1-K1-A3

 Method
 BLASTN

 NCBI GI
 g170067

 BLAST score
 108

E value 7.0e-54
Match length 244
% identity 86

NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP3)

gene, complete cds

Seq. No. 37556

Seq. ID LIB3074-038-Q1-K1-B10

Method BLASTX
NCBI GI g1730118
BLAST score 158
E value 9.0e-11
Match length 58
% identity 60

NCBI Description FUMARATE HYDRATASE PRECURSOR (FUMARASE)

>gi 469103 emb CAA55314 (X78576) fumarase [Rhizopus

oryzae]

Seq. No. 37557

Seq. ID LIB3074-038-Q1-K1-D10

Method BLASTX
NCBI GI g136753
BLAST score 166
E value 1.0e-11
Match length 57
% identity 60

NCBI Description GLYCOGEN (STARCH) SYNTHASE, ISOFORM 1

>gi 101338 pir A38326 UDPglucose--starch

glucosyltransferase (EC 2.4.1.11) 1 - yeast (Saccharomyces

cerevisiae) >gi\_172870 (M60919) glycogen synthase [Saccharomyces cerevisiae] >gi\_836770\_dbj\_BAA09254\_ (D50617) glycogen synthase isoform 1 [Saccharomyces cerevisiae] >gi\_1122228\_dbj\_BAA08032\_ (D44599) Glycogen



## synthase GSY1 [Saccharomyces cerevisiae]

```
37558
Seq. No.
Seq. ID
                  LIB3074-038-Q1-K1-D5
                  BLASTX
Method
                  g2347088
NCBI GI
                  225
BLAST score
                  1.0e-18
E value
                  60
Match length
                  70
% identity
                  (U72765) non-specific lipid transfer protein PvLTP-24
NCBI Description
                  [Phaseolus vulgaris]
                  37559
Seq. No.
                  LIB3074-038-Q1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1172995
                  157
BLAST score
                  1.0e-10
E value
                  57
Match length
                  60
% identity
                  60S RIBOSOMAL PROTEIN L22 >gi 1083790 pir__S52084 ribosomal
NCBI Description
                  protein L22 - rat >gi_710295_emb_CAA55204_ (X78444)
                  ribosomal protein L22 [Rattus norvegicus]
                  >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus
                  norvegicus]
Seq. No.
                  37560
                  LIB3074-038-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2493694
                  295
BLAST score
E value
                  1.0e-26
Match length
                  116
% identity
                  53
                  PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII
NCBI Description
                  6.1 KD PROTEIN) >gi_1076268_pir__S53025 photosystem II
                  protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein
                  of photosystem II [Spinacia oleracea]
                  37561
Seq. No.
Seq. ID
                  LIB3074-038-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g2507421
BLAST score
                  199
                  2.0e-15
E value
                  60
Match length
                  70
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277
NCBI Description
                  (U81042) translation initiation factor [Arabidopsis
                  thaliana] >gi 4490709 emb CAB38843.1 (AL035680)
                  translation initiation factor [Arabidopsis thaliana]
```

Seq. No. 37562

Seq. ID LIB3074-038-Q1-K1-G9

Method BLASTN NCBI GI g407800



```
BLAST score
                  1.0e-18
E value
                  73
Match length
                  92
% identity
                  G.hirsutum mRNA for ribosomal protein 41, large subunit
NCBI Description
                  (RL41)
                  37563
Seq. No.
                  LIB3074-039-Q1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170087
BLAST score
                  170
                  9.0e-91
E value
                  274
Match length
                  92
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
Seq. No.
                  37564
                  LIB3074-039-Q1-K1-B8
Seq. ID
Method
                  BLASTN
                  q531828
NCBI GI
                  47
BLAST score
E value
                  9.0e-18
Match length
                  101
% identity
NCBI Description Cloning vector pSport1, complete cds
                  37565
Seq. No.
                  LIB3074-039-Q1-K1-C1
Seq. ID
                  BLASTX
Method
                  g134145
NCBI GI
BLAST score
                  162
E value
                   2.0e-11
Match length
                   81
                   46
% identity
                  STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE
NCBI Description
                   PROTEIN A) >gi_99886_pir _S08511 28K protein - soybean
                   >gi 169898 (M37530) 28 kDa protein [Glycine max] >gi_169975
                   (M76981) vegetative storage protein [Glycine max]
                   >gi 226867_prf 1609232B 28kD glycoprotein [Glycine max]
                   >gi 444325 prf 1906374A vegetative storage protein
                   [Glycine max]
                   37566
Seq. No.
                   LIB3074-039-Q1-K1-C8
Seq. ID
                   BLASTN
Method
                   g303900
NCBI GI
                   98
BLAST score
                   8.0e-48
E value
                   290
Match length
                   49
% identity
```

Seq. No. 37567

Seq. ID LIB3074-039-Q1-K1-D10

NCBI Description Soybean gene for ubiquitin, complete cds

Method BLASTN NCBI GI g170067



```
BLAST score
                   3.0e-53
E value
                  329
Match length
                  83
% identity
                  Soybean (G.max) proline-rich cell wall protein (SbPRP3)
NCBI Description
                  gene, complete cds
                   37568
Seq. No.
                  LIB3074-039-Q1-K1-D5
Seq. ID
Method
                  BLASTX
                  q531829
NCBI GI
                   142
BLAST score
                   6.0e-09
E value
                   62
Match length
% identity
                   48
                   (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
Seq. No.
                   37569
                   LIB3074-039-Q1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3582335
BLAST score
                   160
E value
                   3.0e-13
Match length
                   71
% identity
                   65
                   (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
                   37570
Seq. No.
                   LIB3074-039-Q1-K1-F9
Seq. ID
                   BLASTN
Method
                   g170089
NCBI GI
BLAST score
                   74
                   2.0e-33
E value
                   273
Match length
                   82
% identity
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
                   37571
Seq. No.
Seq. ID
                   LIB3074-039-Q1-K1-G11
                   BLASTN
Method
                   g169974
NCBI GI
                   213
BLAST score
                   1.0e-116
E value
                   361
Match length
                   89
% identity
                   Glycine max vspA gene, complete cds
NCBI Description
                   37572
Seq. No.
Seq. ID
                   LIB3074-040-Q1-K1-A8
Method
                   BLASTN
NCBI GI
                   g170089
BLAST score
                   188
                   1.0e-101
E value
Match length
                   296
                   91
% identity
```

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds



```
37573
Seq. No.
                  LIB3074-040-Q1-K1-D2
Seq. ID
                  BLASTN
Method
                  q1055367
NCBI GI
                  164
BLAST score
                  3.0e-87
E value
                  224
Match length
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
                  37574
Seq. No.
                  LIB3074-040-Q1-K1-F2
Seq. ID
Method
                  BLASTN
                  g2961299
NCBI GI
                  75
BLAST score
                  4.0e-34
E value
                  251
Match length
% identity
                  82
NCBI Description Cicer arietinum mRNA for ribosomal protein L24
                  37575
Seq. No.
                  LIB3074-041-Q1-K1-A11
Seq. ID
Method
                  BLASTX
                  g456568
NCBI GI
BLAST score
                   245
                   6.0e-21
E value
                   54
Match length
                   85
% identity
NCBI Description (L29077) ubiquitin conjugating enzyme [Pisum sativum]
                   37576
Seq. No.
                   LIB3074-041-Q1-K1-B2
Seq. ID
                   BLASTN
Method
NCBI GI
                   q1055367
BLAST score
                   260
                   1.0e-144
E value
                   371
Match length
% identity
                   93
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   37577
Seq. No.
Seq. ID
                   LIB3074-041-Q1-K1-B8
                   BLASTN
Method
                   q169974
NCBI GI
                   230
BLAST score
E value
                   1.0e-126
                   306
Match length
% identity
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   37578
```

Seq. ID LIB3074-041-Q1-K1-E6

Method BLASTN g170067 NCBI GI



```
BLAST score
E value
                  1.0e-71
                  349
Match length
                  87
% identity
                  Soybean (G.max) proline-rich cell wall protein (SbPRP3)
NCBI Description
                  gene, complete cds
Seq. No.
                  37579
Seq. ID
                  LIB3074-041-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g1277168
BLAST score
                  110
                  8.0e-09
E value
                  62
Match length
                  62
% identity
                  (U51855) cysteine proteinase inhibitor [Glycine max]
NCBI Description
                  37580
Seq. No.
                  LIB3074-041-Q1-K1-E8
Seq. ID
                  BLASTN
Method
                  g170067
NCBI GI
BLAST score
                  72
                  2.0e-32
E value
                  124
Match length
                  90
% identity
                  Soybean (G.max) proline-rich cell wall protein (SbPRP3)
NCBI Description
                   gene, complete cds
                   37581
Seq. No.
                  LIB3074-041-Q1-K1-F1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4335755
BLAST score
                   143
E value
                   5.0e-09
                   70
Match length
                   39
% identity
                  (AC006284) putative hydroxyproline-rich glycoprotein
NCBI Description
                   [Arabidopsis thaliana]
                   37582
Seq. No.
Seq. ID
                  LIB3074-041-Q1-K1-F2
Method
                   BLASTN
                   g170089
NCBI GI
BLAST score
                   63
E value
                   4.0e-27
                   143
Match length
                   86
% identity
                  G.max vegetative storage protien mRNA (VSP27), complete cds
NCBI Description
                   37583
Seq. No.
                   LIB3074-041-Q1-K1-F6
Seq. ID
Method
                   BLASTN
                   q170091
NCBI GI
BLAST score
                   309
E value
                   1.0e-173
Match length
                   405
```

94

% identity



NCBI Description Glycine max vegetative storage protein (vspB) gene, complete cds

Seq. No. 37584

Seq. ID LIB3074-041-Q1-K1-H7

Method BLASTN
NCBI GI g169974
BLAST score 89
E value 1.0e-42
Match length 201
% identity 86

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 37585

Seq. ID LIB3087-001-Q1-K1-A12

Method BLASTX
NCBI GI g2288999
BLAST score 218
E value 1.0e-17
Match length 92
% identity 57

NCBI Description (AC002335) electron transfer flavoprotein ubiquinone

oxidoreductase isolog [Arabidopsis thaliana]

Seq. No. 37586

Seq. ID LIB3087-001-Q1-K1-A3

Method BLASTX
NCBI GI g2344901
BLAST score 182
E value 1.0e-13
Match length 91
% identity 51

NCBI Description (AC002388) serine/threonine protein kinase isolog

[Arabidopsis thaliana]

Seq. No. 37587

Seq. ID LIB3087-001-Q1-K1-A9

Method BLASTX
NCBI GI g4467153
BLAST score 176
E value 1.0e-12
Match length 45
% identity 71

NCBI Description (AL035540) putative thaumatin-like protein [Arabidopsis

thaliana]

Seq. No. 37588

Seq. ID LIB3087-001-Q1-K1-B9

Method BLASTX
NCBI GI g2275211
BLAST score 165
E value 2.0e-11
Match length 42
% identity 76

NCBI Description (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No. 37589

LIB3087-001-Q1-K1-C11 Seq. ID BLASTX Method q1903034 NCBI GI 174 BLAST score 1.0e-12 E value Match length 82 % identity NCBI Description (X94625) amp-binding protein [Brassica napus] Seq. No. 37590 LIB3087-001-Q1-K1-E10 Seq. ID Method BLASTN NCBI GI q1813328 BLAST score 146 2.0e-76 E value Match length 250 % identity NCBI Description Canavalia gladiata mRNA for HMG-1, complete cds 37591 Seq. No. LIB3087-001-Q1-K1-F2 Seq. ID Method BLASTX NCBI GI q4406792 BLAST score 175 1.0e-12 E value 114 Match length % identity (AC006304) putative reverse transcriptase [Arabidopsis NCBI Description thaliana] Seq. No. 37592 LIB3087-001-Q1-K1-G6 Seq. ID Method BLASTX NCBI GI g2832661 BLAST score 180 3.0e-13E value 87 Match length % identity 44 (AL021710) pherophorin - like protein [Arabidopsis NCBI Description thaliana] 37593 Seq. No. LIB3087-001-Q1-K1-H4 Seq. ID Method BLASTN g2661127 NCBI GI 87 BLAST score 3.0e-41E value Match length 265 % identity 84 NCBI Description Glycine max arginase (pAG1) mRNA, complete cds 37594 Seq. No.

Seq. ID LIB3087-001-Q1-K1-H8

BLASTN Method g2369713 NCBI GI BLAST score 160 1.0e-84 E value



```
Match length
% identity
                  86
NCBI Description Beta vulgaris cDNA for elongation factor
Seq. No.
                  37595
Seq. ID
                  LIB3087-002-Q1-K1-B11
Method
                  BLASTX
```

NCBI GI g3786007 BLAST score 182 E value 2.0e-13 Match length 58 % identity 53

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. ID LIB3087-002-Q1-K1-C8 Method BLASTX NCBI GI q2129826 BLAST score 527 E value 8.0e-54 128 Match' length

Seq. No.

80 % identity NCBI Description dynamin-like protein phragmoplastin 5 - soybean >gi 1218004 (U36430) SDL5A [Glycine max]

Seq. No. 37597

LIB3087-002-01-K1-D9 Seq. ID

37596

Method BLASTX NCBI GI g3522954 BLAST score 291 E value 3.0e-26Match length 94 59 % identity

NCBI Description (AC004411) IAA20 [Arabidopsis thaliana]

Seq. No. 37598

LIB3087-003-Q1-K1-B2 Seq. ID

Method BLASTX NCBI GI g4210451 229 BLAST score 6.0e-19 E value Match length 82 % identity 63

NCBI Description (AB016472) ARR2 protein [Arabidopsis thaliana]

Seq. No. 37599

LIB3087-003-Q1-K1-B9 Seq. ID

BLASTXMethod NCBI GI g3334299 BLAST score 251 7.0e-22 E value 64 Match length % identity 81

PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE NCBI Description COMPLEX ALPHA SUBUNIT) >gi 2315211 emb CAA74725 (Y14339)



```
Seq. No.
Seq. ID
                  LIB3087-003-Q1-K1-C8
                  BLASTX
Method
NCBI GI
                  g3482967
BLAST score
                  262
E value
                  6.0e-23
                  67
Match length
% identity
                  76
NCBI Description
                  (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
                  thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585)
                  protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3087-003-Q1-K1-F11
                  BLASTX
Method
NCBI GI
                  g2462749
BLAST score
                  213
                  3.0e-17
E value
Match length
                  76
% identity
                  64
                   (AC002292) Putative Serine/Threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                  37602
Seq. No.
Seq. ID
                  LIB3087-003-Q1-K1-F2
Method
                  BLASTN
NCBI GI
                  q944814
BLAST score
                  42
                  2.0e-14
E value
                  146
Match length
                  82
% identity
NCBI Description
                  Pueraria lobata mRNA for chalcone flavanone isomerase,
                  complete cds
Seq. No.
                  37603
Seq. ID
                  LIB3087-004-Q1-K1-A4
Method
                  BLASTX
                  g1169451
NCBI GI
BLAST score
                  311
E value
                  8.0e-29
Match length
                  99
% identity
                  60
NCBI Description
                  PROBABLE GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE A6 PRECURSOR
                  ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                  (BETA-1,3-ENDOGLUCANASE) >gi_322510_pir__S31906
                  beta-1,3-glucanase homolog - Arabidopsis thaliana
                  >gi_22677_emb_CAA49853 (X70409) A6 [Arabidopsis thaliana]
                  >gi_2244764_emb_CAB10187_ (Z97335) AMP-binding protein
                  [Arabidopsis thaliana]
Seq. No.
                  37604
Seq. ID
                  LIB3087-004-Q1-K1-B4
```

Method BLASTN NCBI GI g169980 BLAST score 300 E value 1.0e-168 Match length 335

% identity

61

NCBI Description Xenopus laevis cDNA clone 27A6-1



```
% identity
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                  37605
Seq. No.
                  LIB3087-004-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3402711
BLAST score
                  326
E value
                  2.0e-30
Match length
                  109
% identity
NCBI Description
                  (AC004261) putative RNA-binding protein [Arabidopsis
                  thaliana]
                  37606
Seq. No.
Seq. ID
                  LIB3087-004-Q1-K1-C3
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  8.0e-11
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  37607
Seq. ID
                  LIB3087-004-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q2494132
BLAST score
                  385
E value
                  1.0e-37
Match length
                  84
% identity
                  81
NCBI Description
                  (AC002376) Contains similarity to human dimethylaniline
                  monooxygenase (gb M64082). [Arabidopsis thaliana]
                  37608
Seq. No.
Seq. ID
                  LIB3087-004-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  q461735
BLAST score
                  184
                  3.0e-14
E value
Match length
                  72
                  57
% identity
                  MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR
NCBI Description
                  >gi 478785 pir S29315 chaperonin 60 - cucurbit
                  >gi 12544 emb CAA50217 (X70867) chaperonin 60 [Cucurbita
                   sp.]
                  37609
Seq. No.
Seq. ID
                  LIB3087-004-Q1-K1-H2
                  BLASTN
Method
NCBI GI
                  q3821780
BLAST score
                  36
                   6.0e-11
E value
Match length
                  37
```

% identity

NCBI Description

thaliana]



```
37610
Seq. No.
                  LIB3087-005-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  g3548808
NCBI GI
BLAST score
                  331
                  5.0e-31
E value
Match length
                  113
% identity
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
Seq. No.
                  37611
                  LIB3087-005-Q1-K1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1675195
                   65
BLAST score
                   2.0e-28
E value
Match length
                   129
                   88
% identity
                  Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
NCBI Description
                   complete cds
Seq. No.
                   37612
                   LIB3087-005-Q1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1168493
BLAST score
                   156
E value
                   2.0e-10
Match length
                   97
                   47
% identity
                   ARGINASE >gi 602422 (U15019) arginase [Arabidopsis
NCBI Description
                   thaliana] >gi 4325373 gb AAD17369 (AF128396) Arabidopsis
                   thaliana arginase (SW:P46637) (Pfam: PF00491, Score=419.6,
                   E=3.7e-142 N=1) [Arabidopsis thaliana]
                   37613
Seq. No.
                   LIB3087-005-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   q2501597
NCBI GI
                   165
BLAST score
                   2.0e-11
E value
                   58
Match length
                   59
% identity
                   PROTEIN 22A3 >gi_1638838_emb_CAA67982_ (X99668) unknown
NCBI Description
                   [Mus musculus]
                   37614
Seq. No.
Seq. ID
                   LIB3087-005-Q1-K1-G2
                   BLASTX
Method
                   q3927831
NCBI GI
                   257
BLAST score
                   3.0e-22
E value
Match length
                   73
                   37
```

(AC005727) similar to mouse ankyrin 3 [Arabidopsis

```
Seq. No.
                  LIB3087-006-Q1-K1-A3
Seq. ID
                  BLASTX
Method
                  q4510345
NCBI GI
                  162
BLAST score
                  5.0e-11
E value
                  53
Match length
                  53
% identity
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                  37616
Seq. No.
                  LIB3087-006-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                  g1362008
NCBI GI
                  112
BLAST score
                  8.0e-09
E value
                  83
Match length
                  14
% identity
NCBI Description ubiquitin-like protein 12 - Arabidopsis thaliana
                  37617
Seq. No.
                  LIB3087-006-Q1-K1-E4
Seq. ID
                  BLASTX
Method
                  g1621268
NCBI GI
BLAST score
                  161
                  2.0e-18
E value
                  103
Match length
                   54
% identity
                  (Z81012) unknown [Ricinus communis]
NCBI Description
                   37618
Seq. No.
                   LIB3087-006-Q1-K1-G2
Seq. ID
                   BLASTX
Method
                   g1350736
NCBI GI
BLAST score
                   145
                   4.0e-09
E value
                   33
Match length
                   85
% identity
                   60S RIBOSOMAL PROTEIN L37 >gi 629673 pir S44313 ribosomal
NCBI Description
                   protein L37 - tomato >gi_483586_emb_CAA55674_ (X79074)
                   ribosomal protein L37 [Lycopersicon esculentum]
                   37619
Seq. No.
                   LIB3087-006-Q1-K1-H3
Seq. ID
Method
                   BLASTX
                   q3450842
NCBI GI
                   125
BLAST score
                   3.0e-09
E value
Match length
                   66
                   56
% identity
                   (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
```

Seq. No. 37620

Seq. ID LIB3087-006-Q1-K1-H5

sativa]

Method BLASTX NCBI GI g3450842

```
BLAST score
                   2.0e-37
E value
                   88
Match length
                   82
% identity
                   (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                   sativa]
                   37621
Seq. No.
                   LIB3087-007-Q1-K1-A4
Seq. ID
Method
                   BLASTN
                   g21054
NCBI GI
                   59
BLAST score
                   1.0e-24
E value
                   98
Match length
                   92
% identity
NCBI Description P.vulgaris mRNA for tonoplast intrinsic protein
                   37622
Seq. No.
                   LIB3087-007-Q1-K1-D9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2281115
BLAST score
                   581
E value
                   3.0e-60
                   126
Match length
                   91
% identity
                    (AC002330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
                    thaliana]
                    37623
Seq. No.
                   LIB3087-008-Q1-K1-B8
Seq. ID
                   BLASTX
Method
                    g2129630
NCBI GI
BLAST score
                    308
                    3.0e-28
E value
                    69
Match length
                    72
% identity
                   lamin - Arabidopsis thaliana >gi_1262754_emb_CAA65750
NCBI Description
                    (X97023) lamin [Arabidopsis thaliana] >g\overline{i}_33\overline{9}5760 (U7\overline{7}721)
                    unknown [Arabidopsis thaliana]
                    37624
Seq. No.
                    LIB3087-008-Q1-K1-E10
Seq. ID
                    BLASTX
Method
                    g2781357
NCBI GI
                    385
BLAST score
                    3.0e-37
E value
                    103
Match length
                    71
% identity
                   (AC003113) F2401.13 [Arabidopsis thaliana]
NCBI Description
                    37625
Seq. No.
Seq. ID
                    LIB3087-008-Q1-K1-F4
                    BLASTX
Method
                    q3776005
NCBI GI
BLAST score
                    216
                    1.0e-17
E value
```

78

Match length



```
% identity
                  (AJ010466) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  37626
Seq. No.
                  LIB3087-008-Q1-K1-G2
Seq. ID
                  BLASTN
Method
                  q432488
NCBI GI
                  70
BLAST score
                  3.0e-31
E value
                  218
Match length
                  84
% identity
NCBI Description Wheat initiation factor 1A (eIF-1A) mRNA
                  37627
Seq. No.
                  LIB3087-008-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  q2129655
NCBI GI
                   101
BLAST score
                   2.0e-13
E value
                   61
Match length
% identity
NCBI Description OBP32pep protein - Arabidopsis thaliana (fragment)
                   >gi_1022799 (U37698) OBP32pep [Arabidopsis thaliana]
Seq. No.
                   37628
                   LIB3087-009-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   a3811380
NCBI GI
                   247
BLAST score
                   4.0e-21
E value
                   132
Match length
                   46
% identity
                   (AF100956) BING4 [Mus musculus] >gi_4050103 (AF110520)
NCBI Description
                   BING4 [Mus musculus]
                   37629
Seq. No.
                   LIB3087-009-Q1-K1-E3
Seq. ID
                   BLASTX
Method
                   q4262226
NCBI GI
BLAST score
                   263
                   4.0e-23
E value
                   80
Match length
 % identity
                   (AC006200) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   37630
 Seq. No.
                   LIB3087-009-Q1-K1-G1
 Seq. ID
 Method
                   BLASTX
                   q2642648
 NCBI GI
                   407
 BLAST score
                   8.0e-40
 E value
                   130
Match length
 % identity
                   68
                    (AF033852) cytosolic heat shock 70 protein; HSC70-3
 NCBI Description
                   [Spinacia oleracea] >gi 2660768 (AF034616) cytosolic heat
```

shock 70 protein [Spinacia oleracea] >gi\_2660770 (AF034617)

cytosolic heat shock 70 protein [Spinacia oleracea]

NCBI Description



```
37631
Seq. No.
                  LIB3087-009-Q1-K1-G9
Seq. ID
                  BLASTX
Method
                  g1213557
NCBI GI
                  149
BLAST score
                  1.0e-09
E value
                  67
Match length
% identity
                  (U50199) coded for by C. elegans cDNA yk89e9.5; coded for
NCBI Description
                  by C. elegans cDNA cm7g5; coded for by C. elegans cDNA
                  cm14b9; coded for by C. elegans cDNA yk52g5.5; coded for by
                  C. elegans cDNA yk76e5.5; coded for by C. elegans cDNA
                  yk131f11.5; c
                   37632
Seq. No.
                  LIB3087-009-Q1-K1-H1
Seq. ID
                  BLASTX
Method
                   g1335862
NCBI GI
                   113
BLAST score
                   1.0e-11
E value
                   115
Match length
                   42
% identity
                  (U42608) clathrin heavy chain [Glycine max]
NCBI Description
                   37633
Seq. No.
                   LIB3087-009-Q1-K1-H12
Seq. ID
                   BLASTN
Method
                   q1675195
NCBI GI
                   98
BLAST score
                   9.0e-48
E value
                   214
Match length
% identity
                   Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
NCBI Description
                   complete cds
                   37634
Seq. No.
                   LIB3087-010-Q1-K1-A8
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3318610
                   54
BLAST score
                   5.0e-22
E value
                   106
Match length
                   88
% identity
                   Glycine max mRNA for mitochondrial phosphate transporter,
NCBI Description
                   complete cds
                   37635
Seq. No.
                   LIB3087-010-Q1-K1-C12
 Seq. ID
Method
                   BLASTX
                   g3641837
 NCBI GI
                   280
 BLAST score
                   3.0e-25
 E value
                   82
Match length
                   65
 % identity
                    (AL023094) Nonclathrin coat protein gamma - like protein
```

[Arabidopsis thaliana]



```
Seq. No.
                  37636
                  LIB3087-010-Q1-K1-C3
Seq. ID
Method
                  BLASTN
                  q1711035
NCBI GI
                  115
BLAST score
E value
                  6.0e-58
                  279
Match length
                  85
% identity
NCBI Description Pisum sativum hydroxyproline rich glycoprotein PsHRGP1
                  mRNA, partial cds
                  37637
Seq. No.
                  LIB3087-010-Q1-K1-C6
Seq. ID
                  BLASTN
Method
                  a1848272
NCBI GI
BLAST score
                  97
                  3.0e-47
E value
Match length
                  157
                  90
% identity
NCBI Description Lathyrus sativus phytochrome type A (phyA) gene, complete
Seq. No.
                  37638
                  LIB3087-010-Q1-K1-C7
Seq. ID
                  BLASTX
Method
                  g3319355
NCBI GI
                  272
BLAST score
                  5.0e-24
E value
Match length
                  61
                  85
% identity
                  (AF077407) similar to chaperonin containing TCP-1 complex
NCBI Description
                  gamma chain [Arabidopsis thaliana]
                   37639
Seq. No.
                  LIB3087-010-Q1-K1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                   q2444419
BLAST score
                   72
E value
                   2.0e-32
Match length
                   160
                   86
% identity
                  Glycine max ribosome-associated protein p40 mRNA, complete
NCBI Description
                   37640
Seq. No.
                   LIB3087-010-Q1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2661179
                   304
BLAST score
E value
                   7.0e-28
Match length
                   82
                   70
% identity
NCBI Description (U80984) AtZW10 [Arabidopsis thaliana]
```

5791

37641

LIB3087-010-Q1-K1-F8

Seq. No.

Seq. ID

Match length



```
BLASTN
Method
                  g1150683
NCBI GI
                  54
BLAST score
                  1.0e-21
E value
                  250
Match length
                  82
% identity
NCBI Description V.radiata atpB, rbcL and trnK genes
                   37642
Seq. No.
                  LIB3087-010-Q1-K1-H8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2344898
                   221
BLAST score
                   4.0e-18
E value
Match length
                   45
                   82
% identity
                   (AC002388) 60S ribosomal protein L30 isolog [Arabidopsis
NCBI Description
                   thaliana]
                   37643
Seq. No.
                   LIB3087-010-Q1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3927835
                   486
BLAST score
                   3.0e-49
E value
                   109
Match length
% identity
                   80
                   (AC005727) similar to Streptomyces PapA [Arabidopsis
NCBI Description
                   thaliana]
                   37644
Seq. No.
                   LIB3087-011-Q1-K1-E6
Seq. ID
Method
                   BLASTX
                   g4115936
NCBI GI
                   202
BLAST score
                   1.0e-15
E value
                   80
Match length
                   53
% identity
                  (AF118223) No definition line found [Arabidopsis thaliana]
NCBI Description
                   37645
Seq. No.
                   LIB3087-011-Q1-K1-E7
Seq. ID
                   BLASTX
Method
                   g4115936
NCBI GI
                   119
BLAST score
                   9.0e-12
E value
                   68
Match length
                   47
% identity
                   (AF118223) No definition line found [Arabidopsis thaliana]
NCBI Description
                   37646
Seq. No.
Seq. ID
                   LIB3087-011-Q1-K1-F6
                   BLASTX
Method
                   g629654
NCBI GI
BLAST score
                   205
                   4.0e-16
E value
```



% identity 5'-phosphoribosyl-4-(N-succinocarboxamide )-5-ami NCBI Description noimidazole synthetase - moth bean

37647 Seq. No.

LIB3087-011-Q1-K1-H5 Seq. ID

BLASTX Method q4090257 NCBI GI 298 BLAST score 6.0e-27 E value 70 Match length 80 % identity

NCBI Description (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]

37648 Seq. No.

LIB3087-012-Q1-K1-A4 Seq. ID

BLASTX Method q3355477 NCBI GI 163 BLAST score 5.0e-13 E value 76 Match length 66 % identity

NCBI Description (AC004218) putative P-glycoprotein, pgpl [Arabidopsis

thaliana]

37649. Seq. No.

LIB3087-012-Q1-K1-B11 Seq. ID

BLASTX Method q461753 NCBI GI 173 BLAST score 2.0e-12 E value 103 Match length 43 % identity

ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG NCBI Description

PRECURSOR >gi\_419773\_pir\_\_S31164 ATP-dependent ClpB

proteinase regulatory chain homolog precursor, chloroplast garden pea >gi\_169128 (L09547) nuclear encoded precursor

to chloroplast protein [Pisum sativum]

37650 Seq. No.

LIB3087-012-Q1-K1-C10 Seq. ID

BLASTX Method q3868756 NCBI GI 288 BLAST score 7.0e-26 E value 118 Match length % identity

(D86611) catalase [Oryza sativa] NCBI Description

37651 Seq. No.

LIB3087-012-Q1-K1-C12 Seq. ID

BLASTN Method q1184986 NCBI GI 124 BLAST score 3.0e-63 E value 256 Match length % identity 87



```
Nicotiana tabacum GTP-binding protein NTGB1 mRNA, partial
NCBI Description
Seq. No.
                  37652
Seq. ID
                  LIB3087-012-Q1-K1-C9
Method
                  BLASTX
                  g2980795
NCBI GI
BLAST score
                  315
                  4.0e-29
E value
Match length
                  115
% identity
                  58
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  37653
                  LIB3087-012-Q1-K1-D11
Seq. ID
Method
                  BLASTX
                  q3928097
NCBI GI
BLAST score
                  264
E value
                  6.0e-23
                  73
Match length
                  70
% identity
                  (AC005770) unknown protein, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  37654
                  LIB3087-012-Q1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3158376
                  233
BLAST score
                  2.0e-19
E value
                  99
Match length
% identity
                  49
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
                  37655
Seq. No.
Seq. ID
                  LIB3087-012-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  g3318611
BLAST score
                  113
E value
                  8.0e-12
Match length
                  101
% identity
                  54
                  (AB016063) mitochondrial phosphate transporter [Glycine
NCBI Description
                  max]
                  37656
Seq. No.
Seq. ID
                  LIB3092-001-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g3126967
BLAST score
                  286
E value
                  6.0e-26
Match length
                  80
```

Seq. No. 37657

% identity

Seq. ID LIB3092-001-Q1-K1-A8

13

NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]

BLAST score

E value Match length 333 3.0e-31

105

```
Method
NCBI GI
                  q4115379
                  106
BLAST score
                  5.0e-10
E value
                  80
Match length
                  51
% identity
NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis
                  thaliana]
                  37658
Seq. No.
                  LIB3092-001-Q1-K1-C1
Seq. ID
                  BLASTX
Method
                  g384332
NCBI GI
BLAST score
                  211
                  5.0e-17
E value
                  101
Match length
                  44
% identity
NCBI Description invertase [Lycopersicon esculentum]
                  37659
Seq. No.
                  LIB3092-001-Q1-K1-D10
Seq. ID
                  BLASTN
Method
                  g18764
NCBI GI
BLAST score
                  188
E value
                  1.0e-101
                  244
Match length
                   95
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
                   37660
Seq. No.
                  LIB3092-001-Q1-K1-D3
Seq. ID
                  BLASTN
Method
                   g1055367
NCBI GI
BLAST score
                   230
                   1.0e-126
E value
                   362
Match length
                   91
% identity
NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small
                   subunit mRNA, complete cds
                   37661
Seq. No.
                   LIB3092-001-Q1-K1-D9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g18764
BLAST score
                   276
                   1.0e-154
E value
                   319
Match length
                   97
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
Seq. No.
                   37662
                   LIB3092-001-Q1-K1-F9
Seq. ID
Method
                   BLASTX
                   g1076510
NCBI GI
```



% identity 60
NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean
>gi\_829119\_emb\_CAA52414\_ (X74403) cyclophilin [Phaseolus
vulgaris]

Seq. No. 37663

Seq. ID LIB3092-001-Q1-K1-G1

Method BLASTX
NCBI GI g2832625
BLAST score 180
E value 2.0e-13
Match length 77
% identity 55

NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 37664

Seq. ID LIB3092-001-Q1-K1-G7

Method BLASTN
NCBI GI g170073
BLAST score 175
E value 8.0e-94
Match length 221
% identity 95

NCBI Description Soybean calmodulin (SCaM-3) mRNA, complete cds

Seq. No. 37665

Seq. ID LIB3092-001-Q1-K1-H10

Method BLASTX
NCBI GI g544184
BLAST score 194
E value 2.0e-28
Match length 113
% identity 61

NCBI Description 4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE)

(DISPROPORTIONATING ENZYME) (D-ENZYME)

>gi\_322785\_pir\_\_A45049 4-alpha-glucanotransferase (EC
2.4.1.25) - potato >gi\_296692\_emb\_CAA48630\_ (X68664)

4-alpha-glucanotransferase [Solanum tuberosum]

Seq. No. 37666

Seq. ID LIB3092-001-Q1-K1-H12

Method BLASTN
NCBI GI 94324966
BLAST score 157
E value 4.0e-83
Match length 193
% identity 95

NCBI Description Glycine max ADP-ribosylation factor mRNA, partial cds

Seq. No. 37667

Seq. ID LIB3092-002-Q1-K1-A6

Method BLASTX
NCBI GI g3297815
BLAST score 176
E value 1.0e-16
Match length 64
% identity 67



```
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
```

Seq. No. 37668

Seq. ID LIB3092-002-Q1-K1-C9

Method BLASTN
NCBI GI g3821780
BLAST score 37
E value 3.0e-11

E value 3.0 Match length 49 % identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 37669

Seq. ID LIB3092-002-Q1-K1-D10 Method BLASTN

Method BLASTN
NCBI GI g2331300
BLAST score 294
E value 1.0e-165
Match length 329
% identity 98

NCBI Description Zea mays ribosomal protein S4 type I (rps4) mRNA, complete

cds

Seq. No. 37670

Seq. ID LIB3092-002-Q1-K1-E3

Method BLASTN
NCBI GI g984307
BLAST score 58
E value 3.0e-24
Match length 106
% identity 89

NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial

cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. No. 37671

Seq. ID LIB3092-002-Q1-K1-G2

Method BLASTX
NCBI GI g1854443
BLAST score 138
E value 7.0e-09
Match length 56
% identity 52

NCBI Description (D83970) CPRD8 protein [Vigna unguiculata]

Seq. No. 37672

Seq. ID LIB3092-003-Q1-K1-B1

Method BLASTX
NCBI GI g1617274
BLAST score 280
E value 4.0e-25
Match length 100
% identity 54

NCBI Description (Z72152) AMP-binding protein [Brassica napus]



```
Seq. No.
                  LIB3092-003-Q1-K1-B8
Seq. ID
                  BLASTX
Method
                  g4105798
NCBI GI
                  543
BLAST score
E value
                  2.0e-59
Match length
                  122
                  76
% identity
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.
Seq. ID
                  LIB3092-003-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2245005
BLAST score
                  243
E value
                  9.0e-21
Match length
                  100
% identity
                  53
                  (Z97341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  37675
                  LIB3092-003-Q1-K1-G11
Seq. ID
Method
                  BLASTN
                  g1575726
NCBI GI
                  296
BLAST score
                   1.0e-166
E value
Match length
                   336
% identity
                   96
NCBI Description Glycine max 14-3-3 related protein SGF14B mRNA, partial cds
                   37676
Seq. No.
Seq. ID
                   LIB3092-004-Q1-K1-B1
Method
                  BLASTN
NCBI GI
                   q1161253
BLAST score
                   145
                   9.0e-76
E value
                   287
Match length
                   99
% identity
NCBI Description Glycine max protein kinase (SPK-4) mRNA, complete cds
                   37677
Seq. No.
Seq. ID
                   LIB3092-004-Q1-K1-B5
Method
                   BLASTX
NCBI GI
                   g2832357
BLAST score
                   165
E value
                   2.0e-11
                   110
Match length
                   38
% identity
                  (Y14071) HMG protein [Arabidopsis thaliana] >gi 3068715
NCBI Description
                   (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                   37678
```

Seq. ID LIB3092-004-Q1-K1-D10

Method BLASTX
NCBI GI g3355483
BLAST score 273
E value 4.0e-24



```
Match length
                  71
% identity
                  (AC004218) gibberellin-regulated protein (GASA5)-like
NCBI Description
                  [Arabidopsis thaliana]
                  37679
Seq. No.
                  LIB3092-004-Q1-K1-F12
Seq. ID
Method
                  BLASTN
                  q1055367
NCBI GI
                  93
BLAST score
                  7.0e-45
E value
Match length
                  272
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
                  37680
Seq. No.
                  LIB3092-004-Q1-K1-G6
Seq. ID
                  BLASTN
Method
                  q169036
NCBI GI
                  95
BLAST score
                  6.0e-46
E value
Match length
                  227
% identity
                  85
NCBI Description Pisum sativum L. aldolase gene, 3' end cds
                  37681
Seq. No.
                  LIB3092-004-Q1-K1-H8
Seq. ID
Method
                  BLASTN
                  q516853
NCBI GI
                   47
BLAST score
                   2.0e-17
E value
                   67
Match length
% identity
                   42
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
                   37682
Seq. No.
                   LIB3092-005-Q1-K1-A2
Seq. ID
Method
                   BLASTX
                   g2129726
NCBI GI
                   165
BLAST score
                   1.0e-11
E value
                   66
Match length
% identity
                   53
                  RNA polymerase II third largest chain RPB35.5A -
NCBI Description
                   Arabidopsis thaliana >gi_514318 (L34770) RNA polymerase II
                   third largest subunit [Arabidopsis thaliana]
                   >gi_4544370_gb_AAD22281.1_AC006920_5 (AC006920) RNA
                   polymerase II, third largest subunit [Arabidopsis thaliana]
                   37683
Seq. No.
                   LIB3092-005-Q1-K1-B1
Seq. ID
                   BLASTX
Method
```

g625547

9.0e-27

295

87

NCBI GI

E value

BLAST score

Match length



% identity chlorophyll a/b-binding protein type I - common tobacco NCBI Description >qi 493723 emb CAA45523 (X64198) photosystem I light-harvesting chlorophyll a/b-binding protein [Nicotiana tabacum] Seq. No. 37684 LIB3092-005-Q1-K1-C7 Seq. ID BLASTX Method q1174626 NCBI GI BLAST score 169 4.0e-12

E value Match length 66 % identity 56

TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) NCBI Description

(P23) >gi\_1072463\_pir\_\_A38959 IgE-dependent histamine-releasing factor homolog - potato

>gi\_587546\_emb\_CAA85519\_ (Z37160) P23 protein [Solanum

tuberosum]

37685 Seq. No.

LIB3092-006-Q1-K1-A10 Seq. ID

Method BLASTX NCBI GI q124224 BLAST score 221 E value 3.0e-23 102 Match length 62 % identity

INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) NCBI Description

>gi\_100345\_pir\_\_S21060 translation initiation factor eIF-5A

common tobacco >gi\_19887\_emb\_CAA45105\_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No. 37686

LIB3092-006-Q1-K1-A3 Seq. ID

BLASTN Method NCBI GI g18764 298 BLAST score E value 1.0e-167 Match length 367 95 % identity

G.max tefS1 gene for elongation factor EF-1a NCBI Description

Seq. No. 37687

LIB3092-006-Q1-K1-C9 Seq. ID

Method BLASTX NCBI GI g1351408 BLAST score 167 1.0e-18 E value 107 Match length 54 % identity

VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) NCBI Description

>gi 1076563 pir \_\_S51117 cystein proteinase - sweet orange >gi 633185 emb CAA87720 (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi\_1588548\_prf\_\_2208463A

vascular processing protease [Citrus sinensis]



```
Seq. No.
                  LIB3092-006-Q1-K1-D4
Seq. ID
Method
                  BLASTX
                  g132086
NCBI GI
BLAST score
                  151
E value
                   5.0e-19
Match length
                  126
                   55
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 1) >gi 68053 pir RKSYS
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) small chain
                  precursor SRS1 - soybean >gi 18742_emb_CAA23736_ (V00458)
                   rubpcase [Glycine max]
                   37689
Seq. No.
Seq. ID
                  LIB3092-006-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                   g2749982
BLAST score
                   225
                   2.0e-18
E value
                   57
Match length
                   68
% identity
                   (AF036705) Similar to phytoene desaturase; coded for by C.
NCBI Description
                   elegans cDNA CEESX74F; coded for by C. elegans cDNA
                   yk303f4.3; coded for by C. elegans cDNA yk257d4.3; coded
                   for by C. elegans cDNA yk303f4.5; coded for by C. elegans
                   cDNA yk257d4.5;
Seq. No.
                   37690
Seq. ID
                   LIB3092-006-Q1-K1-F3
Method
                   BLASTX
NCBI GI
                   g3759184
BLAST score
                   167
E value
                   1.0e-11
Match length
                   96
% identity
                   45
                  (AB018441) phi-1 [Nicotiana tabacum]
NCBI Description
Seq. No.
                   37691
                   LIB3092-006-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   g2739364
NCBI GI
BLAST score
                   120
                   7.0e-15
E value
                   88
Match length
                   49
% identity
                  (AC002505) serpin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   37692
Seq. ID
                   LIB3092-006-Q1-K1-H12
                   BLASTX
Method
NCBI GI
                   g2827710
BLAST score
                   215
```

NCBI Description (AL021684) lysosomal Pro-X carboxypeptidase - like protein 5801

5.0e-27

136

57

E value

Match length

% identity



## [Arabidopsis thaliana]

Seq. No. 37693

Seq. ID LIB3092-007-Q1-K1-A1

Method BLASTN
NCBI GI g257814
BLAST score 204
E value 1.0e-111
Match length 348
% identity 93

NCBI Description phenylalanine ammonia-lyase [soybeans, mRNA, 1427 nt]

Seq. No. 37694

Seq. ID LIB3092-007-Q1-K1-A9

Method BLASTX
NCBI GI g3549667
BLAST score 472
E value 2.0e-47
Match length 121
% identity 74

NCBI Description (AL031394) Arabidopsis dynamin-like protein ADL2

[Arabidopsis thaliana]

Seq. No. 37695

Seq. ID LIB3092-007-Q1-K1-F12

Method BLASTX
NCBI GI g1350548
BLAST score 285
E value 2.0e-25
Match length 97
% identity 58

NCBI Description (L47609) heat shock-like protein [Picea glauca]

Seq. No. 37696

Seq. ID LIB3092-007-Q1-K1-F4

Method BLASTX
NCBI GI g3193324
BLAST score 226
E value 1.0e-18
Match length 118
% identity 47

NCBI Description (AF069299) contains similarity to WD domains, G-beta

repeats (Pfam: G-beta.hmm, score: 22.80 and 35.84)

[Arabidopsis thaliana]

Seq. No. 37697

Seq. ID LIB3092-007-Q1-K1-G3

Method BLASTX
NCBI GI g4218535
BLAST score 214
E value 2.0e-17
Match length 74
% identity 54

NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]

Seq. No. 37698

Seq. ID LIB3092-007-Q1-K1-H6

Match length

100



```
Method
                  BLASTX
                  g2465010
NCBI GI
                  219
BLAST score
                  9.0e-18
E value
                  99
Match length
                  48
% identity
                  (AJ001446) acyl carrier protein [Fragaria vesca]
NCBI Description
                  37699
Seq. No.
                  LIB3092-007-Q1-K1-H7
Seq. ID
                  BLASTX
Method
                  g1922242
NCBI GI
                  101
BLAST score
                  4.0e-10
E value
Match length
                  70
% identity
                  51
                  (Y10084) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  37700
Seq. No.
                  LIB3092-008-Q1-K1-A10
Seq. ID
                  BLASTX
Method
                   g2827710
NCBI GI
BLAST score
                   522
                   3.0e-53
E value
                   141
Match length
% identity
                   73
                   (ALO21684) lysosomal Pro-X carboxypeptidase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   37701
Seq. No.
                   LIB3092-008-Q1-K1-A11
Seq. ID
                   BLASTN
Method
                   g2225884
NCBI GI
                   74
BLAST score
                   2.0e-33
E value
                   150
Match length
                   87
% identity
                   Solanum tuberosum mRNA for eukaryotic initiation factor
NCBI Description
                   5A5, complete cds
Seq. No.
                   37702
                   LIB3092-008-Q1-K1-A9
Seq. ID
                   BLASTN
Method
                   g19701
NCBI GI
BLAST score
                   118
E value
                   1.0e-59
                   333
Match length
                   85
% identity
NCBI Description N.plumbaginifolia mRNA NeIF-5A2 for initiation factor 5A(2)
Seq. No.
                   37703
                   LIB3092-008-Q1-K1-B3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1644289
                   215
BLAST score
E value
                   2.0e-17
```

5803



Seg. No. 37704

Seq. ID LIB3092-008-Q1-K1-D4

Method BLASTN
NCBI GI g3821780
BLAST score 33
E value 4.0e-09
Match length 33
% identity 58

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 37705

Seq. ID LIB3092-008-Q1-K1-E12

Method BLASTX
NCBI GI g2749982
BLAST score 186
E value 6.0e-14
Match length 63
% identity 54

NCBI Description (AF036705) Similar to phytoene desaturase; coded for by C.

elegans cDNA CEESX74F; coded for by C. elegans cDNA yk303f4.3; coded for by C. elegans cDNA yk257d4.3; coded for by C. elegans cDNA yk303f4.5; coded for by C. elegans

cDNA yk257d4.5;

Seq. No. 37706

Seq. ID LIB3092-008-Q1-K1-E7

Method BLASTX
NCBI GI g4468803
BLAST score 385
E value 3.0e-37
Match length 128
% identity 51

NCBI Description (AL035601) cytochrome P450-like protein [Arabidopsis

thaliana]

Seq. No. 37707

Seq. ID LIB3092-008-Q1-K1-F8

Method BLASTX
NCBI GI g1169586
BLAST score 310
E value 1.0e-28
Match length 97
% identity 68

NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (CY-F1) >gi\_542079\_pir\_\_S41287 fructose-bisphosphatase (EC 3.1.3.11) - potato >gi\_440591\_emb\_CAA54265\_ (X76946)

fructose-1,6-bisphosphatase [Solanum tuberosum]

Seq. No. 37708

Seq. ID LIB3092-010-Q1-K1-C2

Method BLASTN NCBI GI g170087

E value

Match length

2.0e-26 144



```
BLAST score
                  2.0e-57
E value
                  309
Match length
                  85
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
                  37709
Seq. No.
                  LIB3092-010-Q1-K1-G10
Seq. ID
                  BLASTX
Method
                  g3785983
NCBI GI
                  102
BLAST score
                  1.0e-09
E value
                  74
Match length
                  42
% identity
NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]
                  37710
Seq. No.
                  LIB3092-010-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                   q1086249
NCBI GI
                   436
BLAST score
                   2.0e-43
E value
                   123
Match length
                   68
% identity
                  subtilisin-like protease - Alnus glutinosa
NCBI Description
                   >gi_757522_emb_CAA59964_ (X85975) subtilisin-like protease
                   [Alnus glutinosa]
                   37711
Seq. No.
                   LIB3092-011-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   g1805618
NCBI GI
                   249
BLAST score
                   2.0e-21
E value
                   87
Match length
                   59
% identity
NCBI Description (D49704) OSH45 transcript [Oryza sativa]
                   37712
Seq. No.
                   LIB3092-011-Q1-K1-E3
Seq. ID
                   BLASTX
Method
                   q125578
NCBI GI
                   155
BLAST score
                   2.0e-10
E value
                   81
Match length
                   48
% identity
                   PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >gi_167266 (M73707) phosphoribulokinase
                   [Mesembryanthemum crystallinum]
Seq. No.
                   37713
                   LIB3092-011-Q1-K1-E5
Seq. ID
                   BLASTX
Method
                   g2832304
NCBI GI
                   294
BLAST score
```

```
% identity 44
NCBI Description (AF044489) receptor-like protein kinase [Oryza sativa]
Seq. No. 37714
```

 Seq. ID
 LIB3092-012-Q1-K1-A11

 Method
 BLASTN

 NCBI GI
 g166379

 BLAST score
 167

 E value
 6.0e-89

Match length 287 % identity 90

NCBI Description Alfalfa glucose-regulated endoplasmic reticular protein

mRNA, complete cds

 Seq. No.
 37715

 Seq. ID
 LIB3092-012-Q1-K1-B7

 Method
 BLASTX

NCBI GI g3249084
BLAST score 135
E value 4.0e-09
Match length 56
% identity 23

NCBI Description (AC004473) Similar to red-1 (related to thioredoxin) gene

gb\_X92750 from Mus musculus. ESTs gb\_AA712687 and gb\_Z37223 come from this gene [Arabidopsis thaliana]

<u>.</u>,

Seq. No. 37716

Seq. ID LIB3092-012-Q1-K1-H2

Method BLASTN
NCBI GI g2905777
BLAST score 37
E value 1.0e-11
Match length 69
% identity 88

NCBI Description Glycine max ribosomal protein L41 mRNA, partial cds

Seq. No. 37717

Seq. ID LIB3092-012-Q1-K1-H4

Method BLASTN
NCBI GI g169897
BLAST score 279
E value 1.0e-156
Match length 390
% identity 93

NCBI Description G.max 28 kDa protein, complete cds

Seq. No. 37718

Seq. ID LIB3092-012-Q1-K1-H6

Method BLASTN
NCBI GI g2598656
BLAST score 116
E value 1.0e-58
Match length 232
% identity 88

NCBI Description Vicia faba mRNA for elongation factor 1-alpha (EF1-a)

Seq. No. 37719

5806



LIB3092-013-Q1-K1-D3 Seq. ID Method BLASTN NCBI GI q1053215 BLAST score 400 E value 0.0e + 00427 Match length 98 % identity NCBI Description Glycine max chlorophyll a/b-binding protein (cab3) mRNA, nuclear gene encoding chloroplast protein, complete cds 37720 Seq. No. LIB3092-013-Q1-K1-E1 Seq. ID BLASTN Method g21004 NCBI GI BLAST score 68 8.0e-30 E value Match length 172 85 % identity NCBI Description French Bean mRNA for plastid-located glutamine synthetase (EC 6.3.1.2)37721 Seq. No. Seq. ID LIB3092-013-Q1-K1-F10 Method BLASTX NCBI GI q4406372 148 BLAST score E value 5.0e-10 Match length 70 % identity 49 (AF109156) thiosulfate sulfurtransferase [Datisca NCBI Description glomerata] Seq. No. 37722 Seq. ID LIB3092-013-Q1-K1-F12 BLASTN Method NCBI GI g1619902 BLAST score 89 1.0e-42 E value 157 Match length % identity 89 NCBI Description Glycine max thiol protease isoform B mRNA, partial cds Seq. No. 37723 LIB3092-015-Q1-K1-A5 Seq. ID Method BLASTX g1353352 NCBI GI 396 BLAST score 2.0e-38 E value 108 Match length % identity 69 NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No. 37724

Seq. ID LIB3092-015-Q1-K1-B5

Method BLASTX NCBI GI g4138166

```
BLAST score
                   4.0e-12
E value
Match length
                  92
                   40
% identity
                  (AJ005341) MLO [Linum usitatissimum]
NCBI Description
                  37725
Seq. No.
                  LIB3092-015-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1616785
BLAST score
                  239
                   4.0e-20
E value
Match length
                  83
                   63
% identity
                  (U71121) pyruvate decarboxylase [Arabidopsis thaliana]
NCBI Description
                   37726
Seq. No.
                   LIB3092-015-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   q3901012
NCBI GI
BLAST score
                   356
E value
                   8.0e-34
                   100
Match length
                   73
% identity
                   (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                   sylvatica]
                   37727
Seq. No.
Seq. ID
                   LIB3092-015-Q1-K1-D6
Method
                   BLASTN
                   g2052028
NCBI GI
BLAST score
                   353
                   0.0e+00
E value
                   374
Match length
                   98
% identity
                  G.max mRNA for glutathione transferase
NCBI Description
                   37728
Seq. No.
                   LIB3092-015-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   g2262100
NCBI GI
                   558
BLAST score
```

2.0e-57 E value 130 Match length 78 % identity

(AC002343) unknown protein [Arabidopsis thaliana] NCBI Description

37729 Seq. No.

LIB3092-015-Q1-K1-G8 Seq. ID

BLASTX Method g3367594 NCBI GI BLAST score 205 4.0e-16 E value 101 Match length 47 % identity

(AL031135) putative protein [Arabidopsis thaliana] NCBI Description



```
37730
Seq. No.
                  LIB3092-016-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3461822
BLAST score
                  389
E value
                  1.0e-37
                  122
Match length
                  58
% identity
NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  37731
                  LIB3092-016-Q1-K1-C1
Seq. ID
                  BLASTX
Method
                  q4468986
NCBI GI
                  148
BLAST score
E value
                   6.0e-10
Match length
                   65
                   43
% identity
                  (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
                   37732
Seq. No.
                  LIB3092-016-Q1-K1-E7
Seq. ID
                  BLASTX
Method
                   g2500725
NCBI GI
                   154
BLAST score
                   2.0e-10
E value
Match length
                   84
% identity
                  PREPROTEIN TRANSLOCASE SECA SUBUNIT PRECURSOR
NCBI Description
                   >gi 939976_emb_CAA88933_ (Z49124) SecA [Spinacia oleracea]
                   37733
Seq. No.
Seq. ID
                   LIB3092-016-Q1-K1-F2
Method
                   BLASTX
                   g3582340
NCBI GI
BLAST score
                   241
E value
                   3.0e-20
Match length
                   117
% identity
                  (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
                   37734
Seq. No.
                   LIB3092-016-Q1-K1-H11
Seq. ID
                   BLASTX
Method
                   q3868758
NCBI GI
                   186
BLAST score
                   2.0e-14
E value
Match length
                   60
                   67
% identity
                  (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
                   37735
Seq. No.
                   LIB3092-017-Q1-K1-C9
Seq. ID
                   BLASTX
Method
```

5809

g82078

7.0e-18

219

NCBI GI

E value

BLAST score



```
Match length
% identity
                 chlorophyll a/b-binding protein type I precursor (cab-6A) -
NCBI Description
                  tomato >gi 170388 (M17633) chlorophyll a/b-binding protein
                  [Lycopersicon esculentum] >gi 225895 prf 1402358A
                  photosystem I protein CAB [Lycopersicon esculentum]
Seq. No.
                  37736
                  LIB3092-017-Q1-K1-D5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1518539
BLAST score
                  123
E value
                  7.0e-63
                  235
Match length
                  91
% identity
NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds
                  37737
Seq. No.
                  LIB3092-017-Q1-K1-E7
Seq. ID
Method
                  BLASTX
                  q1076418
NCBI GI
                  244
BLAST score
E value
                  7.0e-21
Match length
                  106
% identity
                  45
                  thioredoxin reductase (NADPH) (EC 1.6.4.5) B - Arabidopsis
NCBI Description
                  thaliana
Seq. No.
                  37738
                  LIB3092-017-Q1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129808
BLAST score
                  146
E value
                  4.0e-10
Match length
                  86
% identity
                  50
                  CATIONIC PEROXIDASE 2 PRECURSOR >gi 99873 pir B38265
NCBI Description
                  peroxidase (EC 1.11.1.7) precursor, cationic (clone PNC2) -
                  peanut >qi 166475 (M37637) cationic peroxidase [Arachis
                  hypogaea]
                  37739
Seq. No.
                  LIB3092-017-Q1-K1-G12
Seq. ID
Method
                  BLASTX
                  q1161566
NCBI GI
                  150
BLAST score
E value
                  5.0e-10
Match length
                  84
% identity
                  45
                  (X94943) peroxidase [Lycopersicon esculentum]
NCBI Description
```

37740 Seq. No.

Seq. ID LIB3092-017-Q1-K1-H7

Method BLASTX NCBI GI g3759184 BLAST score 293 E value 2.0e-26



```
Match length 106
% identity 55
```

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 37741

Seq. ID LIB3092-018-Q1-K1-A11

Method BLASTN
NCBI GI g2815245
BLAST score 74
E value 2.0e-33

Match length 250 % identity 82

NCBI Description C.arietinum mRNA for class I type 2 metallothionein (clone:

CanMT-2)

Seq. No. 37742

Seq. ID LIB3092-018-Q1-K1-A3

Method BLASTX
NCBI GI g119905
BLAST score 255
E value 3.0e-22
Match length 100
% identity 57

NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)

>gi\_81898\_pir\_\_S04030 ferredoxin--NADP+ reductase (EC
1.18.1.2) precursor - garden pea >gi\_20722\_emb\_CAA30978\_
(X12446) ferredoxin-NADH+ reductase preprotein (AA -52 to
308) [Pisum sativum] >gi\_226545\_prf\_\_1601517A ferredoxin

NADP reductase [Arachis hypogaea]

Seq. No. 37743

Seq. ID LIB3092-018-Q1-K1-A6

Method BLASTX
NCBI GI g119905
BLAST score 273
E value 3.0e-24
Match length 86
% identity 64

NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)

>gi\_81898\_pir\_\_S04030 ferredoxin--NADP+ reductase (EC
1.18.1.2) precursor - garden pea >gi\_20722\_emb\_CAA30978\_
(X12446) ferredoxin-NADH+ reductase preprotein (AA -52 to
308) [Pisum sativum] >gi\_226545\_prf\_\_1601517A ferredoxin

NADP reductase [Arachis hypogaea]

Seq. No. 37744

Seq. ID LIB3092-018-Q1-K1-C1

Method BLASTX
NCBI GI g1483213
BLAST score 482
E value 1.0e-48
Match length 126
% identity 76

NCBI Description (X96480) PAC [Arabidopsis thaliana]

Seq. No. 37745

Seq. ID LIB3092-018-Q1-K1-C10

```
Method
                  BLASTX
NCBI GI
                  g1894791
                  172
BLAST score
                  2.0e-12
E value
Match length
                  88
% identity
                  41
NCBI Description (X91617) 5'-3' exonuclease [Mus musculus]
                  37746
Seq. No.
Seq. ID
                  LIB3092-018-Q1-K1-C11
Method
                  BLASTN
NCBI GI
                  g456713
BLAST score
                  293
                  1.0e-164
E value
Match length
                  393
% identity
                  30
NCBI Description Glycine max gene for ubiquitin, complete cds
                  37747
Seq. No.
                  LIB3092-018-Q1-K1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g516853
BLAST score
                  52
E value
                  2.0e-20
Match length
                  100
% identity
                  46
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
Seq. No.
                  37748
Seq. ID
                  LIB3092-018-Q1-K1-F10
                  BLASTX
Method
NCBI GI
                  g2828147
                  195
BLAST score
                  4.0e-15
E value
                  53
Match length
                  68
% identity
NCBI Description (AF042384) BC-2 protein [Homo sapiens]
                  37749
Seq. No.
Seq. ID
                  LIB3092-018-Q1-K1-H2
Method
                  BLASTX
                  g2232254
NCBI GI
                  309
BLAST score
                  2.0e-28
E value
Match length
                  121
% identity
                  51
NCBI Description (AF005237) old-yellow-enzyme homolog [Catharanthus roseus]
Seq. No.
                  37750
                  LIB3092-019-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3582000
BLAST score
                  258
E value
                  2.0e-22
Match length
                  67
                  79
% identity
```

NCBI Description (AJ010942) hexose transporter protein [Lycopersicon

BLAST score

Match length % identity

E value

176 6.0e-13

62

56



## esculentum]

```
37751
Seq. No.
                  LIB3092-019-Q1-K1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1698547
BLAST score
                  45
E value
                  3.0e-16
Match length
                  137
                  83
% identity
                  Nicotiana tabacum calmodulin-binding protein (TCB60) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  37752
                  LIB3092-019-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1353352
BLAST score
                  468
                  6.0e-47
E value
Match length
                  136
% identity
NCBI Description
                  (U31975) alanine aminotransferase [Chlamydomonas
                  reinhardtii]
                  37753
Seq. No.
Seq. ID
                  LIB3092-019-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  q1001312
BLAST score
                  110
                  2.0e-11
E value
Match length
                  99
% identity
                  41
                  (D64006) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                  37754
                  LIB3092-020-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                  g119905
NCBI GI
BLAST score
                  201
                  9.0e-16
E value
                  81
Match length
                  56
% identity
                  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                  >qi 81898 pir S04030 ferredoxin--NADP+ reductase (EC
                   1.18.1.2) precursor - garden pea >gi_20722_emb_CAA30978
                   (X12446) ferredoxin-NADH+ reductase preprotein (AA -52 to
                   308) [Pisum sativum] >gi 226545_prf__1601517A ferredoxin
                  NADP reductase [Arachis hypogaea]
                  37755
Seq. No.
                  LIB3092-021-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g114734
```



NCBI Description AUXIN-INDUCED PROTEIN AUX28 >gi 81759\_pir\_\_A28993 aux28 protein - soybean >gi\_169921 (JO3919) auxin-regulated protein (Aux28) [Glycine max]

Seq. No. 37756

LIB3092-021-Q1-K1-B12 Seq. ID

Method BLASTX g3882356 NCBI GI BLAST score 153 2.0e-10 E value Match length 90 % identity 46

NCBI Description (U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis

thalianal

37757 Seq. No.

Seq. ID LIB3092-021-Q1-K1-B3

Method BLASTX NCBI GI g2370253 BLAST score 303 E value 1.0e-27 Match length 81 72 % identity

NCBI Description (Y13273) putative protein kinase [Lycopersicon esculentum]

37758 Seq. No.

Seq. ID LIB3092-021-Q1-K1-B7

BLASTX Method q2780192 NCBI GI BLAST score 183 1.0e-13 E value 78 Match length % identity 47

NCBI Description (AJ222713) unnamed protein product [Arabidopsis thaliana]

37759 Seq. No.

LIB3092-021-Q1-K1-B8 Seq. ID

BLASTN Method NCBI GI g4115334 BLAST score 96 E value 1.0e-46 Match length 119 % identity 21

NCBI Description Pisum sativum (Alaska) ubiquitin (PUB2) gene, complete cds

37760 Seq. No.

LIB3092-021-Q1-K1-E9 Seq. ID

Method BLASTX NCBI GI g2462741 BLAST score 254 7.0e-22 E value 97 Match length 74 % identity

NCBI Description (AC002292) Highly similar to auxin-induced protein

(aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 37761

```
LIB3092-021-Q1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1326160
BLAST score
                  50
                  4.0e-19
E value
Match length
                  122
% identity
                  95
                 Phaseolus vulgaris dehydrin mRNA, complete cds
NCBI Description
                  37762
Seq. No.
                  LIB3092-022-Q1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g309672
BLAST score
                  98
                  9.0e-48
E value
Match length
                  194
                  88
% identity
NCBI Description
                 Pisum sativum chloroplast photosystem I 24 kDa light
                  harvesting protein (lhca3) mRNA, complete cds
Seq. No.
Seq. ID
                  37763
                  LIB3092-022-Q1-K1-C11
Method
                  BLASTN
NCBI GI
                  q904153
BLAST score
                  59
E value
                  5.0e-25
Match length
                  123
% identity
                  87
                  Glycine max FAD2-2 microsomal omega-6 desaturase mRNA,
NCBI Description
                  complete cds
                   37764
Seq. No.
Seq. ID
                  LIB3092-022-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  q4469019
BLAST score
                  282
                  2.0e-25
E value
                  108
Match length
% identity
                  54
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                   37765
                  LIB3092-022-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3152606
BLAST score
                  310
                  2.0e-28
E value
                  87
Match length
                  64
% identity
                  (AC004482) putative ring zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
```

 Seq. No.
 37766

 Seq. ID
 LIB3092-022-Q1-K1-E1

 Method
 BLASTX

 NCBI GI
 q1750376

BLAST score 242

- French

```
E value
                  69
Match length
% identity
                  68
                  (U80808) ubiquitin activating enzyme [Arabidopsis thaliana]
NCBI Description
                  >gi 3150409 (AC004165) ubiquitin activating enzyme (UBA1)
                   [Arabidopsis thaliana]
                  37767
Seq. No.
                  LIB3092-022-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                   g1053059
NCBI GI
                   337
BLAST score
                   1.0e-31
E value
                   118
```

% identity 62 (U38423) histone H3 [Triticum aestivum] NCBI Description

37768 Seq. No. LIB3092-022-Q1-K1-G5 Seq. ID BLASTX Method g68200 NCBI GI 207 BLAST score 2.0e-16

E value 75 Match length % identity 61

Match length

fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description chloroplast - spinach >gi\_22633\_emb\_CAA47293\_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

37769 Seq. No.

LIB3092-027-Q1-K1-A2 Seq. ID

BLASTX Method q4325338 NCBI GI BLAST score 296 7.0e-27 E value Match length 115 61 % identity

(AF128392) No definition line found [Arabidopsis thaliana] NCBI Description

37770 Seq. No.

LIB3092-027-Q1-K1-A6 Seq. ID

BLASTN Method g1370177 NCBI GI 123 BLAST score E value 1.0e-62 167 Match length 93 % identity

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB5A

Seq. No.

LIB3092-027-Q1-K1-B9 Seq. ID

BLASTN Method q2062705 NCBI GI 33 BLAST score 6.0e-09 E value 37 Match length 59 % identity



NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 37772

Seq. ID LIB3092-027-Q1-K1-D12

Method BLASTX
NCBI GI g3913008
BLAST score 342
E value 1.0e-32
Match length 83

Match length83% identity81

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi 3021338\_emb\_CAA06308\_ (AJ005041) cytosolic

fructose-1,6-bisphosphate aldolase [Cicer arietinum]

Seq. No. 37773

Seq. ID LIB3092-028-Q1-K1-A4

Method BLASTX
NCBI GI 94234955
BLAST score 483
E value 1.0e-48
Match length 137
% identity 69

NCBI Description (AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]

Seq. No. 37774

Seq. ID LIB3092-028-Q1-K1-F9

Method BLASTX
NCBI GI g541943
BLAST score 221
E value 2.0e-18
Match length 65
% identity 66

NCBI Description metallothionein - soybean >gi\_228682\_prf\_\_1808316A

metallothionein-like protein [Glycine max]

Seq. No. 37775

Seq. ID LIB3092-028-Q1-K1-G4

Method BLASTN
NCBI GI g1663536
BLAST score 47
E value 2.0e-17
Match length 123
% identity 85

NCBI Description Glycine max clone RLG1 disease resistance protein homolog

gene, partial cds

Seq. No. 37776

Seq. ID LIB3092-028-Q1-K1-G7

Method BLASTN
NCBI GI g2924257
BLAST score 40
E value 5.0e-13
Match length 132
% identity 92

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 37777

BLAST score

Match length

E value

33 6.0e-09

81

```
LIB3092-029-Q1-K1-D1
Seq. ID
                  BLASTN
Method
                  g2052028
NCBI GI
                  108
BLAST score
                  6.0e-54
E value
Match length
                  211
                  90
% identity
                  G.max mRNA for glutathione transferase
NCBI Description
Seq. No.
                  37778
                  LIB3092-029-Q1-K1-D2
Seq. ID
Method
                  BLASTX
                  g4263818
NCBI GI
BLAST score
                  182
                  8.0e-14
E value
Match length
                  69
                   46
% identity
                  (AC006067) unknown protein [Arabidopsis thaliana]
NCBI Description
                   37779
Seq. No.
Seq. ID
                  LIB3092-029-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  q3334144
BLAST score
                  142
                   1.0e-08
E value
Match length
                   47
                   62
% identity
                  G1/S-SPECIFIC CYCLIN C-TYPE >gi_1695698_dbj_BAA13181_
NCBI Description
                   (D86925) C-type cyclin [Oryza sativa]
                   37780
Seq. No.
                   LIB3092-030-Q1-K1-B3
Seq. ID
Method
                   BLASTN
                   g310562
NCBI GI
BLAST score
                   275
                   1.0e-153
E value
                   354
Match length
                   95
% identity
NCBI Description Glycine max calmodulin (SCaM-5) mRNA, complete cds
                   37781
Seq. No.
                   LIB3092-030-Q1-K1-C9
Seq. ID
                   BLASTX
Method
                   g1076678
NCBI GI
                   292
BLAST score
                   2.0e-26
E value
                   82
Match length
                   76
% identity
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
                   37782
Seq. No.
Seq. ID
                   LIB3092-030-Q1-K1-D12
                   BLASTN
Method
                   g2564046
NCBI GI
```

Seq. No.

Seq. ID



```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MGI19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  37783
                  LIB3092-030-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g20729
BLAST score
                  405
E value
                  1.0e-39
Match length
                  101
% identity
                  81
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                  37784
Seq. No.
                  LIB3092-030-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1669591
BLAST score
                  141
E value
                  3.0e-09
Match length
                  56
                  54
% identity
                  (D88742) O-methyltransferase [Glycyrrhiza echinata]
NCBI Description
                  37785
Seq. No.
Seq. ID
                  LIB3092-032-Q1-K1-A1
Method
                  BLASTN
NCBI GI
                  q516853
BLAST score
                  50
E value
                  4.0e-19
                  70
Match length
% identity
                  34
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
Seq. No.
                  37786
                  LIB3092-032-Q1-K1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1592672
                  198
BLAST score
                  2.0e-15
E value
                  74
Match length
                  55
% identity
NCBI Description (X91921) germin1 [Arabidopsis thaliana]
                  37787
Seq. No.
Seq. ID
                  LIB3092-032-Q1-K1-B6
                  BLASTX
Method
                  g2145426
NCBI GI
BLAST score
                  276
                  9.0e-25
E value
                  83
Match length
                   65
% identity
                  (X91633) phosphoenolpyruvate carboxylase [Chiloschista
NCBI Description
                  pusilla]
```

5819

7.5

LIB3092-032-Q1-K1-C6

37788

```
Method
                   BLASTN
                   q2924257
NCBI GI
BLAST score
                   48
                   5.0e-18
E value
Match length
                   108
% identity
                   87
                  Tobacco chloroplast genome DNA
NCBI Description
                   37789
Seq. No.
                   LIB3092-032-Q1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4220477
BLAST score
                   155
                   3.0e-10
E value
Match length
                   104
% identity
                   34
                   (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   37790
                   LIB3092-032-Q1-K1-F7
Seq. ID
Method
                   BLASTN
NCBI GI
                   q18764
BLAST score
                   228
E value
                   1.0e-125
Match length
                   340
% identity
                   92
                  G.max tefS1 gene for elongation factor EF-la
NCBI Description
                   37791
Seq. No.
                   LIB3092-032-Q1-K1-H3
Seq. ID
                   BLASTN
Method
                   g596077
NCBI GI
BLAST score
                   62
                   3.0e-26
E value
Match length
                   142
% identity
                   86
                   Zea mays thiamine biosynthetic enzyme (thi1-1) mRNA,
NCBI Description
                   complete cds
                   37792
Seq. No.
Seq. ID
                   LIB3092-033-Q1-K1-F7
                   BLASTX
Method
NCBI GI
                   g2760830
BLAST score
                   515
E value
                   1.0e-52
                   119
Match length
% identity
                   (ACO03105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
```

37793 Seq. No. Seq. ID LIB3092-033-Q1-K1-G12 BLASTN Method

NCBI GI q493019 BLAST, score 76 E value 1.0e-34 Match length 243



```
% identity
                  Glycine max delta-aminolevulinic acid dehydratase (Alad)
NCBI Description
                  mRNA, complete cds
                  37794
Seq. No.
                  LIB3092-034-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                  q4406372
NCBI GI
                  147
BLAST score
                  2.0e-09
E value
                  60
Match length
                  55
% identity
                  (AF109156) thiosulfate sulfurtransferase [Datisca
NCBI Description
                  glomerata]
                  37795
Seq. No.
                  LIB3092-034-Q1-K1-F4
Seq. ID
                  BLASTX
Method
                  g123593
NCBI GI
                   200
BLAST score
                   2.0e-23
E value
                   101
Match length
                   66
% identity
                  HEAT SHOCK 70 KD PROTEIN >gi_82697_pir__A25089 heat shock
NCBI Description
                   protein 70 - maize
                   37796
Seq. No.
                   LIB3092-034-Q1-K1-F9
Seq. ID
                   BLASTN
Method
                   g1575724
NCBI GI
BLAST score
                   48
                   3.0e-18
E value
                   128
Match length
% identity
                   Glycine max 14-3-3 related protein SGF14A mRNA, complete
NCBI Description
                   37797
Seq. No.
                   LIB3092-034-Q1-K1-G4
Seq. ID
Method
                   BLASTX
                   q861170
NCBI GI
                   265
BLAST score
                   1.0e-23
E value
                   78
Match length
% identity
                   71
                  (X03697) heat shock protein 70 [Zea mays]
NCBI Description
                   37798
Seq. No.
                   LIB3092-034-Q1-K1-G5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g123613
                   237
BLAST score
                   4.0e-30
 E value
                   110
Match length
                   70
 % identity
                   HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_100222_pir__S14949
 NCBI Description
```

heat shock cognate protein 70 - tomato

Seq. No.

37804

>gi\_19256\_emb\_CAA37970\_ (X54029) heat shock protein cognate
70 [Lycopersicon esculentum]

```
37799
Seq. No.
                  LIB3092-034-Q1-K1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170019
                  40
BLAST score
                  2.0e-13
E value
                  171
Match length
% identity
NCBI Description Soybean maturation protein (MAT1) gene, complete cds
                  37800
Seq. No.
                  LIB3092-034-Q1-K1-H8
Seq. ID
Method
                  BLASTN
                  g1491775
NCBI GI
BLAST score
                  104
                  2.0e-51
E value
                  324
Match length
                  83
% identity
                  Arachis hypogaea cationic peroxidase (PNC1) mRNA, complete
NCBI Description
                  cds
                  37801
Seq. No.
Seq. ID
                  LIB3092-035-Q1-K1-A4
                  BLASTX
Method
                   q1771158
NCBI GI
BLAST score
                   145
                   2.0e-09
E value
Match length
                   67
                   40
% identity
NCBI Description (Y07861) MFP1 protein [Lycopersicon esculentum]
Seq. No.
                   37802
                   LIB3092-035-Q1-K1-B12
Seq. ID
                   BLASTX
Method
                   q4185509
NCBI GI
                   251
BLAST score
                   1.0e-21
E value
                   95
Match length
                   51
% identity
                   (AF102821) actin depolymerizing factor 3 [Arabidopsis
NCBI Description
                   thaliana]
                   37803
Seq. No.
                   LIB3092-035-Q1-K1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3860263
                   120
BLAST score
                   1.0e-08
E value
                   120
Match length
                   42
% identity
                   (AC005824) putative cytochrome p450 protein [Arabidopsis
NCBI Description
                   thaliana]
```



```
LIB3092-035-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501189
                  276
BLAST score
E value
                  2.0e-24
                  114
Match length
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thil-1
                  - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  37805
Seq. ID
                  LIB3092-035-Q1-K1-C7
                  BLASTX
Method
                  q1899025
NCBI GI
                  287
BLAST score
E value
                  1.0e-25
                  141
Match length
                  49
% identity
                  (U28215) hexokinase 2 [Arabidopsis thaliana] >gi_3687232
NCBI Description
                   (AC005169) hexokinase [Arabidopsis thaliana]
Seq. No.
                  37806
                  LIB3092-035-Q1-K1-D11
Seq. ID
                  BLASTN
Method
                  q1055367
NCBI GI
                   392
BLAST score
                  0.0e+00
E value
                   400
Match length
                   99
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   37807
Seq. No.
Seq. ID
                   LIB3092-035-Q1-K1-E7
Method
                   BLASTX
                   g2213882
NCBI GI
BLAST score
                   152
                   2.0e-21
E value
Match length
                   81
% identity
                   70
                   (AF004165) 2-isopropylmalate synthase [Lycopersicon
NCBI Description
                   pennellii]
                   37808
Seq. No.
                   LIB3092-035-Q1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2213882
                   169
BLAST score
                   7.0e-17
E value
                   104
Match length
                   50
% identity
                   (AF004165) 2-isopropylmalate synthase [Lycopersicon
```

7

Seq. No. 37809

pennellii]

NCBI Description

Method

NCBI GI BLAST score



```
LIB3092-035-Q1-K1-F6
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                    q1055367
 BLAST score
                    429
                    0.0e+00
 E value
                    461
 Match length
 % identity
                    98
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
 NCBI Description
                    subunit mRNA, complete cds
 Seq. No.
                    37810
 Seq. ID
                    LIB3092-035-Q1-K1-H12
 Method
                    BLASTX
                    q4455294
 NCBI GI
 BLAST score
                    270
                    9.0e-24
 E value
                    116
 Match length
 % identity
                   (AL035528) putative protein [Arabidopsis thaliana]
 NCBI Description
                    37811
 Seq. No.
 Seq. ID
                    LIB3092-035-Q1-K1-H6
 Method
                    BLASTX
 NCBI GI
                    q3860263
                    279

    BLAST score

                    9.0e-25
 E value
                    68
 Match length
                    71
 % identity
                    (AC005824) putative cytochrome p450 protein [Arabidopsis
 NCBI Description
                    thaliana]
                    37812
 Seq. No.
                    LIB3092-036-Q1-K1-A10
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g169980
 BLAST score
                    157
                    5.0e-83
 E value
                    273
 Match length
 % identity
                    89
 NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                    37813
 Seq. No.
                    LIB3092-036-Q1-K1-D12
 Seq. ID
 Method
                    BLASTX
                    g3885513
 NCBI GI
                    434
 BLAST score
                    7.0e-43
 E value
 Match length
                    91
                    87
 % identity
                    (AF084201) similar to chloroplast 50S ribosomal protein L31
 NCBI Description
                    [Medicago sativa]
                    37814
 Seq. No.
 Seq. ID
                    LIB3092-036-Q1-K1-E1
                    BLASTN
```

g310566

77



```
2.0e-35
E value
Match length
                  173
% identity
                  Soybean glutamate 1-semialdehyde aminotransferase mRNA,
NCBI Description
                  complete cds
                  37815
Seq. No.
                  LIB3092-036-Q1-K1-F3
Seq. ID
                  BLASTX
Method
                  q4056462
NCBI GI
BLAST score
                  211
                  6.0e-17
E value
Match length
                   99
                   58
% identity
                   (AC005990) Strong similarity to gb_Y09876 aldehyde
NCBI Description
                  dehydrogenase (NAD+) from Nicotiana tabacum and a member of
                   the aldehyde dehydrogenase family PF_00171. ESTs
                   gb_F15117, gb_R83958 and gb_586262 come from this gene.
                   [Arabidopsis thaliana]
                   37816
Seq. No.
                   LIB3092-036-Q1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q417148
BLAST score
                   218
                   6.0e-18
E value
                   76
Match length
                   51
% identity
                   PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A)
NCBI Description
                   (G2-4) >gi 99912_pir__A33654 heat shock protein 26A -
                   soybean > gi_169981 (M20363) Gmhsp26-A [Glycine max]
                   37817
Seq. No.
                   LIB3092-037-Q1-K1-A4
Seq. ID
                   BLASTN
Method
                   q2815245
NCBI GI
BLAST score
                   79
                   2.0e-36
E value
                   243
Match length
% identity
                  C.arietinum mRNA for class I type 2 metallothionein (clone:
NCBI Description
                   CanMT-2)
                   37818
 Seq. No.
                   LIB3092-038-Q1-K1-A1
 Seq. ID
                   BLASTN
Method
                   g12158
 NCBI GI
```

32 BLAST score 9.0e-09 E value 60 Match length % identity 90

Pea gpal gene for subunit A of chloroplast NCBI Description

glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.13)

37819 Seq. No.

LLB3092-038-Q1-K1-A11 Seq. ID

BLASTX Method

```
NCBI GI
BLAST score
                   201
                   1.0e-15
E value
Match length
                   144
                   43
% identity
                  ssb protein homolog - common tobacco chloroplast
NCBI Description
                   >gi 225266 prf 1211235DB ssb-like ORF 273 [Nicotiana
                   tabacum]
                   37820
Seq. No.
Seq. ID
                   LIB3092-038-Q1-K1-B6
                   BLASTX
Method
                   g2760330
NCBI GI
                   191
BLAST score
                   4.0e-15
E value
                   79
Match length
                   57
% identity
```

(AC002130) F1N21.15 [Arabidopsis thaliana] NCBI Description

```
37821
Seq. No.
Seq. ID
                   LIB3092-038-Q1-K1-B8
Method
                   BLASTN
                   g4336433
NCBI GI
                   50
BLAST score
                   2.0e-19
E value
```

74 Match length 92 % identity

Lotus japonicus nodule-enhanced protein phosphatase type 2C NCBI Description

(NPP2C1) mRNA, complete cds

37822 Seq. No. Seq. ID LIB3092-038-Q1-K1-B9

Method BLASTX g1361983 NCBI GI BLAST score 169 9.0e-18 E value Match length 114 50 % identity

ARP protein - Arabidopsis thaliana >gi 886434 emb CAA89858\_ NCBI Description

(Z49776) ARP protein [Arabidopsis thaliana]

37823 Seq. No.

Seq. ID LIB3092-038-Q1-K1-C10

Method BLASTX q4185509 NCBI GI 151 BLAST score E value 6.0e-10 Match length 86 % identity

(AF102821) actin depolymerizing factor 3 [Arabidopsis NCBI Description

thaliana]

Seq. No. 37824

Seq. ID LIB3092-038-Q1-K1-D8

Method BLASTN NCBI GI q1053215 BLAST score 255



81

69

Match length % identity

NCBI Description

```
1.0e-141
E value
                  331
Match length
% identity
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                  nuclear gene encoding chloroplast protein, complete cds
Seq. No.
                  LIB3092-038-Q1-K1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3059094
BLAST score
                  89
E value
                  1.0e-42
Match length
                   166
                   89
% identity
                  Glycine max mRNA for magnesium chelatase subunit
NCBI Description
Seq. No.
                   37826
                   LIB3092-038-Q1-K1-H2
Seq. ID
                   BLASTX
Method
                   q1710112
NCBI GI
                   228
BLAST score
                   5.0e-19
E value
Match length
                   88
% identity
                   57
                  (U53864) PRH19 [Arabidopsis thaliana]
NCBI Description
                   37827
Seq. No.
                   LIB3092-039-Q1-K1-C4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1808591
BLAST score
                   95
                   4.0e-46
E value
Match length
                   199
                   87
% identity
NCBI Description C.arietinum mRNA for SAM-synthetase
                   37828
Seq. No.
                   LIB3092-040-Q1-K1-B3
Seq. ID
Method
                   BLASTX
                   q531829
NCBI GI
                   152
BLAST score
                   5.0e-10
E value
                   70
Match length
                   47
% identity
                   (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
Seq. No.
                   37829
                   LIB3092-040-Q1-K1-D4
Seq. ID
Method
                   BLASTX
                   g2852449
NCBI GI
BLAST score
                   234
                   1.0e-19
E value
```

(D88207) protein kinase [Arabidopsis thaliana] >gi 2947061

1

(AC002521) putative protein kinase [Arabidopsis thaliana]



```
37830
Seq. No.
                  LIB3092-040-Q1-K1-E9
Seq. ID
                  BLASTX
Method
                  g4455196
NCBI GI
                  274
BLAST score
                  3.0e-24
E value
                  86
Match length
                   62
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   37831
Seq. No.
                  LIB3092-040-Q1-K1-H9
Seq. ID
                  BLASTX
Method
                   g4206122
NCBI GI
                   99
BLAST score
                   2.0e-10
E value
Match length
                   84
% identity
                   41
                   (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
NCBI Description
                   crystallinum]
Seq. No.
                   37832
Seq. ID
                   LIB3092-042-Q1-K1-B3
Method
                   BLASTX
                   g3687652
NCBI GI
BLAST score
                   172
                   5.0e-13
E value
                   116
Match length
                   47
% identity
                  (AF047352) rubisco activase precursor [Datisca glomerata]
NCBI Description
Seq. No.
                   37833
                   LIB3092-042-Q1-K1-B7
Seq. ID
Method
                   BLASTX
                   q3676069
NCBI GI
BLAST score
                   352
                   2.0e-33
E value
                   109
Match length
                   61
% identity
                  (Y17899) ERG protein [Antirrhinum majus]
NCBI Description
                   37834
Seq. No.
                   LIB3092-042-Q1-K1-E11
Seq. ID
                   BLASTX
Method
                   g3738297
NCBI GI
                   228
BLAST score
                   9.0e-19
E value
                   130
Match length
                   13
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                   37835
Seq. No.
                   LIB3092-042-Q1-K1-F2
Seq. ID
                   BLASTX
Method
```

g2828292

283

NCBI GI BLAST score

```
3.0e-25
E value
                   100
Match length
                   59
% identity
                   (AL021687) neoxanthin cleavage enzyme-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   37836
Seq. No.
Seq. ID
                   LIB3092-042-Q1-K1-F7
Method
                   BLASTX
NCBI GI
                   g4337178
BLAST score
                   293
                   2.0e-26
E value
                   130
Match length
% identity
                   53
                   (AC006416) T31J12.5 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   37837
Seq. ID
                   LIB3092-042-Q1-K1-G3
Method
                   BLASTX
                   g1785716
NCBI GI
BLAST score
                   168
E value
                   1.0e-11
Match length
                   94
% identity
                   41
                  (Y08501) orf160 [Arabidopsis thaliana]
NCBI Description
                   37838
Seq. No.
Seq. ID
                   LIB3092-043-Q1-K1-A1
Method
                   BLASTN
                   g2598656
NCBI GI
BLAST score
                   98
                   6.0e-48
E value
Match length
                   158
                   91
% identity
                  Vicia faba mRNA for elongation factor 1-alpha (EF1-a)
NCBI Description
                   37839
Seq. No.
```

Seq. ID LIB3092-043-Q1-K1-A5

Method BLASTN
NCBI GI g2598656
BLAST score 243
E value 1.0e-134
Match length 379
% identity 91

NCBI Description Vicia faba mRNA for elongation factor 1-alpha (EF1-a)

Seq. No.

Seq. ID LIB3092-043-Q1-K1-A7

37840

Method BLASTN
NCBI GI g2598656
BLAST score 46
E value 8.0e-17
Match length 58
% identity 95

NCBI Description Vicia faba mRNA for elongation factor 1-alpha (EF1-a)

Seq. No. 37841



LIB3092-043-Q1-K1-B5 Seq. ID BLASTX Method g3287695 NCBI GI 419 BLAST score 3.0e-41E value Match length 94 % identity 85 (AC003979) Similar to hypothetical protein C34B7.2 NCBI Description gb 1729503 from C. elegans cosmid gb\_Z83220. [Arabidopsis thaliana] Seq. No. 37842 LIB3092-043-Q1-K1-C4 Seq. ID Method BLASTX NCBI GI g2443348 239 BLAST score E value 4.0e-20 126 Match length % identity 39 (AB001379) cytochrome P450 [Glycyrrhiza echinata] NCBI Description Seq. No. 37843 Seq. ID LIB3092-043-Q1-K1-E9 Method BLASTX NCBI GI q3738306 BLAST score 312 1.0e-28 E value Match length 142 % identity 47 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana] Seq. No. 37844 Seq. ID LIB3092-043-Q1-K1-G11 Method BLASTX NCBI GI q4406530 BLAST score 334 3.0e-31E value 119 Match length % identity 65 (AF126870) rubisco activase [Vigna radiata] NCBI Description 37845 Seq. No. Seq. ID LIB3092-043-Q1-K1-G5 Method BLASTX NCBI GI g1352186 BLAST score 246 5.0e-21 E value Match length 118 42 % identity ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) NCBI Description (CYTOCHROME P450 74)  $>gi_404866$  (U00428) allene oxide synthase [Linum usitatissimum]

Seq. No. 37846

Seq. ID LIB3092-043-Q1-K1-H10

Method BLASTN NCBI GI g4406529



BLAST score E value 4.0e-65 257 Match length 87 % identity

Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene NCBI Description

encoding chloroplast protein, complete cds

37847 Seq. No.

LIB3092-044-Q1-K1-A4 Seq. ID

BLASTX Method NCBI GI q1654140 BLAST score 183 E value 1.0e-29 151 Match length 52 % identity

(U37840) lipoxygenase [Lycopersicon esculentum] NCBI Description

37848 Seq. No.

LIB3092-044-Q1-K1-A6 Seq. ID

BLASTX Method q3249070 NCBI GI BLAST score 145 E value 4.0e-09 Match length 77 % identity 43

(AC004473) Contains similarity to siah binding protein 1 NCBI Description

(SiahBP1) gb\_U51586 from Homo sapiens. ESTs gb\_T43314,

gb T43315 and gb R90521, gb T75905 [Arabidopsis thaliana]

37849 Seq. No.

LIB3092-044-Q1-K1-B10 Seq. ID

Method BLASTX NCBI GI q266893 BLAST score 108 4.0e-12 E value Match length 106 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE NCBI Description

PRECURSOR (RUBISCO ACTIVASE) >gi\_322416 pir S28172 ribulose-bisphosphate carboxylase activase - cucumber >qi 18284 emb CAA47906 (X67674) rubisco activase [Cucumis

sativus]

Seq. No. 37850

LIB3092-044-Q1-K1-E10 Seq. ID

Method BLASTX NCBI GI q3080427 BLAST score 148 E value 2.0e-09 76 Match length 49 % identity

(AL022604) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 37851

LIB3092-044-Q1-K1-G3 Seq. ID

BLASTX Method g3202028 NCBI GI



BLAST score 136
E value 1.0e-08
Match length 55
% identity 58
NCBI Description (AF069317) cystathionine gamma-synthase [Mesembryanthemum crystallinum]

Seq. No. 37852
Seq. ID LIB3092-044-Q1-K1-H1

Seq. ID LIB3092-04
Method BLASTX
NCBI GI 94544434
BLAST score 169
E value 7.0e-12
Match length 98
% identity 45

NCBI Description (AC006955) putative DNA-directed RNA polymerase II

[Arabidopsis thaliana]

Seq. No. 37853

Seq. ID LIB3092-044-Q1-K1-H5

Method BLASTX
NCBI GI g2911075
BLAST score 255
E value 5.0e-22
Match length 124
% identity 44

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 37854

Seq. ID LIB3092-045-Q1-K1-B10

Method BLASTN
NCBI GI g1053215
BLAST score 155
E value 7.0e-82
Match length 306
% identity 88

NCBI Description Glycine max chlorophyll a/b-binding protein (cab3) mRNA,

nuclear gene encoding chloroplast protein, complete cds

Seq. No. 37855

Seq. ID LIB3092-045-Q1-K1-B11

Method BLASTN
NCBI GI g1053215
BLAST score 117
E value 3.0e-59
Match length 313
% identity 84

NCBI Description Glycine max chlorophyll a/b-binding protein (cab3) mRNA,

nuclear gene encoding chloroplast protein, complete cds

Seq. No. 37856

Seq. ID LIB3092-045-Q1-K1-D5

Method BLASTX
NCBI GI g2842490
BLAST score 322
E walue 9.0e-30
Match length 98



```
% identity
                  (AL021749) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                  37857
Seq. No.
                  LIB3092-045-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                  g2924325
NCBI GI
                  200
BLAST score
                  9.0e-16
E value
                  92
Match length
                  47
% identity
                  (Z93765) hypothetical protein [Malus domestica]
NCBI Description
Seq. No.
                  37858
                  LIB3092-045-Q1-K1-G12
Seq. ID
Method
                  BLASTX
                  q4454464
NCBI GI
BLAST score
                  159
E value
                  1.0e-10
                  75
Match length
% identity
                  41
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                  37859
Seq. No.
                  LIB3092-045-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q857395
BLAST score
                   164
                   3.0e-11
E value
Match length
                   97
% identity
                   54
                  (D50869) mitotic cyclin a2-type [Glycine max]
NCBI Description
Seq. No.
                   37860
                   LIB3092-045-Q1-K1-H7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3096947
BLAST score
                   343
E value
                   3.0e-32
Match length
                   112
% identity
                   61
                   (Y16327) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   37861
                   LIB3092-046-Q1-K1-D7
Seq. ID
Method
                   BLASTX
                   g4325282
NCBI GI
BLAST score
                   213
                   3.0e-17
E value
                   72
Match length
                   58
% identity
                   (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
NCBI Description
                   >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
```

Seq. No. \*37862

[Arabidopsis thaliana]



```
LIB3092-046-Q1-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q169980
BLAST score
                  77
                  3.0e-35
E value
                  213
Match length
% identity
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
NCBI Description
                  37863
Seq. No.
                  LIB3092-046-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3659909
                  384
BLAST score
E value
                  4.0e-37
                  118
Match length
                  71
% identity
                  (AF020715) histidyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                  37864
Seq. No.
                  LIB3092-047-Q1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3335366
BLAST score
                  269
                  1.0e-23
E value
                  117
Match length
                   47
% identity
                  (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
                   37865
Seq. No.
                  LIB3092-047-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2244905
BLAST score
                   171
E value
                   3.0e-12
Match length
                   119
% identity
                   35
                   (Z97339) indole-3-acetate beta-glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   37866
Seq. No.
                   LIB3092-047-Q1-K1-C8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g131384
                   201
BLAST score
                   4.0e-27
E value
                   111
Match length
                   64
% identity
NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                   THYLAKOID MEMBRANE PROTEIN) >gi 81934 pir_S04132
                   photosystem II oxygen-evolving complex protein 1 precursor
                   - garden pea >gi_20621_emb_CAA33408 (X15350) precursor (AA
                   -81 to 248) [Pisum satīvum] >gi_344004_dbj_BAA02554_
                   (D13297) precursor for 33-kDa protein of photosystem II
                   [Pisum sativum] >gi_226937_prf__1611461A O2 evolving
```

complex 33kD protein [Arachis hypogaea]



```
Seq. No.
                   37867
                  LIB3092-047-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4335758
BLAST score
                   234
E value
                   2.0e-19
                   105
Match length
% identity
                   51
                   (AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   378.68
Seq. ID
                   LIB3092-047-Q1-K1-F4
Method
                   BLASTX
NCBI GI
                   q2119719
                   176
BLAST score
                   6.0e-13
E value
Match length
                   106
% identity
                   40
NCBI Description heat-shock cognate protein 70-3 - tomato >gi_762844
                   (L41253) Hsc70 [Lycopersicon esculentum]
Seq. No.
                   37869
Seq. ID
                   LIB3092-047-Q1-K1-G4
                   BLASTX
Method
                   g3935138
NCBI GI
                   220
BLAST score
                   8.0e-18
E value
Match length
                   90
                   50
% identity
                  (AC005106) T25N20.2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   37870
                   LIB3092-047-Q1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3915826
BLAST score
                   451
E value
                   5.0e-45
Match length
                   108
% identity
                   79
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                   37871
Seq. ID
                   LIB3092-048-Q1-K1-C9
Method
                   BLASTN
                   g1166432
NCBI GI
BLAST score
                   157
E value
                   4.0e-83
                   257
Match length
                   91
% identity
                  Helianthus annuus mitochondrion DNA for tRNA-Ile and
NCBI Description
                   tRNA-Ala genes
```

Seq. No. 37872

Seq. ID LIB3092-048-Q1-K1-F4

Method BLASTX 92270994

```
BLAST score 154
E value 2.0e-10
Match length 106
% identity 34
NCBI Description (AF004809) Ca+2-binding EF hand protein [Glycine max]
Seq. No. 37873
Seq. ID LIB3092-048-Q1-K1-H4
Method BLASTX
```

Method BLASTX
NCBI GI g2736147
BLAST score 367
E value 3.0e-35
Match length 79
% identity 81

NCBI Description (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis thaliana] >gi\_3132481 (AC003096) fatty acid hydroxylase,

FAH1 [Arabidopsis thaliana]

LIB3092-049-Q1-K1-A3

Method BLASTN
NCBI GI g20670
BLAST score 50
E value 3.0e-19
Match length 158
% identity 84

NCBI Description P.sativum Lhcb3 gene for chlorophyll a/b-binding protein

Seq. No. 37875

Seq. ID LIB3092-049-Q1-K1-A5

Method BLASTX
NCBI GI g2499703
BLAST score 342
E value 4.0e-32
Match length 144
% identity 46

NCBI Description PHOSPHOLIPASE D1 (PLD 1) (CHOLINE PHOSPHATASE 1)

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D1)
>gi\_1185463 (U38545) phospholipase D1 [Homo sapiens]
>gi\_4505873 ref\_NP\_002653.1\_pPLD1\_ phospholipase D1,

phophatidylcholine-specific (NOTE: redefinition of symbol)

Seq. No. 37876

Seq. ID LIB3092-049-Q1-K1-A6

Method BLASTX
NCBI GI g2505870
BLAST score 152
E value 7.0e-10
Match length 41
% identity 66

NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No.

37877

Seq. ID LIB3092-049-Q1-K1-B7

Method BLASTX
NCBI GI g1184075
BLAST score 183



E value 2.0e-13 Match length 127 % identity 3

NCBI Description (U42444) Cf-2.1 [Lycopersicon pimpinellifolium] >qi 1587673 prf 2207203A Cf-2 gene [Lycopersicon

esculentum]

Seq. No. 37878

Seq. ID LIB3092-049-Q1-K1-D1

Method BLASTX
NCBI GI g729273
BLAST score 152
E value 2.0e-10
Match length 46
% identity 61

NCBI Description CYPRO4 PROTEIN >gi\_322804\_pir\_\_S28592 cypro4 protein -

cardoon >gi 17959 emb CAA49354 (X69672) cypro4 [Cynara

cardunculus]

Seq. No. 37879

Seq. ID LIB3092-049-Q1-K1-E11

Method BLASTX
NCBI GI g2052029
BLAST score 182
E value 1.0e-13
Match length 91
% identity 49

NCBI Description (Y10820) glutathione transferase [Glycine max]

Seq. No. 37880

Seq. ID LIB3092-049-Q1-K1-G6

Method BLASTX
NCBI GI g2981169
BLAST score 144
E value 6.0e-09
Match length 112
% identity 36

NCBI Description (AF053077) osmotic stress-induced zinc-finger protein

[Nicotiana tabacum]

Seq. No. 37881

Seq. ID LIB3092-049-Q1-K1-H6

Method BLASTN
NCBI GI g16220
BLAST score 146
E value 2.0e-76
Match length 434
% identity 83

NCBI Description A.thaliana mRNA for mitochondrial chaperonin hsp60

Seq. No. 37882

Seq. ID LIB3092-050-Q1-K1-B9

Method BLASTN
NCBI GI g4406805
BLAST score 37
E value 2.0e-11
Match length 113



```
% identity
                  Arabidopsis thaliana chromosome II BAC T27K22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3092-050-Q1-K1-E10
                  BLASTN
Method
NCBI GI
                  g340697
BLAST score
                  40
                  3.0e-13
E value
Match length
                  122
% identity
                  88
                  Soybean chloroplast 16S/23S ribosomal intergenic spacer DNA
NCBI Description
                  37884
Seq. No.
Seq. ID
                  LIB3092-050-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  g2262177
BLAST score
                  538
E value
                  4.0e-55
Match length
                 到49
% identity
                  65
NCBI Description
                   (AC002329) hypothetical protein similar to T18A10.3
                   [Arabidopsis thaliana]
                  37885
Seq. No.
Seq. ID
                  LIB3092-050-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g4220535
                  237
BLAST score
                   6.0e-20
E value
Match length
                  84
% identity
                   61
                   (AL035356) clathrin coat assembly like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  37886
Seq. ID
                  LIB3092-050-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  180
                   2.0e-19
E value
Match length
                  86
% identity
                   66
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  37887
```

LIB3092-050-Q1-K1-G7 Seq. ID

Method BLASTN g984307 NCBI GI BLAST score 131 E value 2.0e-67 Match length 276 88 % identity

NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151



protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precurso

Seq. No. 37888
Seq. ID LIB3092-051-Q1-K1-E10

Method BLASTX
NCBI GI g2827709
BLAST score 518
E value 9.0e-53
Match length 114
% identity 88

NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

Seq. No. 37889

Seq. ID LIB3092-053-Q1-K1-C5

Method BLASTX
NCBI GI g3367593
BLAST score 146
E value 3.0e-09
Match length 100
% identity 32

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

>gi 3805841\_emb\_CAA21461\_ (AL031986) putative protein

[Arabidopsis thaliana]

Seq. No. 37890

Seq. ID LIB3092-053-Q1-K1-E9

Method BLASTN
NCBI GI g340697
BLAST score 43
E value 3.0e-15
Match length 79
% identity 90

NCBI Description Soybean chloroplast 16S/23S ribosomal intergenic spacer DNA

Seq. No. 37891

Seq. ID LIB3092-053-Q1-K1-F5

Method BLASTX
NCBI GI g99902
BLAST score 282
E value 3.0e-25
Match length 112
% identity 54

NCBI Description translation elongation factor eEF-1 alpha chain (gene

tefS1) - soybean

Seq. No. 37892

Seq. ID LIB3092-053-Q1-K1-F7

Method BLASTX
NCBI GI g3378650
BLAST score 219
E value 9.0e-18
Match length 117
% identity 48

NCBI Description (X97606) abscisic acid activated [Medicago sativa]

Seq. No. 37893



```
LIB3092-054-Q1-K1-A2
Seq. ID
                   BLASTX
Method
                   g2129647
NCBI GI
                   209
BLAST score
                   5.0e-17
 E value
Match length
                   52
 % identity
                   69
                   MYB-related protein 33,2K - Arabidopsis thaliana
 NCBI Description
                   >gi 1263097 emb CAA90810_ (Z54137) MYB-related protein
                    [Arabidopsis thaliana]
 Seq. No.
                   37894
                   LIB3092-054-Q1-K1-C1
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g30044
 BLAST score
                   81
 E value
                   9.0e-38
                   276
 Match length
 % identity
                   83
                   Human mRNA for collagen VI alpha-2 C-terminal globular
 NCBI Description
                   domain
 Seq. No.
                   37895
                   LIB3092-054-Q1-K1-F12
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g1174162
 BLAST score
                   150
 E value
                    5.0e-12
                    95
 Match length
 % identity
                    48
                    (U44976) ubiquitin-conjugating enzyme [Arabidopsis
 NCBI Description
                    thaliana] >gi 3746915 (AF091106) E2
                    ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
                    37896
 Seq. No.
                   LIB3092-054-Q1-K1-G2
 Seq. ID
                    BLASTN
 Method
 NCBI GI
                    g23238
 BLAST score
                    40
                    2.0e-13
 E value
                    200
 Match length
                    80
 % identity
 NCBI Description Homo sapiens mRNA for 14kDa beta-galactoside-binding lectin
                    37897
 Seq. No.
                    LIB3092-054-Q1-K1-H12
 Seq. ID
                    BLASTX
 Method
                    g2529662
 NCBI GI
 BLAST score
                    284
                    5.0e-26
 E value
                    70
```

Match length % identity NCBI Description

(ACO02535) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana] >gi 3738278 (AC005309) putative

small nuclear ribonucleoprotein, Sm D2 [Arabidopsis

thaliana]



```
Seq. No.
                  LIB3092-054-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2529662
BLAST score
                  133
                  4.0e-10
E value
Match length
                  93
                  45
% identity
                  (AC002535) putative small nuclear ribonucleoprotein, Sm D2
NCBI Description
                  [Arabidopsis thaliana] >gi 3738278 (AC005309) putative
                  small nuclear ribonucleoprotein, Sm D2 [Arabidopsis
                  thaliana]
                  37899
Seq. No.
                  LIB3092-055-Q1-K1-A7
Seq. ID
Method
                  BLASTN
                  g4105179
NCBI GI
BLAST score
                  75
                  5.0e-34
E value
                  151
Match length
% identity
                  Pisum sativum plastoglobule associated protein PG1
NCBI Description
                  precursor, mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  37900
Seq. No.
                  LIB3092-055-Q1-K1-B12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g975703
BLAST score
                   42
                  2.0e-14
E value
Match length
                   95
% identity
                   56
NCBI Description
                  P.sativum GR gene
Seq. No.
                   37901
                   LIB3092-055-Q1-K1-G4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q169897
BLAST score
                   35
                   2.0e-10
E value
Match length
                   117
% identity
                   90
                  G.max 28 kDa protein, complete cds
NCBI Description
                   37902
Seq. No.
                   LIB3092-055-Q1-K1-G5
Seq. ID
Method
                   BLASTN
```

NCBI GI q169974 93 BLAST score 7.0e-45E value 221 Match length 86 % identity

Glycine max vspA gene, complete cds NCBI Description

37903 Seq. No.

Seq. ID LIB3092-055-Q1-K1-H12

BLAST score



```
BLASTX
    Method
                        q3169073
    NCBI GI
                        154
    BLAST score
* E value
                        2.0e-10
                        67
    Match length
                        48
    % identity
                        (AL023705) phenylalanyl-trna synthetase
    NCBI Description
                        [Schizosaccharomyces pombe]
                        37904
    Seq. No.
                        LIB3092-056-Q1-K1-E1
    Seq. ID
    Method
                        BLASTN
    NCBI GI
                        q1236948
                        56
    BLAST score
                        3.0e-23
    E value
    Match length
                        112
                        88
     % identity
    NCBI Description Glycine max lipoxygenase L-5 (vlxB) mRNA, complete cds
                        37905
     Seq. No.
                        LIB3092-056-Q1-K1-G11
     Seq. ID
                        BLASTX
    Method
     NCBI GI
                        g4263818
     BLAST score
                        141
                        1.0e-08
     E value
                        113
     Match length
                        34
     % identity
                        (AC006067) unknown protein [Arabidopsis thaliana]
     NCBI Description
                        37906
     Seq. No.
                        LIB3092-056-Q1-K1-H11
     Seq. ID
     Method
                        BLASTX
     NCBI GI
                        q1657948
                        176
     BLAST score
                        1.0e-13
     E value
                        80
     Match length
                        57
     % identity
                        (U73466) MipC [Mesembryanthemum crystallinum]
    NCBI Description
                        37907
     Seq. No.
                        LIB3092-057-Q1-K1-C10
     Seq. ID
                        BLASTX
     Method
                        g547712
     NCBI GI
                        279
     BLAST score
                        5.0e-25
     E value
                        104
     Match length
                         59
     % identity
                        EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)
     NCBI Description
                        >gi_542153_pir_ S38358 translation initiation factor eIF-4A
                         - \overline{\text{rice}} > \overline{\text{gi}}_303844 dbj_BAA02152_ (D12627) eukaryotic
                         initiation factor 4A [Oryza sativa]
                         37908
     Seq. No.
                        LIB3092-057-Q1-K1-F2
     Seq. ID
                        BLASTX
     Method
                         g2982297
     NCBI GI
```



```
E value
                  7.0e - 38
Match length
                  112
% identity
                  67
                  (AF051233) KIAA0107-like protein [Picea mariana]
NCBI Description
Seq. No.
                  37909
                  LIB3092-057-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3868758
BLAST score
                  146
E value
                  2.0e-09
Match length
                  62
% identity
                  42
                  (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
                  37910
Seq. No.
Seq. ID
                  LIB3092-057-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g541943
BLAST score
                  180
                  3.0e-13
E value
Match length
                  61
% identity
                  67
NCBI Description
                  metallothionein - soybean >gi_228682_prf__1808316A
                  metallothionein-like protein [Glycine max]
Seq. No.
                  37911
Seq. ID
                  LIB3092-057-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g3043428
BLAST score
                  216
E value
                  1.0e-17
Match length
                  75
% identity
                  59
NCBI Description
                  (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
Seq. No.
                  37912
                  LIB3092-057-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g541943
BLAST score
                  221
                   4.0e-18
E value
                  77
Match length
% identity
                  57
                  metallothionein - soybean >gi_228682 prf__1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
Seq. No.
                  37913
Seq. ID
                  LIB3092-058-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g140551
BLAST score
                  229
                  5.0e-19
E value
Match length
                  118
% identity
                   47
                  HYPOTHETICAL 250 KD PROTEIN (ORF 2131)
NCBI Description
```

>gi 81505 pir S01446 hypothetical protein 2131 - spinach

. દર્





chloroplast >gi\_12246\_emb\_CAA30743\_ (X07908) ORF 2131 (AA
1-2131) [Spinacia oleracea]

37914 Seq. No. Seq. ID LIB3092-058-Q1-K1-G2 Method BLASTN NCBI GI g2661020 BLAST score 52 2.0e-20 E value Match length 136 % identity 85 NCBI Description Glycine max catalase (cat4) mRNA, complete cds Seq. No. 37915 Seq. ID LIB3092-060-Q1-K1-H10 Method BLASTX NCBI GI g2252863 BLAST score 233 E value 5.0e-20 Match length 135

NCBI Description (AF013294) similar to nucleolin protein [Arabidopsis

thaliana]

Seq. No. 37916

% identity

Seq. ID LIB3092-060-Q1-K1-H8

47

Method BLASTX
NCBI GI g4559353
BLAST score 200
E value 4.0e-16
Match length 67
% identity 64

NCBI Description (AC006585) putative extragenic suppressor protein

[Arabidopsis thaliana]

Seq. No. 37917

Seq. ID LIB3092-061-Q1-K1-A6

Method BLASTN
NCBI GI g2055227
BLAST score 44
E value 8.0e-16
Match length 48
% identity 98

NCBI Description Glycine max mRNA for SRC1, complete cds

Seq. No. 37918

Seq. ID LIB3092-061-Q1-K1-C7

Method BLASTX
NCBI GI g131399
BLAST score 184
E value 5.0e-14
Match length 80
% identity 54

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE

TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi\_82277\_pir\_\_S00411

photosystem II 10K protein precursor - potato

>gi\_21489\_emb\_CAA28450\_ (X04753) ST-LS1 protein [Solanum



## tuberosum]

```
37919
Seq. No.
                  LIB3092-061-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4417288
BLAST score
                  329
                  1.0e-30
E value
                  108
Match length
% identity
                  (AC007019) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  37920
                  LIB3092-061-Q1-K1-G6
Seq. ID
                  BLASTX
Method
                  q3687654
NCBI GI
                  223
BLAST score
E value
                  1.0e-18
                  86
Match length
                  53
% identity
                  (AF047975) putative ethylene receptor; ETR2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   37921
                  LIB3092-061-Q1-K1-G8
Seq. ID
Method
                  BLASTN
                  q18551
NCBI GI
                   126
BLAST score
E value
                   1.0e-64
                   280
Match length
                   87
% identity
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                  protein
Seq. No.
                   37922
Seq. ID
                   LIB3092-062-Q1-K1-B6
Method
                   BLASTN
                   g20728
NCBI GI
BLAST score
                   90
                   5.0e-43
E value
Match length
                   292
                   88
% identity
                   Pea chloroplast GAPA mRNA encoding
NCBI Description
                   glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A
                   (EC 1.2.1.13)
                   37923
Seq. No.
Seq. ID
                   LIB3092-062-Q1-K1-B7
Method
                   BLASTX
                   q1170781
NCBI GI
BLAST score
                   233
                   2.0e-19
E value
                   83
Match length
                   51
% identity
NCBI Description LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)
                   (ALDOKETOMUTASE) (GLYOXALASE I) >gi_629615_pir__S47177
```

lactoylglutathione lyase (EC 4.4.1.5) - soybean



>gi\_505585\_emb\_CAA48717\_ (X68819) lactoylglutathione lyase
[Glycine max]

 Seq. No.
 37924

 Seq. ID
 LIB3092-062-Q1-K1-B8

 Method
 BLASTN

 NCBI GI
 g505584

 BLAST score
 83

 E value
 8.0e-39

Match length 283 % identity 82

NCBI Description G.max mRNA for Glyoxalase I

Seq. No. 37925

Seq. ID LIB3092-062-Q1-K1-C7

Method BLASTX
NCBI GI 94512684
BLAST score 249
E value 3.0e-21
Match length 97
% identity 55

NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]

>gi\_4559324\_gb\_AAD22986.1\_AC007087\_5 (AC007087) unknown

protein [Arabidopsis thaliana]

Seq. No. 37926

Seq. ID LIB3092-062-Q1-K1-D11

Method BLASTX
NCBI GI g3108209
BLAST score 190
E value 2.0e-14
Match length 79
% identity 53

NCBI Description (AF028809) eukaryotic cap-binding protein [Arabidopsis

thaliana]

Seq. No. 37927

Seq. ID LIB3092-062-Q1-K1-D12

Method BLASTX
NCBI GI g3108209
BLAST score 161
E value 6.0e-11
Match length 67
% identity 51

NCBI Description (AF028809) eukaryotic cap-binding protein [Arabidopsis

thaliana]

Seq. No. 37928

Seq. ID LIB3092-062-Q1-K1-D3

Method BLASTN
NCBI GI g20834
BLAST score 58
E value 7.0e-24
Match length 162
% identity 85

NCBI Description P.sativum PHSP1 mRNA for HSP70

Seq. No.



```
Seq. No.
Seq. ID
                  LIB3092-062-Q1-K1-E7
Method
                  BLASTX
                  q2244904
NCBI GI
BLAST score
                  158
E value
                  5.0e-11
Match length
                  63
% identity
                  54
                  (Z97339) similar to hypothetical protein C02F5.7 - Caenorha
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  37930
Seq. ID
                  LIB3092-062-Q1-K1-F10
Method
                  BLASTN
NCBI GI
                  q18764
BLAST score
                  103
E value
                  1.0e-50
Match length
                  291
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-la
Seq. No.
                  37931
Seq. ID
                  LIB3093-001-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  q2160189
BLAST score
                  167
E value
                  1.0e-11
Match length
                  67
% identity
                  42
                  (ACO00132) Similar to A. thaliana receptor-like protein
NCBI Description
                  kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  37932
Seq. ID
                  LIB3093-001-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  g2706515
BLAST score
                  167
                  9.0e-12
E value
Match length
                  42
                  71
% identity
                  (Y12689) isoflavone reductase-like protein [Citrus x
NCBI Description
                  paradisi]
                  37933
Seq. No.
Seq. ID
                  LIB3093-001-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g129805
BLAST score
                  267
E value
                  2.0e-23
                  79
Match length
                  73
% identity
                  CATIONIC PEROXIDASE 1 PRECURSOR >gi 99872 pir A38265
NCBI Description
                  peroxidase (EC 1.11.1.7) precursor, cationic (clone PNC1) -
                  peanut
```

Seq. ID



```
LIB3093-001-Q1-K1-H6
 Seq. ID
                   BLASTX
Method
                   g4559358
NCBI GI
_BLAST score
                   166
                   1.0e-11
 E value
 Match length
                   74
 % identity
                   41
                   (AC006585) putative steroid binding protein [Arabidopsis
 NCBI Description
                   thaliana]
                   37935
 Seq. No.
 Seq. ID
                   LIB3093-002-Q1-K1-A4
 Method
                   BLASTN
                   q758693
 NCBI GI
 BLAST score
                   47
                   2.0e-17
 E value
 Match length
                   142
 % identity
                   83
 NCBI Description Catharanthus roseus S-adenosyl-L-methionine decarboxylase
                   proenzyme mRNA, complete cds
 Seq. No.
                   37936
 Seq. ID
                   LIB3093-002-Q1-K1-B4
 Method
                   BLASTX
                   g1806140
 NCBI GI
                   238
 BLAST score
                   3.0e-20
 E value
 Match length
                   98
 % identity
                   52
 NCBI Description (X97314) cdc2MsC [Medicago sativa]
                   37937
 Seq. No.
 Seq. ID
                   LIB3093-002-Q1-K1-D3
                   BLASTN
 Method
 NCBI GI
                   q4324966
 BLAST score
                   43
                   3.0e-15
 E value
 Match length
                   95
 % identity
                   86
 NCBI Description Glycine max ADP-ribosylation factor mRNA, partial cds
                   37938
 Seq. No.
 Seq. ID
                   LIB3093-002-Q1-K1-D6
                   BLASTX
 Method
 NCBI GI
                   g2129581
 BLAST score
                   341
                   3.0e-32
 E value
 Match length
                   108
 % identity
                   62
                   envelope Ca2+-ATPase precursor - Arabidopsis thaliana
 NCBI Description
                   >gi 471089 dbj BAA03091 (D13984) chloroplast envelope
                   Ca2+-ATPase precursor [Arabidopsis thaliana]
                    >gi_4165448_emb_CAA49558_ (X69940) envelope Ca2+-ATPase
                    [Arabidopsis thaliana]
 Seq. No.
                   37939
```

LIB3093-002-Q1-K1-E2



```
Method
                  BLASTN
                  q256142
NCBI GI
BLAST score
                  177
                  7.0e-95
E value
Match length
                  395
% identity
                  87
                  cytosolic glutamine synthetase [Glycine max=soybeans, var
NCBI Description
                  Prize, mRNA, 1450 nt]
Seq. No.
                  37940
                  LIB3093-002-Q1-K1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q18764
BLAST score
                  106
                  8.0e-53
E value
Match length
                  206
% identity
                  88
NCBI Description G.max tefS1 gene for elongation factor EF-1a
Seq. No.
                  37941
                  LIB3093-002-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2924781
BLAST score
                  226
E value
                  3.0e-19
Match length
                  59
                  73
% identity
NCBI Description
                  (AC002334) putative cellulose synthase [Arabidopsis
                  thaliana]
Seq. No.
                  37942
                  LIB3093-003-Q1-K1-B4
Seq. ID
Method
                  BLASTX
                  g4038030
NCBI GI
BLAST score
                  250
                  2.0e-21
E value
Match length
                  86
% identity
                  60
                  (AC005936) putative protein kinase, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
                  37943
Seq. No.
Seq. ID
                  LIB3093-003-Q1-K1-B8
Method
                  BLASTN
NCBI GI
                  g170025
BLAST score
                  56
E value
                  1.0e-22
Match length
                  307
% identity
                  80
NCBI Description Soybean malate synthase (MS) mRNA, 3' end
                  37944
Seq. No.
```

Seq. ID LIB3093-003-Q1-K1-C7

Method BLASTX g2499553 NCBI GI BLAST score 624 E value 3.0e-65



Match length 85 % identity CRYPTOCHROME 1 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR) NCBI Description >gi 629524 pir S39058 probable deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - Arabidopsis thaliana >gi 442529 bbs 139743 (S66907) flavin-type blue-light photoreceptor, HY4=DNA photolyase/tropomyosin A homolog [Arabidopsis thaliana, ecotype Columbia, Peptide, 681 aa] [Arabidopsis thaliana] 37945 Seq. No. Seq. ID LIB3093-003-Q1-K1-D10 BLASTX Method g2674203 NCBI GI BLAST score 143 2.0e-09 E value Match length 62 % identity 50 (AF036328) CLP protease regulatory subunit CLPX NCBI Description [Arabidopsis thaliana] Seq. No. 37946 LIB3093-003-Q1-K1-D11 Seq. ID Method BLASTN 辩. q170080 NCBI GI 77 BLAST score 3.0e-35 E value Match length 165 75 % identity NCBI Description Soybean seed lectin gene transposable element tgm1 37947 Seq. No. Seq. ID LIB3093-003-Q1-K1-D4 Method BLASTX g1705678 NCBI GI BLAST score 241 7.0e-21E value 75 Match length 61 % identity CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING NCBI Description PROTEIN HOMOLOG) (VCP) >gi\_862480 (U20213) valosin-containing protein [Glycine max] 37948 Seq. No. Seq. ID LIB3093-003-Q1-K1-D5 BLASTX Method NCBI GI g3935139 BLAST score 408 7.0e-40 E value Match length 102 % identity

NCBI Description (AC005106) T25N20.3 [Arabidopsis thaliana]

37949 Seq. No.

Seq. ID LIB3093-003-Q1-K1-F5

Method BLASTN NCBI GI g303900

```
BLAST score
                  1.0e-108
E value
                  339
Match length
                  32
% identity
                  Soybean gene for ubiquitin, complete cds
NCBI Description
                  37950
Seq. No.
Seq. ID
                  LIB3093-003-Q1-K1-H6
                  BLASTX
Method
NCBI GI
                  q2501578
                  583
BLAST score
                  2.0e-60
E value
                  128
Match length
                  92
% identity
                  ETHYLENE-INDUCIBLE PROTEIN HEVER >gi 2129913_pir__$60047
NCBI Description
                  ethylene-responsive protein 1 - Para rubber tree
                  >gi 1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
                  37951
Seq. No.
Seq. ID
                  LIB3093-004-Q1-K1-B6
Method
                  BLASTX
                  g3176076
NCBI GI
BLAST score
                  161
                  2.0e-11
E value
Match length
                  49
% identity
                  71
                  (AJ002487) protein phosphatase 1 catalitic subunit
NCBI Description
                   [Medicago sativa]
                  37952
Seq. No.
Seq. ID
                  LIB3093-004-Q1-K1-D1
```

Method BLASTX

NCBI GI g3024021 BLAST score 171 3.0e-12 E value 93 Match length 43 % identity

INITIATION FACTOR 5A-4 (EIF-5A) (EIF-4D) NCBI Description

>qi 2225883 dbj BAA20878 (AB004825) eukaryotic initiation

factor 5A4 [Solanum tuberosum]

Seq. No. 37953

Seq. ID LIB3093-004-Q1-K1-E7

BLASTX Method g4455338 NCBI GI BLAST score 148 7.0e-15 E value 129 Match length 40 % identity

(AL035525) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

Seq. ID LIB3093-004-Q1-K1-G8

37954

Method BLASTN NCBI GI q2055227 BLAST score 152

Match length

% identity

133



```
5.0e-80
E value
Match length
                  261
                  92
% identity
                  Glycine max mRNA for SRC1, complete cds
NCBI Description
                  37955
Seq. No.
Seq. ID
                  LIB3093-005-Q1-K1-D11
                  BLASTX
Method
NCBI GI
                  g2706515
BLAST score
                  227
                  6.0e-19
E value
                  65
Match length
                  68
% identity
                  (Y12689) isoflavone reductase-like protein [Citrus x
NCBI Description
                  paradisi]
                  37956
Seq. No.
                  LIB3093-005-Q1-K1-F7
Seq. ID
Method
                  BLASTX
                  g2950210
NCBI GI
BLAST score
                  170
                  2.0e-12
E value
                  62
Match length
                  56
% identity
                  (Y14615) Importin alpha-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  37957
Seq. ID
                  LIB3093-005-Q1-K1-G2
                  BLASTN
Method
NCBI GI
                  g601786
BLAST score
                   62
E value
                   3.0e-26
                  138
Match length
                   86
% identity
                  Arabidopsis thaliana protein kinase (AFC1) mRNA, complete
NCBI Description
                   cds
                   37958
Seq. No.
                  LIB3093-005-Q1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                  g1825645
                   230
BLAST score
E value
                   3.0e-19
Match length
                   72
% identity
                   61
                  (U88173) weak similarity to Arabidopsis thaliana
NCBI Description
                  ubiquitin-like protein 8 [Caenorhabditis elegans]
                   37959
Seq. No.
                  LIB3093-006-Q1-K1-D5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2511590
BLAST score
                   460
                   5.0e-46
E value
```

NCBI Description (Y13692) multicatalytic endopeptidase complex, proteasome



component, beta subunit [Arabidopsis thaliana] >gi\_3421111 (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]

37960 Seq. No. LIB3093-006-Q1-K1-E1 Seq. ID Method BLASTX NCBI GI q136636 BLAST score 427 4.0e-42 E value Match length 85 % identity 89 UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN NCBI Description LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi 1076424 pir\_\_S43781 ubiquitin-conjugating enzyme UBC1 -Arabidopsis thaliana >gi 442594 pdb 1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi\_2981894\_pdb\_2AAK\_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi 431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana] Seq. No. 37961 Seq. ID LIB3093-006-Q1-K1-F10 BLASTX Method q3033401 NCBI GI 222 BLAST score 3.0e-18 E value Match length 91 47 % identity (AC004238) putative potassium transporter [Arabidopsis NCBI Description thaliana] Seq. No. 37962 Seq. ID LIB3093-006-Q1-K1-F9 Method BLASTX g3947735 NCBI GI 163 BLAST score E value 2.0e-11 87 Match length % identity 45 (AJ009720) NL27 [Solanum tuberosum] NCBI Description Seq. No. 37963 LIB3093-007-Q1-K1-B3 Seq. ID Method BLASTN NCBI GI g2330648 BLAST score 47 2.0e-17 E value 114 Match length 87 % identity NCBI Description Pisum sativum mRNA for topoisomerase I

Seq. No. 37964

Seq. ID LIB3093-007-Q1-K1-C4

Method BLASTN NCBI GI g3821780



BLAST score 9.0e-11 E value Match length 36 100 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No.

37965

LIB3093-007-Q1-K1-C5 Seq. ID Method BLASTX

a2507421 NCBI GI 154 BLAST score 2.0e-10 E value Match length 65 51 % identity

NCBI Description

PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi\_1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi\_4490709\_emb\_CAB38843.1\_ (AL035680)

translation initiation factor [Arabidopsis thaliana]

Seq. No. 37966

Seq. ID LIB3093-007-Q1-K1-D3

Method BLASTX g1495251 NCBI GI BLAST score 303 1.0e-27 E value Match length 80 69 % identity

(Z70314) heat-shock protein [Arabidopsis thaliana] NCBI Description

Seq. No. 37967

Seq. ID LIB3093-007-Q1-K1-E7

Method BLASTX NCBI GI q119640 BLAST score 194 8.0e-15 E value Match length 107 43 % identity

1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN NCBI Description

> E8) >gi 82109 pir S01642 ripening protein E8 - tomato >gi\_19199\_emb\_CAA31789\_ (X13437) E8 protein [Lycopersicon

esculentum]

Seq. No. 37968

Seq. ID LIB3093-007-Q1-K1-F7

Method BLASTX NCBI GI q2244917 BLAST score 151 E value 1.0e-09 Match length 80 % identity 45

NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 37969

Seq. ID LIB3093-007-Q1-K1-G2

Method BLASTX NCBI GI g4512624 BLAST score 220



```
E value
                   5.0e-19
Match length
                  88
% identity
                  56
                  (AC004793) Strong similarity to gi 3033401 F19I3.29
NCBI Description
                  putative potassium transporter from Arabidopsis thaliana
                  BAC gb AC004238
Seq. No.
                  37970
                  LIB3093-008-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1086263
BLAST score
                  271
                  6.0e-24
E value
Match length
                  103
% identity
                  53
                  TMV resistance protein N - tobacco (Nicotiana glutinosa)
NCBI Description
                  >gi 558887 (U15605) N [Nicotiana glutinosa]
Seq. No.
                  37971
Seq. ID
                  LIB3093-008-Q1-K1-C11
Method
                  BLASTN
NCBI GI
                  g1814402
BLAST score
                  151
E value
                  2.0e-79
Match length
                  267
% identity
                  89
NCBI Description
                  Mesembryanthemum crystallinum methionine synthase (MetE)
                  mRNA, complete cds
Seq. No.
                  37972
Seq. ID
                  LIB3093-008-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g1350664
BLAST score
                  302
E value
                  1.0e-27
                  87
Match length
% identity
                  67
NCBI Description
                  60S RIBOSOMAL PROTEIN L13 (CLONE 6.2.1)
                  >gi_1084420 pir S50116 hypothetical protein - common
                  tobacco >gi 467325 (L31416) [Nicotiana tabacum (clone
                   6.2.1) mRNA, complete cds.], gene product [Nicotiana
                  tabacum]
```

Seq. No. 37973

Seq. ID LIB3093-008-Q1-K1-E7

Method BLASTN NCBI GI g169980 BLAST score 58 E value 4.0e-24 Match length 122 % identity 87

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No. 37974

Seq. ID LIB3093-008-Q1-K1-G9

Method BLASTX NCBI GI q1083739



```
BLAST score
E value
                  4.0e-21
                  72
Match length
% identity
                  61
                  nucleolar protein Nopp140, hepatic - rat
NCBI Description
                  >gi_1093316_prf__2103261A nuclear protein NAP57 [Rattus
                  norvegicus]
                  37975
Seq. No.
Seq. ID
                  LIB3093-008-Q1-K1-H6
Method
                  BLASTN
NCBI GI
                  g1055367
BLAST score
                  223
E value
                  1.0e-122
                  449
Match length
% identity
                  99
NCBI Description
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
                  subunit mRNA, complete cds
Seq. No.
                  37976
Seq. ID
                  LIB3093-009-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  q1498168
BLAST score
                  220
E value
                  6.0e-18
Match length
                  105
% identity
                  45
NCBI Description
                   (D86730) endoxyloglucan transferase related protein
                   [Nicotiana tabacum]
                  37977
Seq. No.
Seq. ID
                  LIB3093-009-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g3386607
BLAST score
                  447
                  1.0e-44
E value
Match length
                  129
% identity
                  66
                  (AC004665) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  37978
Seq. ID
                  LIB3093-009-Q1-K1-C3
                  BLASTX
Method
NCBI GI
                  g2978452
BLAST score
                  169
E value
                  2.0e-17
Match length
                  72
                  67
% identity
NCBI Description
                  (AE001274) MCAK; L549.3 [Leishmania major]
                  37979
Seq. No.
Seq. ID
                  LIB3093-009-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g541943
BLAST score
                  295
```

1.0e-26

56

E value Match length



```
% identity
                  metallothionein - soybean >gi_228682_prf__1808316A
metallothionein-like protein [Glycine max]
NCBI Description
Seq. No.
                   37980
Seq. ID
                   LIB3093-009-Q1-K1-E1
Method
                   BLASTX
NCBI GI
                   g3785978
BLAST score
                   218
E value
                   1.0e-17
Match length
                   44
% identity
                   80
NCBI Description
                  (AC005560) unknown protein [Arabidopsis thaliana]
                   37981
Seq. No.
Seq. ID
                   LIB3093-009-01-K1-E12
Method
                   BLASTX
NCBI GI
                   g266945
BLAST score
                   260
E value
                   6.0e-23
Match length
                   74
                   72
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
                   >gi_100065_pir__S19978 ribosomal protein L9 - garden pea
                   >gi_20727_emb_CAA46273 (X65155) GA [Pisum sativum]
                   >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9
                   [Pisum sativum]
Seq. No.
                   37982
Seq. ID
                   LIB3093-009-Q1-K1-F8
Method
                   BLASTX
NCBI GI
                   g4580395
BLAST score
                   213
                   2.0e-17
E value
Match length
                   92
% identity
                   51
NCBI Description
                   (AC007171) putative kinesin-related protein [Arabidopsis
                   thaliana)
Seq. No.
                   37983
Seq. ID
                   LIB3093-010-Q1-K1-A2
Method
                   BLASTX
NCBI GI
                   g2492952
BLAST score
                   334
E value
                   2.0e-31
Match length
                   91
% identity
                   73
                   CHORISMATE SYNTHASE 1 PRECURSOR
NCBI Description
                   (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1)
```

>gi\_542026\_pir\_\_S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi\_410482\_emb\_CAA79859\_ (Z21796)

chorismate synthase 1 [Lycopersicon esculentum]

37984 Seq. No.

Seq. ID LIB3093-010-Q1-K1-E10

Method BLASTX NCBI GI g4038592



```
BLAST score
E value
                  5.0e-10
Match length
                  80
                  44
% identity
NCBI Description
                  (Y10403) RNA-directed RNA polymerase [Lycopersicon
                  esculentum]
                  37985
Seq. No.
Seq. ID
                  LIB3093-010-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2245394
BLAST score
                  156
                  2.0e-10
E value
                  96
Match length
                  45
% identity
NCBI Description
                  (U89771) ARF1-binding protein [Arabidopsis thaliana]
                  37986
Seq. No.
                  LIB3093-010-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g485518
BLAST score
                  325
                  1.0e-30
E value
Match length
                  78
% identity
                  86
                  ubiquitin / ribosomal protein CEP52 - rice
NCBI Description
                  >gi 303857 dbj BAA02154 (D12629) ubiquitin/ribosomal
                  polyprotein [Oryza sativa]
                  37987
Seq. No.
Seq. ID
                  LIB3093-011-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  g2852684
BLAST score
                  150
E value
                  1.0e-09
Match length
                  103
% identity
                  31
NCBI Description
                  (AF017751) resistance protein candidate [Lactuca sativa]
Seq. No.
                  37988
Seq. ID
                  LIB3093-011-Q1-K1-A4
Method
                  BLASTN
NCBI GI
                  g2264309
BLAST score
                  52
                  3.0e-20
E value
                  200
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJJ3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  37989
Seq. ID
                  LIB3093-012-Q1-K1-A2
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1931653
BLAST score 225
E value 1.0e-18
Match length 98

Match length

NCBI Description

% identity

53 81



```
% identity
NCBI Description (U95973) unknown protein [Arabidopsis thaliana]
                  37990
Seq. No.
                  LIB3093-012-Q1-K1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169954
                  131
BLAST score
                  2.0e-67
E value
                  131
Match length
% identity
                  100
NCBI Description
                  Glycine max iron superoxide dismutase (FeSOD) mRNA,
                  complete cds
Seq. No.
                  37991
Seq. ID
                  LIB3093-012-Q1-K1-B12
Method
                  BLASTX
                  g3337361
NCBI GI
BLAST score
                  169
                  7.0e-22
E value
                  94
Match length
                  60
% identity
NCBI Description
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.
                  37992
Seq. ID
                  LIB3093-012-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  q2306981
BLAST score
                  230
E value
                  5.0e-19
Match length
                  54
                  72
% identity
NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]
Seq. No.
                  37993
                  LIB3093-012-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914192
BLAST score
                  155
                  2.0e-10
E value
                  89
Match length
                  39
% identity
                  DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE
NCBI Description
                  DEHYDROGENASE COMPLEX PRECURSOR (E2) (PDC-E2)
                  >gi_3150120_emb_CAA19134_ (AL023595) dihydrolipoamide
                  acetyltransferase component [Schizosaccharomyces pombe]
Seq. No.
                  37994
                  LIB3093-012-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3243274
BLAST score
                  213
E value
                  2.0e-17
```

5859

(AF072134) TCP3 [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                  LIB3093-012-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g3695408
BLAST score
                  293
E value
                  2.0e-26
Match length
                  88
% identity
                  64
NCBI Description
                   (AF096373) contains similarity to Solanum lycopersicum
                   (tomato) wound-induced protein (GB:X59882) [Arabidopsis
                  thaliana] >gi_4538956_emb_CAB39780.1_ (AL049488) probable
                  wound-induced protein [Arabidopsis thaliana]
Seq. No.
                  37996
Seq. ID
                  LIB3093-012-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g1134882
BLAST score
                  149
E value
                  1.0e-09
Match length
                  76
% identity
                  42
NCBI Description
                  (Z68291) cysteine protease [Pisum sativum]
Seq. No.
                  37997
Seq. ID
                  LIB3093-012-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  q3063459
BLAST score
                  219
                  7.0e-36
E value
Match length
                  128
% identity
                  66
                  (AC003981) F22013.21 [Arabidopsis thaliana]
NCBI Description
                  37998
Seq. No.
Seq. ID
                  LIB3093-013-Q1-K1-H10
Method
                  BLASTX
                  q1743354
NCBI GI
BLAST score
                  163
                  2.0e-11
E value
                  66
Match length
                  52
% identity
                  (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
NCBI Description
Seq. No.
                  37999
Seq. ID
                  LIB3093-013-Q1-K2-B7
Method
                  BLASTX
NCBI GI
                  g4467099
BLAST score
                  119
E value
                  2.0e-18
Match length
                  86
                  70
% identity
NCBI Description
                   (AL035538) glycine hydroxymethyltransferase like protein
```

[Arabidopsis thaliana]

38000 Seq. No.

Seq. ID LIB3093-013-Q1-K2-G6 Method BLASTX



```
NCBI GI
                    q1708971
BLAST score
                    230
                    3.0e-19
E value
Match length
                    113
                    45
% identity
                    (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
NCBI Description
                    (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
                   >gi_421871_pir__S32156 mandelonitrile lyase (EC 4.1.2.10) -
black cherry >gi_288116_emb_CAA51194_ (X72617)
mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814)
                    (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus
                    serotina] >gi 1090776 prf 2019441A mandelonitrile lyase
                    [Prunus serotina]
                    38001
Seq. No.
Seq. ID
                    LIB3093-013-Q1-K2-H10
Method
                    BLASTX
                    g1743354
NCBI GI
BLAST score
                    182
E value
                    9.0e-14
Match length
                    50
% identity
                    68
NCBI Description
                   (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
                    38002
Seq. No.
Seq. ID
                    LIB3093-014-Q1-K1-B12
                    BLASTX
Method
NCBI GI
                    g4049354
BLAST score
                    215
                    3.0e-26
E value
Match length
                    108
                    62
% identity
NCBI Description
                   (AL034567) glycine hydroxymethyltransferase (EC
                    2.1.2.1) - like protein [Arabidopsis thaliana]
                    38003
Seq. No.
Seq. ID
                  · LIB3093-014-Q1-K1-C12
Method
                    BLASTN
NCBI GI
                    g2970050
BLAST score
                    200
                    1.0e-108
E value
Match length
                    344
% identity
                    90
NCBI Description Vigna radiata mRNA for ARG10, complete cds
Seq. No.
                    38004
Seq. ID
                    LIB3093-014-Q1-K1-C9
Method
                    BLASTX
NCBI GI
                    g1332579
BLAST score
                    119
                    1.0e-09
E value
                    91
Match length
```

% identity

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

38005 Seq. No.

Seq. ID LIB3093-014-Q1-K1-H12



```
BLASTN
Method
                  g170073
NCBI GI
                  33
BLAST score
                  4.0e-09
E value
                  77
Match length
                  86
% identity
                  Soybean calmodulin (SCaM-3) mRNA, complete cds
NCBI Description
                  38006
Seq. No.
                  LIB3093-014-Q1-K2-C9
Seq. ID
                  BLASTN
Method
                  g303900
NCBI GI
                  177
BLAST score
                  5.0e-95
E value
                  243
Match length
                  27
% identity
                  Soybean gene for ubiquitin, complete cds
NCBI Description
                  38007
Seq. No.
                  LIB3093-014-Q1-K2-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g541943
BLAST score
                  181
                  1.0e-13
E value
                   40
Match length
                  82
% identity
                  metallothionein - soybean >qi 228682 prf 1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
                   38008
Seq. No.
Seq. ID
                  LIB3093-014-Q1-K2-D12
                  BLASTX
Method
                   g1839188
NCBI GI
                   332
BLAST score
                   5.0e-36
E value
                   93
Match length
                   76
% identity
                  (U86081) root hair defective 3 [Arabidopsis thaliana]
NCBI Description
                   38009
Seq. No.
                   LIB3093-014-Q1-K2-F5
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3510343
BLAST score
                   49
                   2.0e-18
E value
Match length
                   117
                   85
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MJC20, complete sequence [Arabidopsis thaliana]
                   38010
Seq. No.
Seq. ID
                   LIB3093-014-Q1-K2-G4
Method
                   BLASTX
NCBI GI
                   g4519671
BLAST score
                   142
```

1.0e-08

59

E value Match length

% identity (AB017693) transfactor [Nicotiana tabacum] NCBI Description 38011 Seq. No. LIB3093-014-Q1-K2-G5 Seq. ID  ${\tt BLASTN}$ Method NCBI GI g602358 72 BLAST score 2.0e-32 E value Match length 152 87 % identity P.sativum mRNA for type II chlorophyll a/b binding protein NCBI Description 38012 Seq. No. Seq. ID LIB3093-014-Q1-K2-H12 BLASTN g170073 67

Method NCBI GI BLAST score 2.0e-29 E value 106 Match length 92 % identity

NCBI Description Soybean calmodulin (SCaM-3) mRNA, complete cds

38013 Seq. No.

Seq. ID LIB3093-015-Q1-K1-A4

Method BLASTN q986968 NCBI GI 63 BLAST score 7.0e-27 E value Match length 215 85 % identity

NCBI Description Glycine max TGACG-motif binding protein (STGA1) mRNA,

complete cds

38014 Seq. No.

Seq. ID LIB3093-015-Q1-K1-A9

BLASTX Method NCBI GI q4433048 BLAST score 543 1.0e-55 E value 132 Match length 81 % identity

(D26578) DNA-binding protein [Daucus carota] NCBI Description

Seq. No.

38015

Seq. ID LIB3093-015-Q1-K1-C10 BLASTX Method

NCBI GI q3860277 291 BLAST score 4.0e-26 E value Match length 64 88 % identity

(AC005824) putative ribosomal protein L10 [Arabidopsis NCBI Description

thaliana] >gi\_4314394\_gb\_AAD15604\_ (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

38016 Seq. No.



Seq. ID LIB3093-015-Q1-K1-H5 Method BLASTX NCBI GI q3063465 BLAST score 196 E value 5.0e-15 Match length 131 40 % identity NCBI Description (AC003981) F22013.27 [Arabidopsis thaliana] 38017 Seq. No. Seq. ID LIB3093-015-Q1-K2-B10 Method BLASTX NCBI GI q2909583 BLAST score 249 2.0e-21 E value Match length 114 % identity 45 NCBI Description (AL021926) oxcA [Mycobacterium tuberculosis] Seq. No. 38018 Seq. ID LIB3093-015-Q1-K2-C10 Method BLASTX NCBI GI g3860277 BLAST score 166 2.0e-11 E value Match length 35 91 % identity NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi\_4314394\_gb\_AAD15604\_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana] Seq. No. 38019 LIB3093-015-Q1-K2-C6 Seq. ID Method BLASTN NCBI GI g2921511 BLAST score 109 2.0e-54 E value Match length 225 % identity 87 Fritillaria agrestis GF14 protein (GRF) mRNA, complete cds NCBI Description Seq. No. 38020 Seq. ID LIB3093-015-Q1-K2-D10 Method BLASTN NCBI GI q169934 BLAST score 48 E value 5.0e-18 Match length 91 89 % identity NCBI Description G.max (soybean) atpH gene encoding CFO-ATPase subunit III, chloroplast gene encoding chloroplast protein, complete cds Seq. No. 38021

Seq. ID LIB3093-016-Q1-K1-A9
Method BLASTX
NCBI GI g3328122
BLAST score 324



```
5.0e-30
E value
Match length
                   112
% identity
                   65
NCBI Description
                   (AF073473) phosphoglycerate kinase precursor [Solanum
                   tuberosum]
                   38022
Seq. No.
Seq. ID
                  LIB3093-016-Q1-K1-B4
Method
                  BLASTN
                  g169980
NCBI GI
BLAST score
                   65
                   3.0e-28
E value
                  157
Match length
                   85
% identity
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                   38023
Seq. No.
Seq. ID
                  LIB3093-016-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                   g3461820
BLAST score
                   187
E value
                   6.0e-14
Match length
                   80
                   46
% identity
                  (AC004138) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   38024
Seq. ID
                  LIB3093-016-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                   g1737492
BLAST score
                   145
E value
                   1.0e-09
Match length
                   48
                   60
% identity
NCBI Description
                  (U81318) poly(A)-binding protein [Triticum aestivum]
Seq. No.
                   38025
                  LIB3093-016-Q1-K2-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832717
BLAST score
                   207
                   1.0e-16
E value
Match length
                   74
% identity
                   54
                  (AJ003114) alkaline/neutral invertase [Lolium temulentum]
NCBI Description
Seq. No.
                   38026
Seq. ID
                  LIB3093-017-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  q2252847
```

BLAST score 225 E value 2.0e-18 Match length 72 57 % identity

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 38027



```
LIB3093-017-Q1-K1-D12
Seq. ID
                  BLASTX
Method
                  g549063
NCBI GI
                  350
BLAST score
                  3.0e-33
E value
Match length
                  106
% identity
                  70
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                  >gi 1072464 pir A38958 IgE-dependent histamine-releasing
                   factor homolog - rice >gi 303835 dbj BAA02151 (D12626)
                  21kd polypeptide [Oryza sativa]
                   38028
Seq. No.
                  LIB3093-017-Q1-K1-G6
Seq. ID
                  BLASTX
Method
                   g3158474
NCBI GI
BLAST score
                   154
                   1.0e-16
E value
Match length
                   80
                   64
% identity
                   (AF067184) aquaporin 1 [Samanea saman]
NCBI Description
Seq. No.
                   38029
                   LIB3093-017-Q1-K1-H10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2055227
BLAST score
                   54
E value
                   9.0e-22
Match length
                   174
                   83
% identity
NCBI Description Glycine max mRNA for SRC1, complete cds
Seq. No.
                   38030
Seq. ID
                   LIB3093-017-Q1-K1-H5
Method
                   BLASTN
                   g2055227
NCBI GI
BLAST score
                   224
                   1.0e-123
E value
                   228
Match length
                   100
% identity
                  Glycine max mRNA for SRC1, complete cds
NCBI Description
                   38031
Seq. No.
                   LIB3093-017-Q1-K2-A10
Seq. ID
                   BLASTN
Method
                   g1675195
NCBI GI
BLAST score
                   65
                   2.0e-28
E value
Match length
                   153
% identity
                   86
                   Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
NCBI Description
                   complete cds
```

5866

38032

BLASTX

g3122671

LIB3093-017-Q1-K2-B12

Seq. No. Seq. ID

Method NCBI GI



BLAST score 148
E value 6.0e-10
Match length 52
% identity 58

NCBI Description HYPOTHETICAL RAE1-LIKE PROTEIN >gi\_2129676\_pir\_\_S71241

probable export protein - Arabidopsis thaliana >gi\_1297188 (U53501) Theoretical protein with similarity to Swiss-Prot

Accession Number P41838 poly A+ RNA export protein

[Arabidopsis thaliana]

Seq. No. 38033

Seq. ID LIB3093-017-Q1-K2-B6

Method BLASTX
NCBI GI g2632105
BLAST score 190
E value 2.0e-14
Match length 78
% identity 51

NCBI Description (298760) arginyl-tRNA synthetase [Arabidopsis thaliana]

>gi\_4539426\_emb\_CAB38959.1\_ (AL049171) arginyl-tRNA

synthetase [Arabidopsis thaliana]

Seq. No. 38034

Seq. ID LIB3093-017-Q1-K2-C2

Method BLASTX
NCBI GI g1076294
BLAST score 264
E value 3.0e-23
Match length 65
% identity 78

NCBI Description ATAF2 protein - Arabidopsis thaliana

Seq. No.

38035

Seq. ID LIB3093-018-Q1-K1-C9

Method BLASTN
NCBI GI g3320378
BLAST score 34
E value 1.0e-09
Match length 58
% identity 90

NCBI Description Medicago sativa putative JUN kinase activation domain

binding protein mRNA, complete cds

Seq. No. 38036

Seq. ID LIB3093-018-Q1-K1-G7

Method BLASTN
NCBI GI g1245452
BLAST score 75
E value 3.0e-34
Match length 135
% identity 89

NCBI Description Medicago sativa 3-deoxy-D-arabino-heptulosonate 7-phosphate

synthase (MsDHS1) mRNA, partial cds

Seq. No. 38037

Seq. ID LIB3093-018-Q1-K1-H8

Method BLASTN



```
q3552012
NCBI GI
BLAST score
                   77
                   3.0e-35
E value
                   93
Match length
                   96
% identity
                  Glycine max proline-rich protein precursor, mRNA, complete
NCBI Description
                   38038
Seq. No.
                   LIB3093-018-Q1-K2-B1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3868852
BLAST score
                   33
E value
                   4.0e-09
Match length
                   41
                   95
% identity
                  Vigna radiata ARG8 mRNA for GPI-anchored protein, complete
NCBI Description
                   38039
Seq. No.
                   LIB3093-018-Q1-K2-C1
Seq. ID
Method
                   BLASTN
                   g967124
NCBI GI
BLAST score
                   156
                   2.0e-82
E value
Match length
                   288
                   90
% identity
                  Vigna radiata Rwilcz calcium dependent protein kinase
NCBI Description
                   (CDPK) mRNA, complete cds
                   38040
Seq. No.
                   LIB3093-018-Q1-K2-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3021271
BLAST score
                   141
E value
                   1.0e-08
Match length
                   118
                   30
% identity
                   (AL022347) serine/threonine kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   38041
                   LIB3093-018-Q1-K2-E5
Seq. ID
Method
                   BLASTX
                   g1946373
NCBI GI
                   159
BLAST score
E value
                   8.0e-11
Match length
                   63
% identity
                   51
                  (U93215) leader peptidase I isolog [Arabidopsis thaliana]
NCBI Description
                   38042
Seq. No.
                   LIB3093-018-Q1-K2-F2
Seq. ID
                   {\tt BLASTX}
Method
                   g421867
NCBI GI
BLAST score
                   229
E value
                   7.0e-19
```

E value

Match length

NCBI Description

% identity

90

92

(Ran-2) mRNA, 3' end

```
Match length
                  50
% identity
                  ubiquitin / ribosomal protein CEP52 - turnip >gi 347064
NCBI Description
                  (L21898) ubiquitin/ribosomal protein [Brassica rapa]
                  >gi_395079_emb_CAA80863_ (Z24738) ubiquitin/ribosomal
                  protein [Brassica rapa]
                  38043
Seq. No.
                  LIB3093-018-Q1-K2-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2208908
BLAST score
                  467
E value
                  7.0e-47
Match length
                  108
% identity
                  (AB004809) phosphate transporter [Catharanthus roseus]
NCBI Description
                  38044
Seq. No.
                  LIB3093-018-Q1-K2-F6
Seq. ID
Method
                  BLASTN
                  q1370202
NCBI GI
                  108
BLAST score
E value
                   8.0e-54
Match length
                   259
                   87
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAN1A
                   38045
Seq. No.
Seq. ID
                   LIB3093-018-Q1-K2-H11
Method
                   BLASTX
NCBI GI
                   g4538913
BLAST score
                   188
E value
                   1.0e-14
Match length
                   60
% identity
                   (AL049482) putative protein [Arabidopsis thaliana]
NCBI Description
                   38046
Seq. No.
                   LIB3093-018-Q1-K2-H3
Seq. ID
                   BLASTX
Method
                   g3075488
NCBI GI
                   139
BLAST score
                   1.0e-08
E value
Match length
                   76
% identity
                   41
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   38047
                   LIB3093-019-Q1-K1-A2
Seq. ID
Method
                   BLASTN
                   q495730
NCBI GI
                   62
BLAST score
                   2.0e-26
```

5869

Arabidopsis thaliana small Ras-like GTP-binding protein



```
Seq. No.
                  38048
Seq. ID
                  LIB3093-019-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  g1838976
BLAST score
                  242
                  2.0e-20
E value
                  74
Match length
% identity
                  69
NCBI Description
                 (X73635) vsf-1 [Lycopersicon esculentum]
Seq. No.
                  38049
                  LIB3093-019-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3986691
BLAST score
                  333
E value
                  3.0e-31
Match length
                  88
                  75
% identity
NCBI Description (AF101421) heat shock protein [Cichorium intybus]
                  38050
Seq. No.
Seq. ID
                  LIB3093-019-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g2498490
BLAST score
                  141
                  6.0e-09
E value
                  65
Match length
% identity
                  49
                  VIRAL INTEGRATION SITE PROTEIN INT-6 >gi 1854579 (L35556)
NCBI Description
                  Int-6 [Mus musculus] >gi_2114363 (U62962) similar to mouse
                  Int-6 [Homo sapiens] >gi 2351382 (U54562) eIF3-p48 [Homo
                  sapiens] >gi 2688818 (U85947) Int-6 [Homo sapiens]
                  >gi 2695701 (U94175) mammary tumor-associated protein INT6
                   [Homo sapiens] >gi_4503521_ref_NP_001559.1_pEIF3S6_ murine
                  mammary tumor integration site 6 (oncogene homolog)
                  38051
Seq. No.
Seq. ID
                  LIB3093-019-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g121769
                  140
BLAST score
E value
                  6.0e-09
                  74
Match length
                  42
% identity
                  GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE
NCBI Description
                  AMIDOTRANSFERASE) (GMP SYNTHETASE) >gi_68651_pir__SYECGU
```

GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) -Escherichia coli >gi\_1310841\_pdb\_1GPM\_A Chain A, Escherichia Coli Gmp Synthetase Complexed With Amp And Pyrophosphate >gi 1310842 pdb 1GPM\_B Chain B, Escherichia Coli Gmp Synthetase Complexed With Amp And Pyrophosphate >gi\_1310843\_pdb\_1GPM\_C Chain C, Escherichia Coli Gmp Synthetase Complexed With Amp And Pyrophosphate >gi 1310844 pdb 1GPM D Chain D, Escherichia Coli Gmp Synthetase Complexed With Amp And Pyrophosphate >gi 146276

(M10101) GMP synthetase [Escherichia coli] >gi\_1788854



(AE000337) GMP synthetase (glutamine-hydrolyzing) [Escherichia coli] >gi\_1805567\_dbj\_BAA16394 (D90880) GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) [Escherichia coli]

Seq. No. 38052 Seq. ID LIB3093-019-Q1-K1-D3 Method BLASTN NCBI GI g609224 BLAST score 107 E value 4.0e-53 Match length 248 % identity 90

NCBI Description P.sativum mRNA for SAMS-2 >gi\_609558\_gb\_L36681\_PEADENSYNB Pisum sativum S-adenosylmethionine synthase mRNA, complete

cds

Method BLASTX
NCBI GI g2160185
BLAST score 366
E value 4.0e-35
Match length 116
% identity 59

NCBI Description (AC000132) Similar to S. pombe ISP4 (gb D83992).

[Arabidopsis thaliana]

Seq. No. 38054

Seq. ID LIB3093-019-Q1-K1-F12

Method BLASTX
NCBI GI g3043596
BLAST score 480
E value 2.0e-48
Match length 129
% identity 67

NCBI Description (AB011108) KIAA0536 protein [Homo sapiens]

Seq. No.

Seq. ID LIB3093-019-Q1-K1-F2

38055

Method BLASTX
NCBI GI g3426036
BLAST score 162
E value 3.0e-15
Match length 110
% identity 46

NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.

38056

Seq. ID LIB3093-019-Q1-K1-G2

Method BLASTN
NCBI GI g984307
BLAST score 167
E value 5.0e-89
Match length 256
% identity 93

NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial



cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precurso

 Seq. No.
 38057

 Seq. ID
 LIB3093-019-Q1-K1-H2

 Method
 BLASTN

 NCBI GI
 g984307

 BLAST score
 67

 E value
 2.0e-29

E value 2.0e-29
Match length 151
% identity 90

NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I

component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. No. 38058

Seq. ID LIB3093-019-Q1-K2-A10

Method BLASTX
NCBI GI g1946367
BLAST score 165
E value 2.0e-11
Match length 56
% identity 57

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 38059

Seq. ID LIB3093-019-Q1-K2-B9

Method BLASTX
NCBI GI g3341695
BLAST score 143
E value 3.0e-10
Match length 78
% identity 54

NCBI Description (AC003672) putative thiamin pyrophosphokinase [Arabidopsis

thaliana]

Seq. No. 38060

Seq. ID LIB3093-019-Q1-K2-D6

Method BLASTX
NCBI GI g3548801
BLAST score 287
E value 1.0e-25
Match length 109
% identity 50

NCBI Description (AC005313) putative transmembrane protein [Arabidopsis

thaliana] >gi\_4335768\_gb\_AAD17445\_ (AC006284) putative

integral membrane protein [Arabidopsis thaliana]

Seq. No. 38061

Seq. ID LIB3093-019-Q1-K2-E10

Method BLASTX NCBI GI g2160185 BLAST score 163

÷.

Match length

% identity

67

81 NCBI Description (U43082) RF2 [Zea mays]



```
E value
                   3.0e-11
Match length
                   72
% identity
                   43
NCBI Description
                   (ACO00132) Similar to S. pombe ISP4 (gb_D83992).
                   [Arabidopsis thaliana]
Seq. No.
                  38062
Seq. ID
                  LIB3093-019-Q1-K2-G9
Method
                 BLASTN
NCBI GI
                  g347458
BLAST score
                  149
E value
                  3.0e-78
Match length
                  224
% identity
                  92
NCBI Description
                  Glycine max brassinosteroid-regulated protein mRNA,
                  complete cds
Seq. No.
                  38063
Seq. ID
                  LIB3093-019-Q1-K2-H9
Method
                  BLASTN
NCBI GI
                  g456713
BLAST score
                  211
E value
                  1.0e-115
Match length
                  303
                  29
% identity
NCBI Description Glycine max gene for ubiquitin, complete cds
Seq. No.
                  38064
Seq. ID
                  LIB3093-022-Q1-K1-A12
Method
                  BLASTN
NCBI GI
                  g169980
BLAST score
                  152
E value
                  6.0e-80
Match length
                  380
                  93
% identity
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.
                  38065
Seq. ID
                  LIB3093-022-Q1-K1-A3
Method
                  BLASTN
NCBI GI
                  g169988
BLAST score
                  114
E value
                  2.0e-57
Match length
                  219
% identity
                  100
NCBI Description Glycine max NADP-specific isocitrate dehydrogenase (idh1)
                  mRNA, 3' end
Seq. No.
                  38066
Seq. ID
                  LIB3093-022-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g1421730
BLAST score
                  290
E value
                  2.0e-26
```

5873

Seq. ID

NCBI GI

Method



```
38067
Seq. No.
Seq. ID
                  LIB3093-022-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                   g3242659
                   194
BLAST score
                   7.0e-16
E value
Match length
                   90
% identity
                   59
NCBI Description (AB015599) spermidine synthase [Coffea arabica]
Seq. No.
                   38068
                   LIB3093-022-Q1-K1-D4
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2462911
                   528
BLAST score
                   6.0e-54
E value
                   146
Match length
% identity
                   68
                   (Z83832) UDP-glucose:sterol glucosyltransferase [Avena
NCBI Description
                   sativa]
Seq. No.
                   38069
Seq. ID
                   LIB3093-022-Q1-K1-E10
Method
                   BLASTX
                   g4531444
NCBI GI
BLAST score
                   370
                   2.0e-35
E value
                   96
Match length
                   70
% identity
                  (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   38070
Seq. ID
                   LIB3093-022-Q1-K1-E8
Method
                   BLASTN
NCBI GI
                   g3341467
BLAST score
                   86
                   1.0e-40
E value
                   190
Match length
                   86
% identity
NCBI Description Nicotiana tabacum BBF1 gene
                   38071
Seq. No.
Seq. ID
                   LIB3093-022-Q1-K1-E9
Method
                   BLASTX
                   g3650032
NCBI GI
BLAST score
                   272
E value
                   6.0e-24
Match length
                   60
                   70
% identity
NCBI Description
                   (AC005396) gibberellin-regulated protein GAST1-like
                   [Arabidopsis thaliana]
Seq. No.
                   38072
```

5874

LIB3093-023-Q1-K1-A8

BLASTX

q4263521



BLAST score E value 3.0e-31 Match length 89 33 % identity NCBI Description (AC004044) putative WD-repeat protein [Arabidopsis thaliana] Seq. No. 38073 Seq. ID LIB3093-023-Q1-K1-B10 Method BLASTX

NCBI GI g1399265
BLAST score 319
E value 2.0e-29
Match length 118
% identity 58
NCBI Description (U31751)

NCBI Description (U31751) calmodulin-domain protein kinase CDPK isoform 9 [Arabidopsis thaliana]

Seq. No. 38074

Seq. ID LIB3093-023-Q1-K1-C10

Method BLASTX
NCBI GI g4455335
BLAST score 527
E value 7.0e-54
Match length 145
% identity 26

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 38075

Seq. ID LIB3093-023-Q1-K1-F3

Method BLASTN
NCBI GI g2739003
BLAST score 129
E value 3.0e-66
Match length 317
% identity 85

NCBI Description Glycine max cytochrome P450 monooxygenase CYP82Clp

(CYP82C1) mRNA, complete cds

Seq. No. 38076

Seq. ID LIB3093-024-Q1-K1-B1

Method BLASTN
NCBI GI g642169
BLAST score 39
E value 1.0e-12
Match length 39
% identity 100

NCBI Description C.agrestis ITS2 and 28S rRNA gene (partial)

Seq. No. 38077

Seq. ID LIB3093-024-Q1-K1-B7

Method BLASTX
NCBI GI g4544464
BLAST score 96
E value 4.0e-09
Match length 51
% identity 59

5875



NCBI Description (AC006580) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No. 38078

Seq. ID LIB3093-024-Q1-K1-C3

Method BLASTX NCBI GI g3894193 BLAST score 331 E value 6.0e-31 Match length 131

% identity NCBI Description (AC005662) putative strictosidine synthase [Arabidopsis

thaliana]

Seq. No. 38079

Seq. ID LIB3093-024-Q1-K1-F2

53

Method BLASTX NCBI GI g2342679 BLAST score 375 E value 4.0e-36 Match length 110 % identity 64

NCBI Description (AC000106) Similar to Vicia sativa ENBP1 (gb X95995).

[Arabidopsis thaliana]

Seq. No. 38080

Seq. ID LIB3093-025-Q1-K1-A11

Method BLASTX NCBI GI g3366930 BLAST score 347 E value 8.0e-33 Match length 112 % identity 65

NCBI Description (AF068745) putative phosphatidylinositol 4-kinase [Solanum

tuberosum]

Seq. No. 38081

Seq. ID LIB3093-025-Q1-K1-C12

Method BLASTN NCBI GI g1150683 BLAST score 57 E value 3.0e-23 Match length 121 % identity 91

NCBI Description V.radiata atpB, rbcL and trnK genes

Seq. No. 38082

LIB3093-025-Q1-K1-C2 Seq. ID Method

BLASTX NCBI GI g2764992 BLAST score 299 E value 4.0e-27 Match length 95 % identity 61

(Y08609) plasma membrane polypeptide [Nicotiana tabacum] NCBI Description

Seq. No. 38083



```
Seq. ID
                   LIB3093-025-Q1-K1-D2
                  BLASTX
Method
NCBI GI
                  g1172635
                   99
BLAST score
                   4.0e-09
E value
Match length
                   76
% identity
                   51
                  26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING
NCBI Description
                  PROTEIN HOMOLOG 2) >gi_556558_dbj_BAA04615_ (D17789) rice
                  homologue of Tat binding protein [Oryza sativa]
Seq. No.
                  38084
Seq. ID
                  LIB3093-025-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  q4580513
BLAST score
                  182
E value
                   9.0e-14
Match length
                  80
% identity
                   45
NCBI Description
                  (AF036300) scarecrow-like 1 [Arabidopsis thaliana]
Seq. No.
                  38085
Seq. ID
                  LIB3093-025-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  q1170878
BLAST score
                  163
E value
                  1.0e-11
Match length
                   69
% identity
                   51
NCBI Description
                  MALATE SYNTHASE, GLYOXYSOMAL (MS) >qi 170026 (L01629)
                  malate synthase [Glycine max]
Seq. No.
                   38086
Seq. ID
                  LIB3093-025-Q1-K1-G4
Method
                  BLASTX
                  g2245020
NCBI GI
BLAST score
                  163
E value
                  2.0e-11
                  77
Match length
                   43
% identity
NCBI Description
                  (Z97341) growth regulator homolog [Arabidopsis thaliana]
Seq. No.
                  38087
Seq. ID
                  LIB3093-027-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g4468817
BLAST score
                  722
E value
                  1.0e-76
Match length
                  159
% identity
                  44
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]
Seq. No.
                  38088
```

Seq. ID LIB3093-027-Q1-K1-E9 Method BLASTX

NCBI GI g3646320 BLAST score 144



```
6.0e-09
E value
                  35
Match length
% identity
                  86
                  (AJ000759) MADS-box protein [Malus domestica]
NCBI Description
                  38089
Seq. No.
                  LIB3093-027-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4455278
BLAST score
                  312
                  9.0e-29
E value
Match length
                  89
% identity
                  65
                  (AL035527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  38090
Seq. No.
Seq. ID
                  LIB3093-028-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  g266945
BLAST score
                  202
                  6.0e-16
E value
Match length
                  89
% identity
                  52
                  60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
NCBI Description
                  >gi_100065_pir__S19978 ribosomal protein L9 - garden pea
                  >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum]
                  >gi 1279645 emb_CAA65987_ (X97322) ribosomal protein L9
                   [Pisum sativum]
                  38091
Seq. No.
                  LIB3093-028-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4371282
                  161
BLAST score
                   5.0e-11
E value
Match length
                   68
% identity
                   57
                   (AC006260) putative 60S ribosomal protein L12 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   38092
                   LIB3093-028-Q1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2959767
BLAST score
                   162
                   2.0e-11
E value
Match length
                   85
% identity
                   42
                   (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292
NCBI Description
                   (AC005309) glutathione-conjugate transporter AtMRP4
                   [Arabidopsis thaliana]
```

Seq. No. 38093

Seq. ID LIB3093-028-Q1-K1-F12

Method BLASTX
NCBI GI g3549679
BLAST score 101



```
4.0e-09
E value
Match length
                   66
% identity
                  (AL031394) putative protein [Arabidopsis thaliana]
NCBI Description
                   38094
Seq. No.
                   LIB3093-029-Q1-K1-D8
Seq. ID
                   BLASTX
Method
                   g3334150
NCBI GI
                   225
BLAST score
                   1.0e-18
E value
                   110
Match length
                   54
% identity
                   MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR
NCBI Description
                   (MG-PROTOPORPHYRIN IX CHELATASE) >gi 2129847_pir__JC4312
                   chlorophyll magnesium chelatase (EC \overline{4}.99.-.-) - \overline{\text{soy}}bean
                   chloroplast >gi_1732469_dbj_BAA08291_ (D45857) Mg chelatase
                   subunit (46 kD) [Glycine max]
                   38095
Seq. No.
                   LIB3093-029-Q1-K1-E10
Seq. ID
                   BLASTN
Method
NCBI GI
                   g18764
BLAST score
                   62
                   2.0e-26
E value
                   102
Match length
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
                   38096
Seq. No.
                   LIB3093-029-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   q4456682
NCBI GI
BLAST score
                   129
                   3.0e-14
E value
Match length
                   97
% identity
                   47
                   (AJ224336) MAP kinase [Medicago sativa]
NCBI Description
Seq. No.
                   38097
                   LIB3093-029-Q1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3860325
BLAST score
                   186
                   5.0e-14
E value
Match length
                   63
                   57
% identity
                   (AJ012689) ribonuclease T2 [Cicer arietinum]
NCBI Description
                   38098
Seq. No.
                   LIB3093-029-Q1-K1-F9
Seq. ID
Method
                   BLASTX
                   g1173103
NCBI GI
BLAST score
                   170
                   3.0e-12
E value
```

55

58

Match length

% identity



RIBONUCLEASE 1 PRECURSOR >gi 561998 (U05206) ribonuclease NCBI Description [Arabidopsis thaliana] >gi\_3461823 (AC004138) ribonuclease, RNS1 [Arabidopsis thaliana] Projection of the Control of the Con 38099 Seq. No. LIB3093-029-Q1-K1-H10 Seq. ID Method BLASTX q2213594 NCBI GI BLAST score 268 1.0e-23 E value Match length 117 % identity 41 NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana] 38100 Seq. No. Seq. ID LIB3093-030-Q1-K1-A7 Method BLASTX NCBI GI q417148 BLAST score 143 4.0e-09 E value 80 Match length % identity 44 NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) (G2-4) >gi\_99912\_pir\_\_A33654 heat shock protein 26A soybean >gi 169981 (M20363) Gmhsp26-A [Glycine max] Seq. No. 38101 LIB3093-030-Q1-K1-B4 Seq. ID Method BLASTX NCBI GI g1857447 BLAST score 172 E value 2.0e-12 Match length 87 % identity 43 NCBI Description (U82367) UDP-glucose glucosyltransferase [Solanum tuberosum] Seq. No. 38102 Seq. ID LIB3093-030-Q1-K1-C12 Method BLASTX NCBI GI q4138608 BLAST score 175 4.0e-13 E value Match length 59 % identity (AJ010455) glutathione peroxidase [Triticum aestivum] NCBI Description Seq. No. 38103 Seq. ID LIB3093-030-Q1-K1-C5

Method BLASTX
NCBI GI g3176965
BLAST score 270
E value 1.0e-23
Match length 104
% identity 57

NCBI Description (AF067967) pyrroline-5-carboxylate synthetase

[Mesembryanthemum crystallinum]



Seq. No.

38104

```
LIB3093-030-Q1-K1-D2
Seq. ID
Method
                  BLASTX
                  g3445416
NCBI GI
                  500
BLAST score
                  1.0e-50
E value
                  151
Match length
                  66
% identity
                  (Y11154) DEAD box-like RNA helicase [Arabidopsis thaliana]
NCBI Description
                  38105
Seq. No.
                  LIB3093-031-Q1-K1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1931642
                  167
BLAST score
                  1.0e-11
E value
                  102
Match length
                   39
% identity
                  (U95973) Ser/Thr protein kinase isolog [Arabidopsis
NCBI Description
                   thaliana]
                   38106
Seq. No.
                   LIB3093-031-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   g169363
NCBI GI
                   255
BLAST score
                   4.0e-22
E value
                   80
Match length
                   64
% identity
NCBI Description (M75856) PVPR3 [Phaseolus vulgaris]
                   38107
Seq. No.
                   LIB3093-031-Q1-K1-A5
Seq. ID
                   BLASTN
Method
                   g2293111
NCBI GI
                   105
BLAST score
                   7.0e-52
E value
                   192
Match length
                   90
% identity
NCBI Description V.faba mRNA for potassium channel
                   38108
Seq. No.
                   LIB3093-031-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   g4239845
NCBI GI
                   208
BLAST score
                   8.0e-17
E value
                   85
Match length
                   51
% identity
NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]
                   38109
Seq. No.
                   LIB3093-031-Q1-K1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3947719
                   191
BLAST score
```

5881



```
2.0e-14
E value
                  65
Match length
                  68
% identity
                  (AJ012653) ribosomal protein S28 [Prunus persica]
NCBI Description
                  >gi 3947721 emb_CAA10102_ (AJ012654) ribosomal protein S28
                  [Prunus persica] >gi_3947723_emb_CAA10103 (AJ012655)
                  ribosomal protein S28 [Prunus persica]
                  38110
Seq. No.
                  LIB3093-031-Q1-K1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4191785
                  249
BLAST score
                  2.0e-21
E value
                  86
Match length
                  58
% identity
                  (AC005917) putative hydrolase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  38111
                  LIB3093-031-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g400578
BLAST score
                  153
                  5.0e-10
E value
Match length
                  61
                  49
% identity
                  NADH-UBIQUINONE OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-18 KD) (CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ)
                  >gi_346531_pir__S28240 NADH dehydrogenase (ubiquinone) (EC
                  1.6.5.3) chain CI-18(IP) - bovine >gi 226 emb CAA44900
                   (X63215) NADH dehydrogenase [Bos taurus]
Seq. No.
                  38112
                  LIB3093-031-Q1-K1-C5
Seq. ID
Method
                  BLASTX
                  g3309084
NCBI GI
                   142
BLAST score
                   4.0e-09
E value
                   51
Match length
                   63
% identity
                   (AF076252) calcineurin B-like protein 2 [Arabidopsis
NCBI Description
                   thaliana]
                   38113
Seq. No.
                   LIB3093-031-Q1-K1-D3
Seq. ID
                   BLASTN
Method
                   q1196896
NCBI GI
                   118
BLAST score
                   1.0e-59
E value
                   232
Match length
                   89
% identity
NCBI Description Glycine max acidic ribosomal protein PO mRNA, complete cds
```

Seq. No. 38114

Seq. ID LIB3093-031-Q1-K1-D4

Method BLASTN NCBI GI g3243255



```
BLAST score
                   2.0e-33
E value
                  146
Match length
% identity
                   88
                  Vigna unguiculata phosphoribosylpyrophosphate
NCBI Description
                   amidotransferase (purl) mRNA, complete cds
                   38115
Seq. No.
                   LIB3093-031-Q1-K1-D8
Seq. ID
Method
                   BLASTX
                   g2213783
NCBI GI
                   278
BLAST score
                   1.0e-24
E value
                   80
Match length
                   72
% identity
                  (U89256) Pti5 [Lycopersicon esculentum]
NCBI Description
                   38116
Seq. No.
                   LIB3093-031-Q1-K1-D9
Seq. ID
Method
                   BLASTN
                   g2218151
NCBI GI
BLAST score
                   200
                   1.0e-108
E value
                   296
Match length
                   92
% identity
                   Vigna unguiculata type IIIa membrane protein cp-wap13 mRNA,
NCBI Description
                   complete cds
                   38117
Seq. No.
                   LIB3093-031-Q1-K1-E7
Seq. ID
                   BLASTX
Method
                   g2853219
NCBI GI
BLAST score
                   399
                   6.0e-39
E value
                   102
Match length
% identity
                   69
                  (AJ000923) glutathione transferase [Carica papaya]
NCBI Description
                   38118
Seq. No.
                   LIB3093-031-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g1174162
NCBI GI
                   357
BLAST score
                   5.0e-34
E value
                   67
Match length
                   94
% identity
                   (U44976) ubiquitin-conjugating enzyme [Arabidopsis
NCBI Description
                   thaliana] >gi_3746915 (AF091106) E2
                   ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
                   38119
 Seq. No.
                   LIB3093-031-Q1-K1-H10
 Seq. ID
                   BLASTX
Method
                   g3695408
NCBI GI
```

5883

143

80

7.0e-09

BLAST score

Match length

E value



% identity (AF096373) contains similarity to Solanum lycopersicum NCBI Description (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi\_4538956\_emb\_CAB39780.1\_ (AL049488) probable wound-induced protein [Arabidopsis thaliana] 38120 Seq. No. LIB3093-031-Q1-K1-H8 Seq. ID BLASTX Method g2809244 NCBI GI 198 BLAST score 2.0e-15 E value 60 Match length 65 % identity (AC002560) F21B7.13 [Arabidopsis thaliana] NCBI Description Seq. No. 38121 LIB3093-032-Q1-K1-C10 Seq. ID BLASTN Method g18731 NCBI GI 302 BLAST score 1.0e-169 E value 455 Match length 98 % identity Soybean RPB1-B1 gene for the largest subunit of RNA NCBI Description polymerase II (EC 2.7.7.6) 38122 Seq. No. LIB3093-032-Q1-K1-E4 Seq. ID BLASTX Method g4545262 NCBI GI BLAST score 165 2.0e-11 E value 42 Match length 69 % identity (AF118230) metallothionein-like protein [Gossypium NCBI Description hirsutum] 38123 Seq. No. LIB3093-032-Q1-K1-E6 Seq. ID BLASTN Method NCBI GI g2654093 BLAST score 147 5.0e-77 E value

323 Match length 86 % identity

NCBI Description

Glycine max aspartate aminotransferase glyoxysomal isozyme AAT1 precursor and aspartate aminotransferase cytosolic

1. T. ( )

isozyme AAT2 (AAT) mRNA, complete cds

Seq. No.

38124

LIB3093-032-Q1-K1-F3 Seq. ID

BLASTX Method q1586940 NCBI GI BLAST score 176 E value 1.0e-12

84 Match length



```
% identity
                   Ser/Thr kinase [Lycopersicon esculentum]
 NCBI Description
                   38125
 Seq. No.
 Seq. ID
                   LIB3093-032-Q1-K1-F9
 Method
                   BLASTX
 NCBI GI
                   q1488521
                   156
 BLAST score
                   1.0e-10
 E value.
                   93
 Match length
                   43
 % identity
                   (X99938) RNA helicase [Arabidopsis thaliana]
 NCBI Description
                   38126
 Seq. No.
 Seq. ID
                   LIB3093-032-Q1-K1-H10
                   BLASTX
 Method
                   g2827143
 NCBI GI
                   157
 BLAST score
                   1.0e-10
 E value
                   100
 Match length
                   41
 % identity
                    (AF027174) cellulose synthase catalytic subunit
 NCBI Description
                    [Arabidopsis thaliana]
                   38127
 Seq. No.
 Seq. ID
                   LIB3093-033-Q1-K1-A2
                   BLASTX
 Method
                   g3548802
 NCBI GI
                   313
 BLAST score
                   5.0e-29
 E value
                   101
 Match length
                    57
 % identity
                    (AC005313) axi 1-like protein [Arabidopsis thaliana]
 NCBI Description
                    >qi 4335769 gb AAD17446 (AC006284) putative axi1 protein
                    [Nicotiana tabacum] [Arabidopsis thaliana]
                    38128
 Seq. No.
                   LIB3093-033-Q1-K1-A6
 Seq. ID
                    BLASTX
 Method
                    g2827992
 NCBI GI
 BLAST score
                    149
                    6.0e-10
 E value
                    41
 Match length
                    71
 % identity
                   (AF034743) UDP-glucuronosyltransferase [Pisum sativum]
 NCBI Description
                    38129
 Seq. No.
 Seq. ID
                    LIB3093-033-Q1-K1-B7
                    BLASTX
 Method
                    g1711512
 NCBI GI
BLAST score
                    438
                    2.0e-43
 E value
 Match length
                    94
                    93
 % identity
                    SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54)
 NCBI Description
                    >gi 1076577_pir__S51598 signal recognition particle 54K
```

protein - tomato (cv. UC82-B) >gi\_556902\_emb\_CAA84288\_



(Z34527) 54-kD signal recognition particle (SRP) specific protein [Lycopersicon esculentum]

38130 Seq. No. Seq. ID LIB3093-033-Q1-K1-C2 BLASTX Method g3249084 NCBI GI 330 BLAST score 7.0e-31 E value Match length 110 % identity 21 (AC004473) Similar to red-1 (related to thioredoxin) gene NCBI Description gb X92750 from Mus musculus. ESTs gb AA712687 and gb Z37223 come from this gene [Arabidopsis thaliana] 38131 Seq. No. LIB3093-033-Q1-K1-C3 Seq. ID Method BLASTX g3293031 NCBI GI BLAST score 294 1.0e-26 E value Match length 79 77 % identity (AJ007574) amino acid carrier [Ricinus communis] NCBI Description 38132 Seq. No. Seq. ID LIB3093-033-Q1-K1-C5 Method BLASTN g3334662 NCBI GI 385 BLAST score 0.0e+00E value 393 Match length % identity 100 G.max mRNA for putative cytochrome P450, clone CP4 NCBI Description Seq. No. 38133 Seq. ID LIB3093-033-Q1-K1-G10 Method BLASTX g3851636 NCBI GI BLAST score 241 E value 2.0e-20 Match length 76 67 % identity (AF098519) unknown [Avicennia marina] >gi 4128206 NCBI Description (AF056316) 40S ribosome protein S7 [Avicennia marina] 38134 Seq. No. Seq. ID LIB3093-033-Q1-K1-G5 BLASTX Method NCBI GI g2267567

BLAST score 395

2.0e-38 E value Match length 87 % identity 85

(AF009003) glycine-rich RNA binding protein 1 [Pelargonium NCBI Description x hortorum] >gi 2267569 (AF009004) glycine-rich RNA binding

protein 2 [Pelargonium x hortorum]



```
38135
Seq. No.
                  LIB3093-034-Q1-K1-C10
Seq. ID
                  BLASTX
Method
                  q4559339
NCBI GI
                  267
BLAST score
                   4.0e-24
E value
Match length
% identity
                   (AC007087) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                   thaliana]
                   38136
Seq. No.
                   LIB3093-034-Q1-K1-F1
Seq. ID
                   BLASTN
Method
                   g2739005
NCBI GI
                   74
BLAST score
                   2.0e-33
E value
                   166
Match length
                   86
% identity
                  Glycine max cytochrome P450 monooxygenase CYP93C1p
NCBI Description
                   (CYP93C1) mRNA, complete cds
                   38137
Seq. No.
                   LIB3093-034-Q1-K1-F10
Seq. ID
                   BLASTN
Method
                   g4567090
NCBI GI
                   38
BLAST score
                   5.0e-12
E value
                   106
Match length
% identity
                   Glycine max SNF-1-like serine/threonine protein kinase
NCBI Description
                   mRNA, complete cds
                   38138
Seq. No.
                   LIB3093-034-Q1-K1-F12
Seq. ID
                   BLASTN
Method
                   q4567090
NCBI GI
                   167
BLAST score
                   4.0e-89
E value
                   276
Match length
                   89
 % identity
                   Glycine max SNF-1-like serine/threonine protein kinase
NCBI Description
                   mRNA, complete cds
                   38139
 Seq. No.
                   LIB3093-035-Q1-K1-C4
 Seq. ID
                   BLASTX
 Method
                   g1854443
 NCBI GI
 BLAST score
                   257
                   6.0e-23
 E value
                   119
 Match length
                   55
 % identity
                   (D83970) CPRD8 protein [Vigna unguiculata]
 NCBI Description
```

5887

38140

LIB3093-035-Q1-K1-C7

Seq. No.

Seq. ID



```
BLASTN
Method
                  g2502086
NCBI GI
                  155
BLAST score
                  8.0e-82
E value
                  314
Match length
                  90
% identity
NCBI Description Vigna radiata adenosine triphosphatase mRNA, complete cds
                  38141
Seq. No.
                  LIB3093-035-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                   g2959767
NCBI GI
                   442
BLAST score
                   5.0e-44
E value
Match length
                   125
                   36
% identity
                   (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292
NCBI Description
                   (AC005309) glutathione-conjugate transporter AtMRP4
                   [Arabidopsis thaliana]
                   38142
Seq. No.
                   LIB3093-035-Q1-K1-E4
Seq. ID
                   BLASTX
Method
                   g134646
NCBI GI
                   214
BLAST score
                   2.0e-17
E value
                   82
Match length
                   56
% identity
                   SUPEROXIDE DISMUTASE, CHLOROPLAST PRECURSOR (FE) >gi 169955
NCBI Description
                   (M64267) Fe-superoxide dismutase [Glycine max]
                   >gi_228415_prf__1803527A Fe superoxide dismutase [Glycine
                   max]
                   38143
Seq. No.
                   LIB3093-035-Q1-K1-E5
Seq. ID
                   BLASTN
Method
                   q3821780°
NCBI GI
                   36
BLAST score
                   1.0e-10
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   38144
Seq. No.
                   LIB3093-035-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   g2262105
NCBI GI
                   339
BLAST score
                   3.0e - 32
 E value
                   78
Match length
 % identity
                   78
                   (AC002343) unknown protein [Arabidopsis thaliana]
 NCBI Description
```

5888

38145

BLASTX q1742961

LIB3093-035-Q1-K1-G2

Seq. No.

Seq. ID Method

NCBI GI

```
BLAST score
                   6.0e-11
E value
Match length
                  105
                   42
% identity
                   (X94756) cystathionine gamma-synthase [Arabidopsis
NCBI Description
                   thaliana]
                   38146
Seq. No.
                   LIB3093-035-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   g4454039
NCBI GI
                   119
BLAST score
                   1.0e-12
E value
                   90
Match length
                   52
% identity
                   (AL035394) putative Na+/H+-exchanging protein [Arabidopsis
NCBI Description
                   thaliana]
                   38147
Seq. No.
                   LIB3093-035-Q1-K1-G6
Seq. ID
                   BLASTX
Method
                   g2511541
NCBI GI
                   281
BLAST score
                   3.0e-25
E value
                   75
Match length
                   76
% identity
                   (AF020787) DNA-binding protein GBP16 [Oryza sativa]
NCBI Description
                   38148
Seq. No.
                   LIB3093-035-Q1-K1-H11
Seq. ID
                   BLASTX
Method
                   q2462828
NCBI GI
                   567
BLAST score
                   2.0e-58
E value
                   148
Match length
                   70
 % identity
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   38149
 Seq. No.
                   LIB3093-036-Q1-K1-C5
 Seq. ID
                   BLASTX
 Method
                   q857395
 NCBI GI
                    306
 BLAST score
 E value
                    5.0e-28
 Match length
                    126
 % identity
                    59
                   (D50869) mitotic cyclin a2-type [Glycine max]
 NCBI Description
 Seq. No.
                    38150
                    LIB3093-036-Q1-K1-D9
 Seq. ID
 Method
                    BLASTX
                    g1170746
 NCBI GI
 BLAST score
                    218
                    8.0e-18
 E value
                    86
 Match length
 % identity
                    58
 NCBI Description DESICCATION PROTECTANT PROTEIN LEA14 HOMOLOG >gi_472850
```



(U08108) putative desiccation protectant protein, homolog of Lea14, GenBank Accession Number M88321 [Glycine max]

```
38151
Seq. No.
                    LIB3093-036-Q1-K1-E3
Seq. ID
                    BLASTX
Method
                    g2129738
NCBI GI
                    231
BLAST score
                    3.0e-19
E value
                     83
Match length
                     63
% identity
                    shaggy-like kinase dzeta - Arabidopsis thaliana >gi_1225913_emb_CAA64408_ (X94938) shaggy-like kinase dzeta [Arabidopsis thaliana] >gi_1669653_emb_CAA70483_ (Y09300)
NCBI Description
                     serine/threonine kinase [Arabidopsis thaliana]
                     38152
Seq. No.
                     LIB3093-036-Q1-K1-G2
Seq. ID
                     BLASTX
Method
                     g2914700
NCBI GI
BLAST score
                     213
                     4.0e-17
E value
                     80
Match length
                     55
% identity
                     (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
                     thaliana]
                     38153
Seq. No.
                     LIB3093-036-Q1-K1-G5
Seq. ID
                     BLASTN
Method
                     g169980
NCBI GI
                     220
BLAST score
                     1.0e-120
E value
                     308
Match length
                     93
% identity
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                     38154
Seq. No.
                     LIB3093-036-Q1-K1-H11
 Seq. ID
Method
                     BLASTX
                     a462195
NCBI GI
                     110
BLAST score
                     1.0e-08
E value
                     74
Match length
                     54
 % identity
                     PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
 NCBI Description
                     >gi_100682_pir__S21636 GOS2 protein - rice
                          20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                          \overline{3789950} (\overline{\text{AF094774}} translation initiation factor [Oryza
```

Seq. No. 38155

Seq. ID LIB3093-037-Q1-K1-C3

sativa]

Method BLASTN
NCBI GI g2055227
BLAST score 144
E value 3.0e-75

5890



Match length 97 % identity

NCBI Description Glycine max mRNA for SRC1, complete cds

38156 Seq. No.

LIB3093-037-Q1-K1-C6 Seq. ID

BLASTX Method g462187 NCBI GI 207 BLAST score 4.0e-25 E value 107 Match length 72 % identity

SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR NCBI Description

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi\_282928\_pir\_\_A42906 serine

hydroxymethyltransferase - garden pea >gi\_169158 (M87649)

serine hydroxymethyltransferase [Pisum sativum]

38157 Seq. No.

LIB3093-037-Q1-K1-E12 Seq. ID

BLASTN Method g20724 NCBI GI BLAST score 36 9.0e-11 E value 80 Match length 86 % identity

NCBI Description P.sativum GA mRNA (clone A)

Seq. No.

38158 LIB3093-037-Q1-K1-F9 Seq. ID

BLASTX Method g2660670 NCBI GI 560 BLAST score 9.0e-58 E value 139 Match length 76 % identity

(AC002342) putative Cu2+-transporting ATPase [Arabidopsis NCBI Description

thaliana]

38159 Seq. No.

LIB3093-037-Q1-K1-G10 Seq. ID

BLASTX Method g1707032 NCBI GI BLAST score 233 1.0e-19 E value 110 Match length % identity

(U80445) coded for by C. elegans cDNA yk13g5.3; coded for NCBI Description

by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA

yk65h8

38160 Seq. No.

LIB3093-037-Q1-K1-G4 Seq. ID

Method BLASTX NCBI GI g4510370

% identity

54



```
BLAST score
E value
                   4.0e-20
Match length
                  73
                   68
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  38161
                  LIB3093-037-Q1-K1-H7
Seq. ID
Method
                  BLASTN
                  q169980
NCBI GI
BLAST score
                   326
E value
                   0.0e + 00
Match length
                   391
                   97
% identity
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                   38162
Seq. No.
Seq. ID
                   LIB3093-038-Q1-K1-A5
Method
                  BLASTN
                   g456713
NCBI GI
                   244
BLAST score
                   1.0e-135
E value
Match length
                   332
% identity
                   27
NCBI Description Glycine max gene for ubiquitin, complete cds
Seq. No.
                   38163
                   LIB3093-038-Q1-K1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1711618
BLAST score
                   147
E value
                   7.0e-19
Match length
                   104
% identity
                   63
                   LOW AFFINITY SULPHATE TRANSPORTER 3 >gi 1085993 pir__S51765
NCBI Description
                   low affinity sulphate transporter - Stylosanthes hamata
                   >gi_607188_emb_CAA57831_ (X82454) low affinity sulphate
                   transporter [Stylosanthes hamata]
                   38164
Seq. No.
                   LIB3093-038-Q1-K1-D10
Seq. ID
                   BLASTN
Method
                   g169980
NCBI GI
BLAST score
                   330
                   0.0e+00
E value
                   386
Match length
% identity
                   96
                   Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
NCBI Description
                   38165
Seq. No.
                   LIB3093-038-Q1-K1-D11
Seq. ID
                   BLASTX
Method
                   g2497543
NCBI GI
BLAST score
                   141
                   1.0e-08
E value
                   48
Match length
```

```
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061 pir S41379
                  pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_
                   (Z29492) pyruvate kinase [Nicotiana tabacum]
                   38166
Seq. No.
                  LIB3093-038-Q1-K1-D7
Seq. ID
                  BLASTX
Method
                  g3287679
NCBI GI
                   512
BLAST score
                   4.0e-52
E value
                   125
Match length
                   78
% identity
                   (AC003979) T22J18.6 [Arabidopsis thaliana]
NCBI Description
                   38167
Seq. No.
                   LIB3093-038-Q1-K1-E7
Seq. ID
                   BLASTN
Method
                   g303900
NCBI GI
                   158
BLAST score
                   1.0e-83
E value
                   289
Match length
                   29
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
                   38168
Seq. No.
                   LIB3093-038-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   q2465923
NCBI GI
                   296
BLAST score
                   9.0e-27
E value
                   140
Match length
                   46
% identity
                   (AF024648) receptor-like serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
                   38169
Seq. No.
                   LIB3093-038-Q1-K1-F12
 Seq. ID
                   BLASTX
Method
                   q1168329
NCBI GI
 BLAST score
                   321
                   6.0e-32
 E value
                   133
```

Match length 55 % identity

ACTIN-LIKE PROTEIN 3 (ACTIN-LIKE PROTEIN 66B) (ACTIN-2) NCBI Description >gi\_558568\_emb\_CAA50674\_ (X71789) actin related protein [Drosophila melanogaster] >gi\_1096138\_prf\_\_2111232A

actin-related protein [Drosophila melanogaster]

38170 Seq. No.

LIB3093-038-Q1-K1-F7 Seq. ID

Method BLASTX g2832304 NCBI GI 299 BLAST score 3.0e-27 E value 98 Match length 58 % identity

્રદ

NCBI Description (AF044489) receptor-like protein kinase [Oryza sativa]

Seq. ID

Method



```
38171
Seq. No.
                  LIB3093-039-Q1-K1-A11
Seq. ID
                  BLASTN
Method
                   q4506742
NCBI GI
                   42
BLAST score
                   2.0e-14
E value
                   58
Match length
                   93
% identity
NCBI Description Homo sapiens ribosomal protein S8 (RPS8) mRNA
                   38172
Seq. No.
                   LIB3093-039-Q1-K1-A4
Seq. ID
Method
                   BLASTX
                   g1061040
NCBI GI
                   202
BLAST score
                   4.0e-16
E value
                   83
Match length
                   53
% identity
                   (X89867) sterol-C-methyltransferase [Arabidopsis thaliana]
NCBI Description
                   >gi 1587694 prf__2207220A sterol C-methyltransferase
                   [Arabidopsis thaliana]
                   38173
Seq. No.
                   LIB3093-039-Q1-K1-A6
Seq. ID
                   BLASTN
Method
                   g18764
NCBI GI
                   126
BLAST score
                   1.0e-64
E value
                   202
Match length
                   92
 % identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
                   38174
 Seq. No.
                   LIB3093-039-Q1-K1-E11
 Seq. ID
                   BLASTX
 Method
                   q2707334
 NCBI GI
                   164
 BLAST score
                   2.0e-11
 E value
                   56
 Match length
                    62
 % identity
                    (AF037368) putative ethylene receptor; Cm-ERS1 [Cucumis
 NCBI Description
                   melo]
                    38175
 Seq. No.
                   LIB3093-039-Q1-K1-E12
 Seq. ID
                   BLASTN
 Method
                    q3821780
 NCBI GI
 BLAST score
                    36
                    8.0e-11
 E value
 Match length
                    36
 % identity
                    100
 NCBI Description Xenopus laevis cDNA clone 27A6-1
                    38176
 Seq. No.
```

5894

LIB3093-040-Q1-K1-A11

BLASTX

BLAST score

E value

460 5.0e-46

```
q4185129
NCBI GI
BLAST score
                  143
                  7.0e-09
E value
                  66
Match length
                  53
% identity
                   (AC005724) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4218012 (AC006135) unknown protein [Arabidopsis
                  thaliana]
Seq. No.
                   38177
                  LIB3093-040-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539383
BLAST score
                   352
                   2.0e-33
E value
                   94
Match length
                   67
% identity
                  (AL035526) putative protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
                   38178
Seq. No.
                   LIB3093-040-Q1-K1-C10
Seq. ID
Method
                   BLASTX
                   q4388728
NCBI GI
                   170
BLAST score
                   2.0e-12
E value
                   59
Match length
                   59
% identity
                  (AC006413) putative grr1-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   38179
Seq. No.
                   LIB3093-040-Q1-K1-C3
Seq. ID
Method
                   BLASTX
                   q1197577
NCBI GI
BLAST score
                   271
E value
                   8.0e-24
Match length
                   131
                   47
% identity
                  (X95277) serpin [Hordeum vulgare]
NCBI Description
                   38180
Seq. No.
                   LIB3093-040-Q1-K1-D1
Seq. ID
Method
                   BLASTX
                   g2880048
NCBI GI
                   507
BLAST score
                   2.0e-51
E value
Match length
                   113
                   82
 % identity
NCBI Description (AC002340) unknown protein [Arabidopsis thaliana]
                 ** 38181
Seq. No.
                   LIB3093-040-Q1-K1-E12
 Seq. ID
                   BLASTX
Method
                   g2832643
 NCBI GI
```

5895

Seq. ID

Method

NCBI GI

BLAST score



```
Match length
% identity
                   81
                   (AL021710) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   38182
Seq. No.
                   LIB3093-040-Q1-K1-F2
Seq. ID
Method
                   BLASTX
                   g3096947
NCBI GI
                   155
BLAST score
                   3.0e-10
E value
                   66
Match length
                   47
% identity
                   (Y16327) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
                   38183
Seq. No.
                   LIB3093-041-Q1-K1-B12
Seq. ID
Method
                   BLASTN
                   q2739005
NCBI GI
                   88
BLAST score
                   6.0e-42
E value
                   176
Match length
% identity
                   Glycine max cytochrome P450 monooxygenase CYP93C1p
NCBI Description
                   (CYP93C1) mRNA, complete cds
Seq. No.
                   LIB3093-041-Q1-K1-C6
Seq. ID
Method
                   BLASTX
                   q2160161
NCBI GI
                   461
BLAST score
E value
                   3.0e-46
                   129
Match length
 % identity
                   13
                   (AC000132) F21M12.7 gene product [Arabidopsis thaliana]
 NCBI Description
                   38185
 Seq. No.
                   LIB3093-041-Q1-K1-F12
 Seq. ID
 Method
                   BLASTX
                   g399046
 NCBI GI
                   157
 BLAST score
                   1.0e-10
 E value
                   57
 Match length
                   56
 % identity
                   ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT)
 NCBI Description
                   >gi_99657_pir__S20867 adenine phosphoribosyltransferase (EC
                   2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_
                    (X58640) adenine phosphoribosyltransferase [Arabidopsis
                   thaliana] >gi 433050 (L19637) adenine
                   phosphoribosyltransferase [Arabidopsis thaliana]
                   >gi 3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]
                    38186
 Seq. No.
```

5896

LIB3093-041-Q1-K1-F8

BLASTN

41

g1041244

% identity

NCBI Description

59

```
E value
                  9.0e-14
Match length
                  53
                  94
% identity
                  A.glutinosa mRNA for enolase
NCBI Description
                  38187
Seq. No.
                  LIB3Q93-041-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                  q3850999
NCBI GI
                  302
BLAST score
                   2.0e-27
E value
Match length
% identity
                   (AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1
NCBI Description
                   [Zea mays]
                   38188
Seq. No.
                   LIB3093-041-Q1-K1-H5
Seq. ID
                   BLASTX
Method
                   q3618320
NCBI GI
                   159
BLAST score
                   9.0e-11
E value
                   98
Match length
                   40
% identity
                  (AB001888) zinc finger protein [Oryza sativa]
NCBI Description
                   38189
Seq. No.
                   LIB3093-042-Q1-K1-A11
Seq. ID
                   BLASTX
Method
                   g4558556
NCBI GI
                   444
BLAST score
                   3.0e-44
E value
Match length
                   116
                   69
% identity
                   (AC007138) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   38190
Seq. No.
                   LIB3093-042-Q1-K1-A9
Seq. ID
Method
                   BLASTN
                   q2905777
NCBI GI
                   34
BLAST score
                   1.0e-09
E value
                   90
Match length
 % identity
NCBI Description Glycine max ribosomal protein L41 mRNA, partial cds
                   38191
 Seq. No.
                   LIB3093-042-Q1-K1-B11
 Seq. ID
 Method
                   BLASTX
                   q4406819
 NCBI GI
                   451
 BLAST score
                   7.0e-45
 E value
                   152
 Match length
```

(AC006201) unknown protein [Arabidopsis thaliana]

NCBI GI



```
38192
Seq. No.
                  LIB3093-042-Q1-K1-C12
Seq. ID
                  BLASTX
Method
                  g1694621
NCBI GI
                  153
BLAST score
                  5.0e-10
E value
                  62
Match length
                  53
% identity
                  (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]
NCBI Description
                   38193
Seq. No.
                   LIB3093-042-Q1-K1-D5
Seq. ID
Method
                  BLASTX
                  q3309243
NCBI GI
                   153
BLAST score
                   5.0e-10
E value
                   68
Match length
% identity
                   57
                   (AF073507) aconitase-iron regulated protein 1 [Citrus
NCBI Description
                   38194
Seq. No.
Seq. ID
                   LIB3093-042-Q1-K1-F4
Method
                   BLASTX
                   q2696804
NCBI GI
                   225
BLAST score
                   1.0e-18
E value
                   65
Match length
% identity
                   (AB009665) water channel protein [Oryza sativa]
NCBI Description
                   38195
Seq. No.
                   LIB3093-042-Q1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4092774
                   157
BLAST score
E value
                   2.0e-10
                   157
Match length
                   32
% identity
                   (AF105140) disease resistance gene homolog 9N [Brassica
NCBI Description
                   napus]
                   38196
Seq. No.
                   LIB3093-042-Q1-K1-G7
Seq. ID
                   BLASTN
Method
                   g1946337
NCBI GI
                   161
 BLAST score
                   2.0e-85
 E value
                   351
Match length
                   87
 % identity
                   Glycine max alternative oxidase (Aox3) mRNA, nuclear gene
 NCBI Description
                   encoding mitochondrial protein, complete cds
                   38197
 Seq. No.
                   LIB3093-042-Q1-K1-H11
 Seq. ID
                   BLASTX
 Method
```

5898

g4539394



```
BLAST score
                  3.0e-11
E value
                  111
Match length
                  7
% identity
                  (AL035526) putative protein [Arabidopsis thaliana]
NCBI Description
                  38198
Seq. No.
                  LIB3093-043-Q1-K1-E11
Seq. ID
                  BLASTN
Method
                  g1217993
NCBI GI
BLAST score
                  196
E value
                   1.0e-106
                   290
Match length
                   95
% identity
NCBI Description Glycine max dynamin-like protein SDL12A mRNA, complete cds
                   38199
Seq. No.
                   LIB3093-044-Q1-K1-D2
Seq. ID
Method
                   BLASTX
                   g4218001
NCBI GI
                   172
BLAST score
                   3.0e-12
E value
Match length
                   101
% identity
                   31
                   (AC006135) putative Ac transposase [Arabidopsis thaliana]
NCBI Description
                   38200
Seq. No.
                   LIB3093-044-Q1-K1-D6
Seq. ID
Method
                   BLASTX
                   g4336610
NCBI GI
BLAST score
                   276
                   2.0e-24
E value
Match length
                   134
                   47
% identity
                   (AF099112) sigma factor; Sig3 [Zea mays]
NCBI Description
                   38201
Seq. No.
                   LIB3093-044-Q1-K1-G3
Seq. ID
Method
                   BLASTX
                   g118514
NCBI GI
                   253
BLAST score
                   7.0e-22
E value
                   104
Match length
                   55
% identity
                   TURGOR-RESPONSIVE PROTEIN 26G >gi 100051 pir S11863
NCBI Description
                   aldehyde dehydrogenase homolog - garden pea
                   >gi_20681_emb_CAA38243_ (X54359) 508 aa peptide [Pisum
                   sativum]
                   38202
Seq. No.
                   LIB3093-044-Q1-K1-G7
Seq. ID
                   BLASTX
Method
                   g3335336
NCBI GI
                   210
BLAST score
                   8.0e-17
E value
```

5899

90

51

Match length

% identity



NCBI Description (AC004512) Contains similarity to DnaJ gene YM8520.10 gb\_825566 from from S. cerevisiae cosmid gb\_Z49705. ESTs gb\_Z47720 and gb\_Z29879 come from this gene. [Arabidopsis thaliana]

Seq. No. 38203

Seq. ID LIB3093-045-Q1-K1-A2

Method BLASTX
NCBI GI g1871187
BLAST score 169
E value 3.0e-12
Match length 84
% identity 46

NCBI Description (U90439) unknown protein [Arabidopsis thaliana]

Seq. No. 38204

Seq. ID LIB3093-045-Q1-K1-B1

Method BLASTX
NCBI GI g3297819
BLAST score 494
E value 5.0e-50
Match length 133
% identity 71

NCBI Description (AL031032) protein kinase - like protein [Arabidopsis

thaliana]

Seq. No. 38205

Seq. ID LIB3093-045-Q1-K1-C8

Method BLASTX
NCBI GI g3341688
BLAST score 140
E value 1.0e-12
Match length 107
% identity 47

NCBI Description (AC003672) putative casein kinase II beta subunit

[Arabidopsis thaliana]

Seq. No. 38206

Seq. ID LIB3093-045-Q1-K1-D1

Method BLASTX
NCBI GI g4406780
BLAST score 143
E value 9.0e-14
Match length 69
% identity 62

NCBI Description (AC006532) putative multispanning membrane protein

[Arabidopsis thaliana]

Seq. No. 38207

Seq. ID LIB3093-045-Q1-K1-E8

Method BLASTN
NCBI GI g170053
BLAST score 58
E value 6.0e-24
Match length 170
% identity 84

NCBI Description Soybean ribosomal protein S11 mRNA, 3' end

1.2



```
38208
Seq. No.
                  LIB3093-045-Q1-K1-E9
Seq. ID
                  BLASTX
Method
                  g4008008
NCBI GI
                  216
BLAST score
E value
                  2.0e-17
                  117
Match length
% identity 🥕
                  (AF084035) receptor-like protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  38209
Seq. No.
                  LIB3093-045-Q1-K1-F3
Seq. ID
                  BLASTX
Method
                  q4263703
NCBI GI
                  154
BLAST score
E value
                  3.0e-10
                  93
Match length
                   43
% identity
                  (AC006223) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   38210
Seq. No.
                   LIB3093-045-Q1-K1-H8
Seq. ID
                   BLASTX
Method
                   q548485
NCBI GI
                   190
BLAST score
                   1.0e-14
E value
                   68
Match length
                   60
% identity
                   POLYGALACTURONASE INHIBITOR PRECURSOR
NCBI Description
                   (POLYGALACTURONASE-INHIBITING PROTEIN)
                   >gi 478677_pir__S23764 polygalacturanase-inhibiting protein
                   precursor - kidney bean >gi_21029_emb_CAA46016_ (X64769)
                   polygalacturanase-inhibiting protein [Phaseolus vulgaris]
Seq. No.
                   38211
                   LIB3093-046-Q1-K1-A5
Seq. ID
                   BLASTX
Method
                   g417148
NCBI GI
                   135
BLAST score
                   8.0e-12
E value
                   107
Match length
                   44
 % identity
                   PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A)
NCBI Description
                   (G2-4) >gi_99912_pir__A33654 heat shock protein 26A -
                   soybean >gi 169981 (M20363) Gmhsp26-A [Glycine max]
                   38212
 Seq. No.
                   LIB3093-046-Q1-K1-A8
 Seq. ID
                   BLASTX
 Method
                   q4097571
 NCBI GI
                   120
 BLAST score
                   7.0e-11
 E value
                   100
 Match length
```

42

NCBI Description (U64916) GMFP5 [Glycine max]

% identity



```
38213
Seq. No.
Seq. ID
                  LIB3093-046-Q1-K1-D6
Method
                  BLASTX
                  q3334195
NCBI GI
                  271
BLAST score
                  6.0e-24
E value
                  120
Match length
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-1 SUBUNIT
NCBI Description
                  (GP-ALPHA-1) >gi_1480298_emb_CAA67845_ (X99485) G protein
                  [Lupinus luteus]
                  38214
Seq. No.
                  LIB3093-046-Q1-K1-D7
Seq. ID
                  BLASTX
Method
                  q3377797
NCBI GI
                  233
BLAST score
                  1.0e-19
E value
                  77
Match length
                  65
% identity
                  (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
                   38215
Seq. No.
                   LIB3093-046-Q1-K1-E3
Seq. ID
                   BLASTX
Method
                   q3377797
NCBI GI
BLAST score
                   278
                   5.0e-27
E value
                   105
Match length
                   65
% identity
                   (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                   by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
                   A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                   R90691 [Ara
                   38216
Seq. No.
Seq. ID
                   LIB3093-046-Q1-K1-E9
                   BLASTX
Method
                   q3717965
NCBI GI
                   155
BLAST score
                   3.0e-10
E value
Match length
                   91
 % identity
                   (AL031640) 1-evidence=predicted by content;
NCBI Description
                   1-method=genefinder;084; 1-evidence_end;
```

2-evidence=predicted by match;
2-match\_accession=SPTREMBL:060878;

2-match\_description=DIA-12C PROTEIN.; 2-match\_species=HOMO

SAPIENS (HUMAN).;

Seq. No. 38217

Seq. ID

Method NCBI GI



```
LIB3093-046-Q1-K1-F3
Seq. ID
                  BLASTX
Method
                  g541943
NCBI GI
BLAST score
                  293
                  2.0e-26
E value
Match length
                  56
                  95
% identity
                  metallothionein - soybean >gi_228682_prf__1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
Seq. No.
                  38218
Seq. ID
                  LIB3093-046-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  q1763063
BLAST score
                  227
                  2.0e-34
E value
Match length
                  162
% identity
                  42
NCBI Description (U68763) SCOF-1 [Glycine max]
                  38219
Seq. No.
Seq. ID
                  LIB3093-047-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g2832672
BLAST score
                  319
                  1.0e-29
E value
Match length
                  114
                  60
% identity
                  (AL021712) nifU-like protein [Arabidopsis thaliana]
NCBI Description
                  38220
Seq. No.
Seq. ID
                  LIB3093-047-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  q3023535
BLAST score
                  392
                  3.0e-38
E value
                  112
Match length
                  69
% identity
                  MOLYBDOPTERIN BIOSYNTHESIS CNX2 PROTEIN (MOLYBDENUM
NCBI Description
                  COFACTOR BIOSYNTHESIS ENZYME CNX2) >gi 662871 emb_CAA88107_
                   (Z48047) Cnx2 [Arabidopsis thaliana]
Seq. No.
                  38221
Seq. ID
                  LIB3093-047-Q1-K1-B9
                  BLASTX
Method
                  g3513737
NCBI GI
BLAST score
                  230
E value
                  5.0e-19
                  67
Match length
                  60
% identity
                  (AF080118) contains similarity to C3HC4-type zinc fingers
NCBI Description
                   (Pfam:zf-C3HC4.hmm, score: 34.87) [Arabidopsis thaliana]
                   38222
Seq. No.
```

5903

LIB3093-047-Q1-K1-F10

BLASTN

q18764



```
BLAST score
                  393
                  0.0e + 00
E value
Match length
                  425
% identity
                  98
NCBI Description G.max tefS1 gene for elongation factor EF-1a
Seq. No.
                  38223
                  LIB3093-048-Q1-K1-A4
Seq, ID
                  BLASTN
Method
                  g169980
NCBI GI
BLAST score
                  34
                  1.0e-09
E value
Match length
                  46
% identity
                  93
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No. Seq. ID
                  38224
                  LIB3093-048-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q3080435
BLAST score
                  533
E value
                  1.0e-54
Match length
                  148
% identity
                  70
NCBI Description (AL022605) putative protein [Arabidopsis thaliana]
                  38225
Seq. No.
Seq. ID
                  LIB3093-048-Q1-K1-C7
                  BLASTX
Method
                  g1236949
NCBI GI
BLAST score
                  148
                  3.0e-14
E value
                  117
Match length
                  49
% identity
NCBI Description (U50075) lipoxygenase L-5 [Glycine max]
                  38226
Seq. No.
Seq. ID
                  LIB3093-048-Q1-K1-D8
Method
                  BLASTN
NCBI GI
                  g1834452
BLAST score
                  379
E value
                  0.0e + 00
Match length
                   461
                   95
% identity
NCBI Description G.max mRNA for alpha subunit of G protein
                  38227
Seq. No.
                  LIB3093-048-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2244912
                  173
BLAST score
```

7.0e-13 E value Match length 54 % identity 67

NCBI Description (Z97339) similar to transketolase [Arabidopsis thaliana]

38228 Seq. No.

E value

Match length

5.0e-15



```
LIB3093-048-Q1-K1-G3
Seq. ID
                  BLASTN
Method
                  g18764
NCBI GI
BLAST score
                   173
                   1.0e-92
E value
                   245
Match length
                   93
% identity
                  G.max tefS1 gene for elongation factor EF-1a
NCBI Description
                   38229
Seq. No.
Seq. ID
                  LIB3093-048-Q1-K1-G8
                  BLASTN
Method
                   g18764
NCBI GI
                   170
BLAST score
                   8.0e-91
E value
                   302
Match length
% identity
                   89
NCBI Description G.max tefS1 gene for elongation factor EF-1a
                   38230
Seq. No.
Seq. ID
                   LIB3093-048-Q1-K1-H5
Method
                   BLASTN
                   g498741
NCBI GI
                   32
BLAST score
                   1.0e-08
E value
Match length
                   56
                   89
% identity
NCBI Description H.vulgare (pMaW25) mRNA for beta-ketoacyl-ACP synthase
                   38231
Seq. No.
Seq. ID
                   LIB3093-049-Q1-K1-A12
Method
                   BLASTX
NCBI GI
                   g3540182
                   294
BLAST score
                   1.0e-26
E value
                   108
Match length
                   57
% identity
                  (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   38232
Seq. No.
Seq. ID
                   LIB3093-049-Q1-K1-A4
Method
                   BLASTN
NCBI GI
                   g2341023
BLAST score
                   101
                   1.0e-49
E value
                   253
Match length
% identity
                   Sequence of BAC F19P19 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
                   38233
Seq. No.
Seq. ID
                   LIB3093-049-Q1-K1-C5
                   BLASTX
Method
NCBI GI
                   g1346809
BLAST score
                   194
```



```
% identity
NCBI Description PATHOGEN-RELATED PROTEIN >gi_499074_emb_CAA34641_ (X16648)
                  pathogenesis related protein [Hordeum vulgare]
                  38234
Seq. No.
                  LIB3093-049-Q1-K1-E9
Seq. ID
                  BLASTX
Method
                  g129808
NCBI GI
                  353
BLAST score
                  2.0e-33
E value
                  107
Match length
                  66
% identity
NCBI Description CATIONIC PEROXIDASE 2 PRECURSOR >gi_99873_pir__B38265
                  peroxidase (EC 1.11.1.7) precursor, cationic (clone PNC2) -
                  peanut >gi_166475 (M37637) cationic peroxidase [Arachis
                  hypogaea]
                  38235
Seq. No.
                  LIB3093-049-Q1-K1-F3
Seq. ID
                  BLASTX
Method
                  q2129559
NCBI GI
                  406
BLAST score
                  1.0e-39
E value
                  142
Match length
                  53
% identity
                  cellulase homolog OR16pep - Arabidopsis thaliana
NCBI Description
                  >gi_1022807 (U37702) cellulase [Arabidopsis thaliana]
                  >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana]
                  >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana]
                  >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN
                   [Arabidopsis thaliana]
                  38236
Seq. No.
                  LIB3093-049-Q1-K1-G8
Seq. ID
                  BLASTN
Method
                  q18764
NCBI GI
BLAST score
                   54
                   4.0e-22
E value
                   82
Match length
% identity
                   93
NCBI Description G.max tefS1 gene for elongation factor EF-1a
Seq. No.
                   38237
                   LIB3093-049-Q1-K1-H2
Seq. ID
Method
                   BLASTX
                   q3913416
NCBI GI
                   511
BLAST score
                   5.0e-52
E value
Match length
                   124
                   79
 % identity
NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                   (SAMDC) >gi_2129920_pir__S68990 adenosylmethionine
                   decarboxylase (EC 4.1.1.50) - Madagascar periwinkle
```

>gi\_758695 (U12573) S-adenosyl-L-methionine decarboxylase
proenzyme [Catharanthus roseus] >gi\_1094441\_prf\_\_2106177A

Met(S-adenosyl) decarboxylase [Catharanthus roseus]



```
Seq. No.
                  LIB3093-049-Q1-K1-H6
Seq. ID
Method
                  BLASTN
                  q3821780
NCBI GI
                   36
BLAST score
                   6.0e-11
E value
                   37
Match length
                   61
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   38239
Seq. No.
                   LIB3093-049-Q1-K1-H8
Seq. ID
                   BLASTX
Method
                   g3287695
NCBI GI
                   148
BLAST score
                   1.0e-09
E value
                   52
Match length
                   50
% identity
                   (ACO03979) Similar to hypothetical protein C34B7.2
NCBI Description
                   gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis
                   thaliana]
                   38240
Seq. No.
                   LIB3093-050-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   g4138722
NCBI GI
                   202
BLAST score
                   6.0e-16
E value
                   45
Match length
                   82
% identity
                  (Y09590) hexose transporter [Vitis vinifera]
NCBI Description
                   38241
Seq. No.
                   LIB3093-050-Q1-K1-A9
Seq. ID
                   BLASTX
Method
                   g3378650
NCBI GI
                   248
BLAST score
                   2.0e-21
E value
                   78
Match length
 % identity
                   65
NCBI Description (X97606) abscisic acid activated [Medicago sativa]
 Seq. No.
                   LIB3093-050-Q1-K1-C6
 Seq. ID
 Method
                   BLASTX
                    g3386621
 NCBI GI
                    211
 BLAST score
                    7.0e-17
 E value
 Match length
                   88
                    53
 % identity
 NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
                    38243
 Seq. No.
                    LIB3093-050-Q1-K1-C8
 Seq. ID
                    BLASTX
 Method
```

g729470

221

NCBI GI

BLAST score



2.0e-18 E value Match length % identity

NCBI Description

MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)

>gi\_542089\_pir\_\_JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi\_297798\_emb\_CAA79702\_ (Z21493) mitochondrial formate dehydrogenase precursor

[Solanum tuberosum]

38244 Seq. No.

LIB3093-050-Q1-K1-G6 Seq. ID

BLASTX Method NCBI GI q4006878 155 BLAST score 3.0e-10 E value 99 Match length 35 % identity

(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana] NCBI Description

Seq. No.

38245 LIB3093-050-Q1-K1-G7 Seq. ID

BLASTX Method g417103 NCBI GI BLAST score 259 3.0e-25 E value 109 Match length 61 % identity

HISTONE H3.2, MINOR >gi 282871 pir S24346 histone NCBI Description

H3.3-like protein - Arabidopsis thaliana

>gi 16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 404825\_emb CAA42958\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa]  $>gi_488567$  ( $\overline{U}09460$ ) histone H3.2 [Medicago sativa] >gi\_488569 ( $\overline{U}$ 09461) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2

[Medicago sativa] >gi 488577 (U09465) histone H3.2

[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone

H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum]

>gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum]  $>g\bar{i}$  38 $\bar{8}$ 5890 (AF $\bar{0}$ 93633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi 4490755 emb\_CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 38246

LIB3093-050-Q1-K1-H6 Seq. ID

BLASTX Method g1825645 NCBI GI 166 BLAST score 8.0e-12 E value Match length 66 58 % identity

NCBI Description (U88173) weak similarity to Arabidopsis thaliana

Seq. No.

38252



## ubiquitin-like protein 8 [Caenorhabditis elegans]

```
Seq. No.
                  LIB3093-051-Q1-K1-B2
Seq. ID
                  BLASTN
Method
                   q170025
NCBI GI
BLAST score
                   141
E value
                   2.0e-73
                   305
Match length
                   87
% identity
                  Soybean malate synthase (MS) mRNA, 3' end
NCBI Description
Seq. No.
                   LIB3093-051-Q1-K1-C9
Seq. ID
                   BLASTX
Method
                   g1174498
NCBI GI
                   388
BLAST score
E value
                   2.0e-37
                   110
Match length
                   64
% identity
                   SYNAPTOBREVIN-RELATED PROTEIN >gi_600710 (M90418) formerly
NCBI Description
                   called HAT24; synaptobrevin-related protein [Arabidopsis
                   thaliana]
                   38249
Seq. No.
                   LIB3093-051-Q1-K1-E11
Seq. ID
                   BLASTN
Method
                   g3510337
NCBI GI
BLAST score
                   34
                   1.0e-09
E value
                   50
Match length
                   92
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K19E20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   38250
                   LIB3093-051-Q1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4097573
                   228
BLAST score
                   9.0e-19
E value
                   114
Match length
% identity
                   45
                   (U64917) GMFP7 [Glycine max]
NCBI Description
                   38251
Seq. No.
                   LIB3093-051-Q1-K1-H10
Seq. ID
Method
                   BLASTN
                   q2687435
NCBI GI
                   180
BLAST score
                   1.0e-96
E value
                   452
Match length
                   85
% identity
                   Hamamelis virginiana large subunit 26S ribosomal RNA gene,
NCBI Description
                   partial sequence
```



```
LIB3093-052-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  g1946360
NCBI GI
                  145
BLAST score
                  1.0e-09
E value
                  51
Match length
                  61
% identity
                  (U93215) elicitor response element binding protein WRKY3
NCBI Description
                  isolog [Arabidopsis thaliana]
                  38253
Seq. No.
                  LIB3093-052-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                  g20725
NCBI GI
BLAST score
                  175
                  8.0e-13
E value
                  80
Match length
                  53
% identity
                  (X65154) GA [Pisum sativum]
NCBI Description
                   38254
Seq. No.
                  LIB3093-052-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                   g542157
NCBI GI
BLAST score
                   139
                   7.0e-09
E value
                   70
Match length
                   43
% identity
NCBI Description ribosomal 5S RNA-binding protein - Rice
                   38255
Seq. No.
                   LIB3093-053-Q1-K1-A11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1743354
                   165
BLAST score
E value
                   1.0e-11
Match length
                   48
                   65
% identity
                  (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
NCBI Description
                   38256
Seq. No.
                   LIB3093-053-Q1-K1-A3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4127877
BLAST score
                   136
                   1.0e-70
E value
                   232
Match length
                   90
% identity
NCBI Description Glycine max mRNA for NDX1 homeobox protein, partial
                   38257
Seq. No.
                   LIB3093-053-Q1-K1-B11
Seq. ID
                   BLASTX
Method
                   g3452263
NCBI GI
BLAST score
                   551
```

1.0e-56

146

E value Match length

% identity



```
% identity
                  (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis
NCBI Description
                  thaliana]
                  38258
Seq. No.
Seq. ID
                  LIB3093-053-Q1-K1-C2
Method
                  BLASTX
                  q4415931
NCBI GI
                  256
BLAST score
                  4.0e-22
E value
Match length
                  82
                  60
% identity
                  (AC006418) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown
                  protein [Arabidopsis thaliana]
                  38259
Seq. No.
                  LIB3093-053-Q1-K1-C6
Seq. ID
                  BLASTX
Method
                  q3334144
NCBI GI
                  127
BLAST score
E value
                  1.0e-09
Match length
                  57
% identity
                  63
NCBI Description G1/S-SPECIFIC CYCLIN C-TYPE >gi 1695698_dbj BAA13181_
                   (D86925) C-type cyclin [Oryza sativa]
                  38260
Seq. No.
                  LIB3093-053-Q1-K1-E11
Seq. ID
                  BLASTX
Method
                  g3451068
NCBI GI
                   465
BLAST score
                   1.0e-46
E value
Match length
                   132
% identity
                  (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                   38261
Seq. No.
                   LIB3093-053-Q1-K1-G11
Seq. ID
Method
                   BLASTN
NCBI GI
                   q18764
BLAST score
                   106
                   1.0e-52
E value
Match length
                   297
% identity
                   85
NCBI Description G.max tefS1 gene for elongation factor EF-1a
                   38262
Seq. No.
                   LIB3093-053-Q1-K1-H2
Seq. ID
Method
                   BLASTN
                   q18743
NCBI GI
                   37
BLAST score
                   2.0e-11
E value
                   49
Match length
                   94
```

NCBI Description G.max mRNA from stress-induced gene (SAM22)



```
38263
Seq. No.
Seq. ID
                  LIB3093-053-Q1-K1-H5
Method
                  BLASTX
                  q3334667
NCBI GI
                  169
BLAST score
                  4.0e-23
E value
Match length
                  137
% identity
                  43
                  (Y10493) putative cytochrome P450 [Glycine max]
NCBI Description
                  38264
Seq. No.
                  LIB3093-053-Q1-K1-H6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q18743
BLAST score
                  96
                  1.0e-46
E value
                  148
Match length
                  91
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
                  38265
Seq. No.
                  LIB3093-056-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3928150
BLAST score
                  446
E value
                  2.0e-44
                  111
Match length
                  77
% identity
                  (AJ131049) hypothetical protein [Cicer arietinum]
NCBI Description
                  38266
Seq. No.
                  LIB3093-056-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2842482
BLAST score
                   149
E value
                  1.0e-09
Match length
                   67
                   42
% identity
                   (AL021749) protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   38267
Seq. No.
                  LIB3093-056-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3882356
BLAST score
                   244
E value
                   6.0e-21
Match length
                   67
% identity
                   70
                   (U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis
NCBI Description
                   thaliana]
                   38268
Seq. No.
```

Seq. ID

Method

LIB3093-056-Q1-K1-B11

NCBI GI

BLASTX g3645985

223 BLAST score



3.0e-18 E value 40 Match length 93 % identity

(AL031581) 1-evidence=predicted by content; NCBI Description 1-method=genefinder;084; 1-method\_score=23.36; 1-evidence\_end; 2-evidence=predicted by match;

2-match accession=AA141041;

2-match description=CK01110.3prime CK Drosophila

melanogaster

Seq. No. 38269

Seq. ID LIB3093-056-Q1-K1-B3

Method BLASTX q1169238 NCBI GI BLAST score 268 7.0e-37 E value 101 Match length % identity 83

GLUTAMATE DECARBOXYLASE (GAD) >gi\_1076648\_pir\_\_A48767 NCBI Description

glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding garden petunia >gi\_294112 (L16797) glutamate decarboxylase

[Petunia hybrida] >gi 309680 (L16977) glutamate

decarboxylase [Petunia hybrida]

38270 Seq. No.

LIB3093-056-Q1-K1-C5 Seq. ID

Method BLASTX NCBI GI q2982243 BLAST score 166 1.0e-11 E value Match length 61 54 % identity

(AF051204) hypothetical protein [Picea mariana] NCBI Description

Seq. No.

38271

LIB3093-056-Q1-K1-D7 Seq. ID

BLASTX Method q2055230 NCBI GI BLAST score 178 4.0e-13 E value 62 Match length 53 % identity

(AB000130) SRC2 [Glycine max] NCBI Description

38272 Seq. No.

LIB3093-056-Q1-K1-F11 Seq. ID

Method BLASTX g3876865 NCBI GI BLAST score 141 1.0e-08 E value 77 Match length 35 % identity

NCBI Description (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL: C09822 comes from this

gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co



```
38273
Seq. No.
                  LIB3093-056-Q1-K1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1335861
                  38
BLAST score
                  6.0e-12
E value
Match length
                  98
                  85
% identity
NCBI Description Glycine max clathrin heavy chain mRNA, complete cds
Seq. No.
Seq. ID
                  LIB3093-056-Q1-K1-F4
Method
                  BLASTX
                  q1170938
NCBI GI
                  365
BLAST score
                  5.0e-35
E value
                  111
Match length
                   68
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
                  >gi_481566_pir__S38875 methionine adenosyltransferase (EC
                   2.5.1.6) - tomato >gi_429106_emb_CAA80866_ (Z24742)
                   S-adenosyl-L-methionine synthetase [Lycopersicon
                   esculentum]
                   38275
Seq. No.
                  LIB3093-056-Q1-K1-F5
Seq. ID
Method
                  BLASTX
                   q4406775
NCBI GI
                   146
BLAST score
E value
                   3.0e-09
                   44
Match length
% identity
                   (AC006836) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   38276
                   LIB3093-056-Q1-K1-G6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2618602
BLAST score
                   45
                   4.0e-16
E value
Match length
                   85
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSJ1, complete sequence [Arabidopsis thaliana]
                   38277
Seq. No.
Seq. ID
                   LIB3093-056-Q1-K1-H3
Method
                   BLASTX
NCBI GI
                   q899608
                   409
BLAST score
                   3.0e-40
E value
                   106
Match length
                   17
% identity
```

Seq. No. 38278

NCBI Description

(U29158) polyubiquitin [Zea mays]

Method

NCBI GI

BLAST score

BLASTX

g3297824 138



```
LIB3093-056-Q1-K1-H8
Seq. ID
                  BLASTX
Method
                  g3894172
NCBI GI
                  251
BLAST score
                  1.0e-21
E value
                  85
Match length
% identity
                  (AC005312) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                  thaliana]
                  38279
Seq. No.
                  LIB3093-057-Q1-K1-A10
Seq. ID
                  BLASTX
Method
                  g4099329
NCBI GI
                  167
BLAST score
                  9.0e-13
E value
                  91
Match length
                  58
% identity
                  (U86384) ATP synthase beta subunit [Euptelea polyandra]
NCBI Description
                  38280
Seq. No.
                  LIB3093-057-Q1-K1-B6
Seq. ID
                  BLASTX
Method
                   g1173027
NCBI GI
                   338
BLAST score
                   1.0e-31
E value
                   108
Match length
% identity
                   65
                  60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal
NCBI Description
                   protein L31 [Nicotiana glutinosa]
Seq. No.
                   38281
                   LIB3093-057-Q1-K1-E7
Seq. ID
                   BLASTN
Method
                   g1066498
NCBI GI
                   189
BLAST score
                   1.0e-102
E value
                   353
Match length
                   88
% identity
NCBI Description Medicago sativa (clone GG16-1) NADH-dependent glutamate
                   synthase gene, complete cds
                   38282
Seq. No.
Seq. ID
                   LIB3093-057-Q1-K1-G3
                   BLASTX
Method
                   q4539305
NCBI GI
BLAST score
                   328
                   1.0e-30
E value
                   115
Match length
                   52
% identity
NCBI Description (AL049480) putative protein [Arabidopsis thaliana]
Seq. No.
                   38283
Seq. ID
                   LIB3093-057-Q1-K1-H4
```



```
1.0e-08
E value
Match length
                   61
% identity
NCBI Description
                   [Arabidopsis thaliana]
```

(AL031032) bZIP transcription factor - like protein

Seq. No. 38284

LIB3093-057-Q1-K1-H9 Seq. ID

Method BLASTX NCBI GI g2500715 BLAST score 251 E value 1.0e-21 Match length 79 61 % identity

PATHOGENESIS-RELATED PROTEIN PR-1 PRECURSOR NCBI Description

>gi\_629627\_pir\_\_S47171 gene PR-1 protein - barrel medic >gi\_505553 emb\_CAA56174\_ (X79778) PR-1 [Medicago

truncatula]

Seq. No. 38285

Seq. ID LIB3093-058-Q1-K1-A2

Method BLASTX NCBI GI q3860272 BLAST score 216 E value 2.0e-17 Match length 73 58 % identity

(AC005824) putative suppressor protein [Arabidopsis NCBI Description

thaliana] >gi\_4314399\_gb\_AAD15609\_ (AC006232) putative skd1

protein [Arabidopsis thaliana]

Seq. No. 38286

Seq. ID LIB3093-058-Q1-K1-C1

Method BLASTX NCBI GI q417744 140 BLAST score 3.0e-10 E value 69 Match length % identity 61

ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE NCBI Description

HYDROLASE) (ADOHCYASE) >gi 169663 (M81885)

S-adenosylhomocysteine hydrolase [Petroselinum crispum]

38287 Seq. No.

Seq. ID LIB3093-058-Q1-K1-C3

 ${\tt BLASTX}$ Method NCBI GI g3386617 BLAST score 124 4.0e-13 E value 102 Match length 50 % identity

(AC004665) putative cell division protein (ftsY) NCBI Description

[Arabidopsis thaliana]

38288 Seq. No.

Seq. ID LIB3093-058-Q1-K1-E11

Method BLASTX

Seq. ID

Method

```
q3759184
NCBI GI
BLAST score
                  182
                  2.0e-23
E value
                  108
Match length
% identity
                  64
                  (AB018441) phi-1 [Nicotiana tabacum]
NCBI Description
                  38289
Seq. No.
                  LIB3093-058-Q1-K1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3142290
                  301
BLAST score
                  2.0e-27
E value
                  88
Match length
                   64
% identity
                   (AC002411) Contains similarity to gb_Z69902 from C.
NCBI Description
                  elegans. [Arabidopsis thaliana]
                  38290
Seq. No.
Seq. ID
                  LIB3093-058-Q1-K1-G12
                  BLASTN
Method
NCBI GI
                  g10790
                   34
BLAST score
                   1.0e-09
E value
                  72
Match length
                   93
% identity
NCBI Description Tetrahymena pyriformis alpha-tubulin gene
                   38291
Seq. No.
                   LIB3093-058-Q1-K1-G5
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1177368
BLAST score
                   74
                   2.0e-33
E value
                   158
Match length
                   87
% identity
NCBI Description Z.mays mRNA for ribosomal protein L39
                   38292
Seq. No.
Seq. ID
                   LIB3094-001-Q1-K1-B6
                   BLASTX
Method
NCBI GI
                   g2618684
BLAST score
                   329
                   1.0e-30
E value
Match length
                   148
                   50
% identity
NCBI Description
                   (AC002510) putative
                   UDP-N-acetylglucosamine--dolichyl-phosphate
                   N-acetylglucosaminephosphotransferase [Arabidopsis
                   thaliana] >gi 3241947 (AC004625) putative
                   UDP-N-acetylglucosamine--dolichyl-phosphate
                   N-acetylglucosaminephosphotransferase [Arabidopsis
                   thaliana]
Seq. No.
                   38293
```

LIB3094-001-Q1-K1-C12

BLASTN

Match length

% identity



```
q2920665
NCBI GI
                  276
BLAST score
                  1.0e-154
E value
                  290
Match length
                  99
% identity
                  Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                   (GSTa) mRNA, complete cds
                  38294
Seq. No.
                  LIB3094-001-Q1-K1-G10
Seq. ID
                  BLASTN
Method
                  g288618
NCBI GI
                  44
BLAST score
                  1.0e-15
E value
                  160
Match length
                  82
% identity
NCBI Description G.max GB-D-II gene for proteinase inhibitor D-II
                  38295
Seq. No.
                  LIB3094-001-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1906828
BLAST score
                   173
                   1.0e-12
E value
                   68
Match length
                   59
% identity
NCBI Description (Y11828) heat shock protein [Arabidopsis thaliana]
                   38296
Seq. No.
                   LIB3094-001-Q1-K1-G7
Seq. ID
                   BLASTN
Method
                   g2791862
NCBI GI
BLAST score
                   34
                   1.0e-09
E value
                   42
Match length
                   95
% identity
                  Danio rerio heat shock protein 90-beta (hsp90beta) mRNA,
NCBI Description
                   complete cds
                   38297
Seq. No.
Seq. ID
                   LIB3094-001-Q1-K1-H2
                   BLASTX
Method
                   g82666
NCBI GI
                   156
BLAST score
                   5.0e-11
E value
                   63
Match length
                   60
% identity
                  ADP, ATP carrier protein G2 - maize
NCBI Description
                   38298
Seq. No.
Seq. ID
                   LIB3094-002-Q1-K1-A4
                   BLASTX
Method
                   g548746
NCBI GI
                   224
BLAST score
                   2.0e-18
E value
```



50S RIBOSOMAL PROTEIN L12, CHLOROPLAST PRECURSOR (CL12) NCBI Description >gi 478604\_pir\_\_S21111 ribosomal protein L12 precursor, chloroplast - wood tobacco >gi\_248303 bbs 93167 (S93166) ribosomal protein L12, CL12 [Nicotiana sylvestris=tobacco, leaf, Peptide Chloroplast, 186 aa] [Nicotiana sylvestris] Seq. No. 38299 LIB3094-002-Q1-K1-B6 Seq. ID BLASTX Method NCBI GI g2764941 BLAST score 207 1.0e-16 E value 78 Match length 51 % identity (X98255) transcriptionally stimulated by gibberellins; NCBI Description expressed in meristematic region, and style [Arabidopsis thaliana] 38300 Seq. No. Seq. ID LIB3094-002-Q1-K1-D7 Method BLASTX g4138583 NCBI GI BLAST score 211 4.0e-17 E value 95 Match length 54 % identity (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum] NCBI Description 38301 Seq. No. Seq. ID LIB3094-002-Q1-K1-D9 Method BLASTN NCBI GI q310575 BLAST score 57 2.0e-23 E value Match length 157 % identity 84 NCBI Description Glycine max nodulin-26 mRNA, complete cds 38302 Seq. No. LIB3094-002-Q1-K1-E6 Seq. ID Method BLASTX q2764941 NCBI GI BLAST score 173 2.0e-12 E value 93 Match length 39 % identity

NCBI Description (X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis

thaliana]

38303 Seq. No.

Seq. ID LIB3094-002-Q1-K1-F2

BLASTX Method NCBI GI g20020 BLAST score 171 E value 5.0e-13 Match length 70



```
% identity
NCBI Description (X62368) ribosomal protein L12-1a [Nicotiana tabacum]
                  38304
Seq. No.
                  LIB3094-002-Q1-K1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3868758
                  200
BLAST score
                  7.0e-16
E value
                  76
Match length
                  50
% identity
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                  38305
Seq. No.
Seq. ID
                  LIB3094-002-Q1-K1-H7
Method
                  BLASTN
NCBI GI
                  g1518539
                  206
BLAST score
                  1.0e-112
E value
                  306
Match length
                  92
% identity
NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds
                  38306
Seq. No.
Seq. ID
                  LIB3094-002-Q1-K1-H9
                  BLASTN
Method
NCBI GI
                  q3342030
                  37
BLAST score
                  2.0e-11
E value
Match length
                  41
                  98
% identity
                  Joinvillea ascendens 18S small subunit ribosomal RNA gene,
NCBI Description
                  complete sequence
                  38307
Seq. No.
Seq. ID
                  LIB3094-005-Q1-K1-A2
                  BLASTX
Method
                  q4469020
NCBI GI
BLAST score
                  176
                  9.0e-13
E value
                  67
Match length
                  54
% identity
                  (AL035602) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                  38308
Seq. No.
Seq. ID
                  LIB3094-005-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g1706329
BLAST score
                  407
                  5.0e-40
E value
Match length
                  104
% identity
                  75
                  PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC)
NCBI Description
                  >gi 2146788 pir S65471 pyruvate decarboxylase (EC 4.1.1.1)
```

>gi 1177605 emb CAA91445 (Z66544) pyruvate decarboxylase

(clone PDC2) - Garden pea (fragment)



## [Pisum sativum]

```
38309
Seq. No.
Seq. ID
                  LIB3094-005-Q1-K1-C5
                  BLASTN
Method
                  g169980
NCBI GI
                  49
BLAST score
E value
                  1.0e-18
                  117
Match length
                  85
% identity
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
NCBI Description
                  38310
Seq. No.
                  LIB3094-006-Q1-K1-A1
Seq. ID
                  BLASTN
Method
                  g1732555
NCBI GI
BLAST score
                   58
                   5.0e-24
E value
                   237
Match length
                   82
% identity
                  Glycine max desiccation protective protein LEA5 (Lea5)
NCBI Description
                  mRNA, complete cds
                   38311
Seq. No.
                   LIB3094-006-Q1-K1-A5
Seq. ID
Method
                   BLASTX
                   g1169840
NCBI GI
                   194
BLAST score
                   8.0e-15
E value
Match length
                   96
% identity
                   43
                   GIBBERELLIN-REGULATED PROTEIN 4 PRECURSOR
NCBI Description
                   >gi 2129591_pir__S71442 GAST1 protein homolog (clone GASA4)
                   - Arabidopsis thaliana >gi 950099 (U15683)
                   qibberellin-regulated [Arabidopsis thaliana]
                   38312
Seq. No.
                   LIB3094-006-Q1-K1-B2
Seq. ID
                   BLASTX
Method
                   g3482979
NCBI GI
BLAST score
                   308
                   3.0e-28
E value
                   95
Match length
                   59
% identity
                   (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4567258 gb AAD23672.1 AC007070_21 (AC007070)
                   hypothetical protein [Arabidopsis thaliana]
                   38313
Seq. No.
                   LIB3094-006-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                   g4580478
NCBI GI
BLAST score
                   141
                   1.0e-08
E value
                   70
Match length
                   56
% identity
NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]
```



```
Seq. No.
                  38314
Seq. ID
                  LIB3094-006-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2764941
BLAST score
                  212
E value
                  6.0e-17
Match length
                  95
                  45
% identity
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis,
                  thaliana]
Seq. No.
                   38315
Seq. ID
                  LIB3094-006-Q1-K1-G1
Method
                  BLASTN
NCBI GI
                  g19394
BLAST score
                  33
E value
                   4.0e-09
                   69
Match length
                  87
% identity
NCBI Description Tomato U3 small nuclear RNA gene
Seq. No.
                   38316
                  LIB3094-007-Q1-K1-A7
Seq. ID
Method
                  BLASTX
                   q4105696
NCBI GI
                   151
BLAST score
E value
                   3.0e-10
                   56
Match length
                   59
% identity
                  (AF049870) beta tubulin 1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   38317
Seq. ID
                   LIB3094-007-Q1-K1-B12
Method
                   BLASTX
                   g4191782
NCBI GI
                   273
BLAST score
                   4.0e-24
E value
Match length
                   130
% identity
                   52
                  (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   38318
Seq. ID
                   LIB3094-007-Q1-K1-B6
                   BLASTN
Method
NCBI GI
                   g2920665
BLAST score
                   93
                   7.0e-45
E value
                   185
Match length
                   88
% identity
                   Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                   (GSTa) mRNA, complete cds
```

5922

38319

BLASTX

LIB3094-007-Q1-K1-C5

Seq. No. Seq. ID

Method



NCBI GI g4193388
BLAST score 344
E value 2.0e-32
Match length 94
% identity 74

NCBI Description (AF091455) translationally controlled tumor protein [Hevea

brasiliensis]

Seq. No. 38320

Seq. ID LIB3094-007-Q1-K1-G10

Method BLASTX
NCBI GI g1706329
BLAST score 465
E value 1.0e-46
Match length 118
% identity 74

NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC)

>gi\_2146788\_pir\_\_S65471 pyruvate decarboxylase (EC 4.1.1.1)

(clone PDC2) - Garden pea (fragment)

>gi\_1177605\_emb\_CAA91445\_ (Z66544) pyruvate decarboxylase

[Pisum sativum]

Seq. No. 38321

Seq. ID LIB3094-007-Q1-K1-G3

Method BLASTX
NCBI GI g3915699
BLAST score 163
E value 2.0e-11
Match length 68
% identity 49

NCBI Description AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T

PROTEIN) >gi\_541970\_pir\_\_S40260 T-protein - garden pea >gi\_1362061\_pir\_\_S56661 glycine decarboxylase T protein precursor - garden pea >gi\_438217\_emb\_CAA81080\_ (Z25861)

T-protein [Pisum sativum] >gi\_3021553\_emb\_CAA10976\_

(AJ222771) T protein [Pisum sativum]

Seq. No. 38322

Seq. ID LIB3094-009-Q1-K1-A1

Method BLASTX
NCBI GI g120669
BLAST score 218
E value 5.0e-18
Match length 69
% identity 68

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 38323

Seq. ID LIB3094-009-Q1-K1-A10

Method BLASTN
NCBI GI g170007
BLAST score 311
E value 1.0e-175



Match length 343 % identity 98

NCBI Description Soybean 18 kD late embryogenesis abundant (Lea) protein

mRNA, complete cds

Seq. No. 38324

Seq. ID LIB3094-009-Q1-K1-C7

Method BLASTN
NCBI GI g1675195
BLAST score 67
E value 2.0e-29
Metab length 213

Match length 213 % identity 83

NCBI Description Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,

complete cds

Seq. No. 38325

Seq. ID LIB3094-009-Q1-K1-D2

Method BLASTX
NCBI GI g2804278
BLAST score 579
E value 5.0e-60
Match length 133
% identity 82

NCBI Description (AB003516) squalene epoxidase [Panax ginseng]

Seq. No. 38326

Seq. ID LIB3094-009-Q1-K1-H10

Method BLASTX
NCBI GI g1172571
BLAST score 170
E value 4.0e-12
Match length 120
% identity 38

NCBI Description PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)

>gi\_1076277\_pir\_\_S52637 phosphoenolpyruvate carboxykinase

(ATP) (EC 4.1.1.49) - cucumber >gi\_567102 (L31899) phosphoenolpyruvate carboxykinase [Cucumis sativus]

Seq. No. 38327

Seq. ID LIB3094-010-Q1-K1-A5

Method BLASTX
NCBI GI g3334196
BLAST score 123
E value 1.0e-09
Match length 67
% identity 54

NCBI Description AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T

PROTEIN) >gi\_2467117\_emb\_CAB16917\_ (Z99769) T-Protein

precursor [Flaveria trinervia]

Seq. No. 38328

Seq. ID LIB3094-010-Q1-K1-B12

Method BLASTX
NCBI GI g4454457
BLAST score 412
E value 2.0e-40



Match length 86 % identity

(AC006234) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

38329

Seq. ID

LIB3094-010-Q1-K1-B9

Method NCBI GI BLASTN g310575 111

BLAST score E value Match length

1.0e-55 296

% identity 87

Glycine max nodulin-26 mRNA, complete cds NCBI Description

Seq. No.

38330

Seq. ID

LIB3094-010-Q1-K1-C1

Method NCBI GI BLAST score BLASTN g1256607 74

E value Match length % identity

9.0e-34 125 90

NCBI Description Glycine max G protein beta subunit mRNA, complete cds

Seq. No.

38331

Seq. ID

LIB3094-010-Q1-K1-C11

Method BLASTX NCBI GI g1710807 BLAST score 206 2.0e-16 E value 60 Match length 72 % identity

NCBI Description

RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60

KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi\_1185390

(U21105) alphacpn60 [Pisum sativum]

Seq. No.

38332

Seq. ID

LIB3094-010-Q1-K1-C6

BLASTX Method g3319682 NCBI GI BLAST score 276 9.0e-25 E value 89 Match length 60 % identity

NCBI Description

(Y17720) SPINDLY protein [Petunia x hybrida]

Seq. No.

38333

Seq. ID

LIB3094-010-Q1-K1-F8

BLASTN Method NCBI GI g2511688 BLAST score 108 1.0e-53 E value 282 Match length % identity 85

NCBI Description

Phaseolus vulgaris Moldavian encoding cysteine proteinase

precursor (clone cp6a)



```
38334
Seq. No.
                  LIB3094-010-Q1-K1-G4
Seq. ID
                  BLASTN
Method
                  g169980
NCBI GI
                  127
BLAST score
E value
                  3.0e-65
                  227
Match length
% identity
                  89
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
NCBI Description
                  38335
Seq. No.
Seq. ID
                  LIB3094-010-Q1-K1-G6
Method
                  BLASTN
NCBI GI
                   g2920665
BLAST score
                   34
                   4.0e-10
E value
Match length
                   58
% identity
                   90
                  Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                   (GSTa) mRNA, complete cds
Seq. No.
                   38336
Seq. ID
                   LIB3094-011-Q1-K1-A1
Method
                   BLASTN
NCBI GI
                   g169980
BLAST score
                   156
                   2.0e-82
E value
Match length
                   276
% identity
                   89
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
NCBI Description
                   38337
Seq. No.
Seq. ID
                   LIB3094-011-Q1-K1-D3
Method
                   BLASTN
NCBI GI
                   g2642237
BLAST score
                   37
                   2.0e-11
E value
Match length
                   217
                   82
% identity
                   Glycine max endoplasmic reticulum HSC70-cognate binding
NCBI Description
                   protein precursor (BIP) mRNA, complete cds
                   38338
Seq. No.
Seq. ID
                   LIB3094-011-Q1-K1-F9
                   BLASTN
Method
NCBI GI
                   g1675195
BLAST score
                   82
                   3.0e-38
E value
                   246
Match length
                   83
% identity
                   Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
NCBI Description
                   complete cds
                   38339
Seq. No.
Seq. ID
                   LIB3094-011-Q1-K1-G4
```

5926

BLASTN

g310575

Method NCBI GI 1.00



```
BLAST score
                   7.0e-98
E value
Match length
                   356
                   90
% identity
```

NCBI Description Glycine max nodulin-26 mRNA, complete cds

Seq. No. Seq. ID

LIB3094-011-Q1-K1-H4

Method BLASTX NCBI GI g2764941 BLAST score 211 E value 7.0e-17 Match length 86 49 % identity

(X98255) transcriptionally stimulated by gibberellins; NCBI Description

expressed in meristematic region, and style [Arabidopsis

thaliana]

Seq. No.

38341 LIB3094-013-Q1-K1-D4 Seq. ID

BLASTN Method q2920665 NCBI GI BLAST score 96 E value 1.0e-46 236 Match length % identity 88

Glycine max 2,4-D inducible glutathione S-transferase NCBI Description

(GSTa) mRNA, complete cds

38342 Seq. No.

LIB3094-013-Q1-K1-F6 Seq. ID

Method BLASTX NCBI GI g1706329 BLAST score 236 1.0e-20 E value Match length 95 % identity 62

PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) NCBI Description

>gi\_2146788\_pir\_\_S65471 pyruvate decarboxylase (EC 4.1.1.1)

(clone PDC2) - Garden pea (fragment)

>qi 1177605 emb CAA91445 (Z66544) pyruvate decarboxylase

[Pisum sativum]

Seq. No. 38343

LIB3094-014-Q1-K1-A6 Seq. ID

Method BLASTX NCBI GI g1708236 BLAST score 253 1.0e-37 E value Match length 116 66 % identity

HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) NCBI Description

(3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)

>gi\_2129617\_pir\_\_JC4567 hydroxymethylglutaryl-CoA synthase

(EC 4.1.3.5) - Arabidopsis thaliana >gi 1143390\_emb\_CAA58763\_ (X83882)

hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]



>gi\_1586548\_prf\_\_2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No. 38344 Seq. ID LIB3094-014-Q1-K1-C8 Method BLASTN g2920665 NCBI GI BLAST score 215 E value 1.0e-117 Match length 315 92 % identity Glycine max 2,4-D inducible glutathione S-transferase NCBI Description (GSTa) mRNA, complete cds 38345 Seq. No. LIB3094-014-Q1-K1-D5 Seq. ID Method BLASTN

Method BLASTN
NCBI GI 9475599
BLAST score 52
E value 1.0e-20

Match length 96 % identity 89

NCBI Description Glycine max Century 84 BiP isoform B mRNA, complete cds

Seq. No. 38346

Seq. ID LIB3094-015-Q1-K1-B3

Method BLASTN
NCBI GI g2511688
BLAST score 81
E value 1.0e-37
Match length 215
% identity 85

NCBI Description Phaseolus vulgaris Moldavian encoding cysteine proteinase

precursor (clone cp6a)

Seq. No. 38347

Seq. ID LIB3094-015-Q1-K1-E2

Method BLASTX
NCBI GI g3372233
BLAST score 289
E value 5.0e-26
Match length 96
% identity 57

NCBI Description (AF019248) RNA polymerase I, II and III 24.3 kDa subunit

[Arabidopsis thaliana]

Seq. No. 38348

Seq. ID LIB3094-015-Q1-K1-H11

Method BLASTX
NCBI GI g1169840
BLAST score 160
E value 6.0e-11
Match length 94
% identity 37

NCBI Description GIBBERELLIN-REGULATED PROTEIN 4 PRECURSOR

>gi\_2129591\_pir\_\_S71442 GAST1 protein homolog (clone GASA4)

- Arabidopsis thaliana >gi 950099 (U15683)

Method

BLASTX



## gibberellin-regulated [Arabidopsis thaliana]

```
38349
Seq. No.
                  LIB3094-017-Q1-K1-A1
Seq. ID
                  BLASTN
Method
                  g3694834
NCBI GI
BLAST score
                  73
E value
                  4.0e-33
                  105
Match length
                  92
% identity
                  Glycine max alcohol dehydrogenase Adh-1 gene, partial cds
NCBI Description
                  38350
Seq. No.
                  LIB3094-017-Q1-K1-G8
Seq. ID
Method
                  BLASTN
                  q1234899
NCBI GI
BLAST score
                  115
                  3.0e-58
E value
Match length
                  199
                  89
% identity
                  G.max mRNA for homeobox-leucine zipper protein
NCBI Description
Seq. No.
                  38351
Seq. ID
                  LIB3094-018-Q1-K1-A11
Method
                  BLASTX
                  g132944
NCBI GI
BLAST score
                  333
E value
                  2.0e-31
Match length
                  94
                  67
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi 81658 pir JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >gi_806279
                   (M32655) ribosomal protein [Arabidopsis thaliana]
                  38352
Seq. No.
Seq. ID
                  LIB3094-018-Q1-K1-D11
                  BLASTN
Method
                  g1326160
NCBI GI
BLAST score
                  44
                  1.0e-15
E value
Match length
                  124
                  94
% identity
NCBI Description Phaseolus vulgaris dehydrin mRNA, complete cds
Seq. No.
                  38353
Seq. ID
                  LIB3094-018-Q1-K1-H11
                  BLASTX
Method
NCBI GI
                  q4210948
BLAST score
                  293
                  2.0e-26
E value
                  91
Match length
% identity
                  71
                  (AF085275) DnaJ protein [Hevea brasiliensis]
NCBI Description
Seq. No.
                  38354
                  LIB3094-020-Q1-K1-B12
Seq. ID
```

% identity



```
NCBI GI
                   q3157943
BLAST score
                  151
                  7.0e-10
E value
Match length
                  78
                   41
% identity
                   (ACO02131) Contains similarity to BAP31 protein gb_X81816
NCBI Description
                  from Mus musculus. [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3094-020-Q1-K1-B2
Method
                  BLASTN
NCBI GI
                  q642357
BLAST score
                   44
E value
                   4.0e-16
Match length
                  84
                   88
% identity
NCBI Description T.aralioides 28S rRNA gene (partial)
                   38356
Seq. No.
Seq. ID
                  LIB3094-020-Q1-K1-G3
Method
                  BLASTX
                   q1710546
NCBI GI
BLAST score
                   202
E value
                   2.0e-16
                   63
Match length
                   67
% identity
                  60S RIBOSOMAL PROTEIN L36 >qi 1276967 (U47095) putative
NCBI Description
                  ribosomal protein [Daucus carota]
Seq. No.
                   38357
                   LIB3094-020-Q1-K1-G6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g169936
                   97
BLAST score
                   3.0e-47
E value
                   241
Match length
% identity
                   85
NCBI Description Glycine max chalcone synthase (chs7) gene, complete cds
Seq. No.
                   38358
                   LIB3094-021-Q1-K1-A10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3551105
BLAST score
                   189
                   1.0e-14
E value
Match length
                   65
% identity
                   60
                  (AB011989) maturase [Rosa rugosa]
NCBI Description
                   38359
Seq. No.
Seq. ID
                   LIB3094-021-Q1-K1-D8
Method
                   BLASTN
NCBI GI
                   q18764
BLAST score
                   194
E value
                   1.0e-105
                   286
Match length
```

Seq. No.

Seq. ID

Method

38365

BLASTN

LIB3094-022-Q1-K1-G3



```
NCBI Description G.max tefS1 gene for elongation factor EF-la
                  38360
Seq. No.
                  LIB3094-021-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  g1707364
NCBI GI
BLAST score
                   406
E value
                  1.0e-39
                  134
Match length
                   60
% identity
                  (X94626) AATP2 [Arabidopsis thaliana]
NCBI Description
                  38361
Seq. No.
Seq. ID
                  LIB3094-022-Q1-K1-D12
                  BLASTX
Method
NCBI GI
                  g3915826
                  173
BLAST score
                   2.0e-13
E value
                  73
Match length
                   63
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L5
                   38362
Seq. No.
                  LIB3094-022-Q1-K1-E9
Seq. ID
Method
                  BLASTX
                   g4454457
NCBI GI
                   242
BLAST score
                   1.0e-20
E value
                   82
Match length
                   61
% identity
NCBI Description
                   (AC006234) unknown protein [Arabidopsis thaliana]
                   38363
Seq. No.
                   LIB3094-022-Q1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3036795
                   99
BLAST score
                                                            .
                   8.0e-10
E value
Match length
                   120
% identity
                   35
NCBI Description
                   (AL022373) putative protein [Arabidopsis thaliana]
                   >gi_3805857_emb_CAA21477_ (AL031986) putative protein
                   [Arabidopsis thaliana]
                   38364
Seq. No.
Seq. ID
                   LIB3094-022-Q1-K1-F3
Method
                   BLASTX
NCBI GI
                   q4454457
BLAST score
                   260
                   1.0e-22
E value
Match length
                   94
% identity
                   55
NCBI Description
                   (AC006234) unknown protein [Arabidopsis thaliana]
```

Match length



```
q3273826
NCBI GI
                  53
BLAST score
                  5.0e-21
E value
                  175
Match length
                   87
% identity
                  Glycine max nodule-enhanced malate dehydrogenase (Mdh)
NCBI Description
                  gene, complete cds
                   38366
Seq. No.
                  LIB3094-023-Q1-K1-B7
Seq. ID
                  BLASTN
Method
NCBI GI
                   q18644
                   32
BLAST score
                   1.0e-08
E value
                   150
Match length
% identity
                   83
                  Soybean mRNA for HMG-1 like protein
NCBI Description
                   38367
Seq. No.
                   LIB3094-023-Q1-K1-E12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g457569
BLAST score
                   40
                   3.0e-13
E value
                   214
Match length
                   79
% identity
                  Soybean mRNA for endo-xyloglucan transferase, partial cds
NCBI Description
                   38368
Seq. No.
                   LIB3094-023-Q1-K1-F4
Seq. ID
                   BLASTN
Method
                   g1675195
NCBI GI
BLAST score
                   84
                   2.0e-39
E value
                   158
Match length
                   89
% identity
                   Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
NCBI Description
                   complete cds
                   38369
Seq. No.
Seq. ID
                   LIB3094-023-Q1-K1-F7
                   BLASTN
Method
                   g2920665
NCBI GI
BLAST score
                   270
                   1.0e-150
E value
                   293
Match length
                   98
% identity
                   Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                   (GSTa) mRNA, complete cds
                   38370
Seq. No.
Seq. ID
                   LIB3094-023-Q1-K1-H10
Method
                   BLASTN
                   g2780193
NCBI GI
BLAST score
                   70
                   2.0e-31
E value
```



```
% identity
NCBI Description Lupinus albus mRNA for adenine nucleotide translocator
                  38371
Seq. No.
                  LIB3094-025-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                  g2129889
NCBI GI
BLAST score
                  311
                  6.0e-29
E value
Match length
                  77
% identity
                  81
NCBI Description methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
                  38372
Seq. No.
                  LIB3094-025-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267079
BLAST score
                  277
                  1.0e-24
E value
Match length
                  109
                  53
% identity
                  TUBULIN BETA-6 CHAIN >gi_320187_pir__JQ1590 tubulin beta-6
NCBI Description
                  chain - Arabidopsis thaliana >gi 166904 (M84703) beta-6
                  tubulin [Arabidopsis thaliana]
                   38373
Seq. No.
                  LIB3094-025-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1326161
BLAST score
                   260
                   7.0e-23
E value
                   72
Match length
% identity
                   83
                  (U54703) dehydrin [Phaseolus vulgaris]
NCBI Description
                   38374
Seq. No.
                   LIB3094-025-Q1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1326161
BLAST score
                   216
                   1.0e-17
E value
                   103
Match length
% identity
                   56
                  (U54703) dehydrin [Phaseolus vulgaris]
NCBI Description
Seq. No.
                   38375
                   LIB3094-025-Q1-K1-C6
Seq. ID
Method
                   BLASTN
```

g1326160 NCBI GI 69 BLAST score 1.0e-30 E value 145 Match length 95 % identity

Phaseolus vulgaris dehydrin mRNA, complete cds NCBI Description

38376 Seq. No.

LIB3094-025-Q1-K1-C7 Seq. ID



```
BLASTX
Method
NCBI GI
                  q4454457
BLAST score
                  186
                  4.0e-14
E value
                  64
Match length
                  56
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                  38377
Seq. No.
                  LIB3094-025-Q1-K1-G4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3449316
BLAST score
                  50
                  4.0e-19
E value
                  167
Match length
                  90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9D7, complete sequence [Arabidopsis thaliana]
                  38378
Seq. No.
                  LIB3094-026-Q1-K1-A3
Seq. ID
Method
                  BLASTX
                  g453980
NCBI GI
BLAST score
                   155
E value
                   9.0e-11
Match length
                   95
                   34
% identity
                  (Z29946) gamma-TIP-like protein [Trifolium repens]
NCBI Description
                   38379
Seq. No.
                   LIB3094-026-Q1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3482979
BLAST score
                   99
                   2.0e-10
E value
Match length
                   94
% identity
                   45
                   (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4567258_gb_AAD23672.1_AC007070_21 (AC007070)
                   hypothetical protein [Arabidopsis thaliana]
                   38380
Seq. No.
                   LIB3094-026-Q1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1708313
BLAST score
                   209
                   3.0e-17
E value
Match length
                   79
% identity
                   68
                   HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396 bbs 163637
NCBI Description
                   (S77849) heat-shock Protein=HSP81-3 [Arabidopsis
                   thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis
                   thaliana]
```

Seq. No. 38381

Seq. ID LIB3094-027-Q1-K1-C10

Method BLASTN

BLAST score



```
g1234899
NCBI GI
BLAST score
                  77
                  3.0e-35
E value
                  191
Match length
                  94
% identity
NCBI Description G.max mRNA for homeobox-leucine zipper protein
                  38382
Seq. No.
Seq. ID
                  LIB3094-028-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  q2894592
BLAST score
                  181
                  3.0e-13
E value
Match length
                  84
% identity
                  46
NCBI Description (AL021889) predicted protein [Arabidopsis thaliana]
Seq. No.
                  38383
                  LIB3094-029-Q1-K1-B3
Seq. ID
Method
                  BLASTX
                  g1706329
NCBI GI
BLAST score
                  328
E value
                  7.0e-33
Match length
                  109
% identity
                  PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC)
NCBI Description
                  >gi_2146788_pir__S65471 pyruvate decarboxylase (EC 4.1.1.1)
                  (clone PDC2) - Garden pea (fragment)
                  >gi 1177605 emb CAA91445 (Z66544) pyruvate decarboxylase
                  [Pisum sativum]
Seq. No.
                  38384
Seq. ID
                  LIB3094-029-Q1-K1-C11
                  BLASTN
Method
                  g2052028
NCBI GI
BLAST score
                  36
                  7.0e-11
E value
Match length
                  124
% identity
                  82
NCBI Description G.max mRNA for glutathione transferase
Seq. No.
                  38385
Seq. ID
                  LIB3094-029-Q1-K1-F7
                  BLASTX
Method
                  g2500354
NCBI GI
BLAST score
                  168
                  1.0e-18
E value
Match length
                  73
                  67
% identity
                  60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462_
NCBI Description
                  (AB001891) QM family protein [Solanum melongena]
Seq. No.
                  38386
Seq. ID
                  LIB3094-030-Q1-K1-B4
                  BLASTX
Method
NCBI GI
                  q133405
```



2.0e-13 E value Match length 63 59 % identity NCBI Description

DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN

>gi\_81956\_pir\_\_S04384 DNA-directed RNA polymerase (EC

2.7.7.6) alpha chain - garden pea chloroplast >gi\_12180 emb\_CAA33668\_ (X15645) RNA polymerase alpha

subunit (AA 1-334) [Pisum sativum]

38387 Seq. No.

LIB3094-030-Q1-K1-E7 Seq. ID

Method BLASTX NCBI GI q2677830 BLAST score 207 E value 1.0e-16 Match length 76 % identity 58

NCBI Description (U93168) ribosomal protein L12 [Prunus armeniaca]

38388 Seq. No.

LIB3094-033-Q1-K1-D4 Seq. ID

Method BLASTX NCBI GI g1762939 BLAST score 191 6.0e-15E value Match length 74 50 % identity

(U66266) ORF; able to induce HR-like lesions [Nicotiana NCBI Description

tabacum]

38389 Seq. No.

Seq. ID LIB3094-034-Q1-K1-H9

Method BLASTX NCBI GI q3452497 BLAST score 193 E value 8.0e-15 Match length 96 51 % identity

NCBI Description (Y17796) ketol-acid reductoisomerase [Pisum sativum]

Seq. No.

38390

Seq. ID LIB3094-035-Q1-K1-B4

Method BLASTX NCBI GI g3421104 278 BLAST score 1.0e-24 E value Match length 101 % identity 51

(AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis NCBI Description

thaliana]

Seq. No. 38391

Seq. ID LIB3094-035-Q1-K1-D9

BLASTX Method g2804278 NCBI GI 429 BLAST score 2.0e-42 E value



```
Match length
                   64
% identity
                   (AB003516) squalene epoxidase [Panax ginseng]
NCBI Description
                   38392
Seq. No.
                   LIB3094-035-Q1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4217999
BLAST score
                   152
                   5.0e-19
E value
Match length
                   74
% identity
                   70
                   (AC006135) putative ubiquitin--protein ligase
NCBI Description
                   (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]
Seq. No.
                   38393
Seq. ID
                   LIB3094-036-Q1-K1-C5
Method
                   BLASTX
NCBI GI
                   g1174626
BLAST score
                   235
                   8.0e-20
E value
Match length
                   99
% identity
                   57
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   (P23) >gi 1072463 pir A38959 IgE-dependent
                   histamine-releasing factor homolog - potato
                   >gi_587546_emb_CAA85519_ (Z37160) P23 protein [Solanum
                   tuberosum]
                   38394
Seq. No.
Seq. ID
                   LIB3094-036-Q1-K1-F12
Method
                   BLASTN
NCBI GI
                   g457569
BLAST score
                   78
                   7.0e-36
E value
Match length
                   281
                   83
% identity
                  Soybean mRNA for endo-xyloglucan transferase, partial cds
NCBI Description
                   38395
Seq. No.
Seq. ID
                   LIB3094-037-Q1-K1-C4
                   BLASTN
Method
NCBI GI
                   g575354
BLAST score
                   134
                   3.0e-69
E value
Match length
                   338
% identity
                   85
                  O.sativa SC34 mRNA for tumor suppressor
NCBI Description
                   38396
Seq. No.
                   LIB3094-037-Q1-K1-C7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4006890
BLAST score
                   153
                   4.0e-10
E value
```

80

50

Match length % identity



```
(Z99708) ubiquitin--protein ligase-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  38397
Seq. No.
                  LIB3094-037-Q1-K1-F11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2624382
                  180
BLAST score
                  9.0e-97
E value
Match length
                  272
% identity
                  92
NCBI Description P.vulgaris mRNA for cinnamate 4-hydroxylase
                  38398
Seq. No.
                  LIB3094-037-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454457
BLAST score
                  222
E value
                  3.0e-18
Match length
                  55
                  75
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                  38399
                  LIB3094-038-Q1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3273826
BLAST score
                  32
                  1.0e-08
E value
Match length
                   60
% identity
                  88
                  Glycine max nodule-enhanced malate dehydrogenase (Mdh)
NCBI Description
                  gene, complete cds
Seq. No.
                   38400
                  LIB3094-038-Q1-K1-F2
Seq. ID
Method
                  BLASTX
                   q399015
NCBI GI
BLAST score
                   298
                   3.0e-27
E value
                   103
Match length
                   62
% identity
                  ADP, ATP CARRIER PROTEIN PRECURSOR (ADP/ATP TRANSLOCASE)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT)
                   >gi_218145_dbj_BAA02161_ (D12637) ATP/ADP translocator
                   [Oryza sativa]
                   38401
Seq. No.
Seq. ID
                   LIB3094-038-Q1-K1-F7
Method
                   BLASTX
                   g3386615
NCBI GI
                   194
BLAST score
                   5.0e-15
E value
```

5938

(AC004665) putative phosphomannomutase [Arabidopsis

103

thaliana]

48

Match length

NCBI Description

% identity

NCBI Description



```
38402
Seq. No.
                  LIB3094-039-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g462195
BLAST score
                  194
                  3.0e-15
E value
Match length
                  78
                  56
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi_100682_pir__S21636 GOS2 protein - rice
                  >qi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                  >qi 3789950 (AF094774) translation initiation factor [Oryza
                   sativa]
                   38403
Seq. No.
Seq. ID
                  LIB3094-039-Q1-K1-A3
Method
                  BLASTN
NCBI GI
                   g170007
BLAST score
                   55
                   3.0e-22
E value
Match length
                   115
% identity
                   87
                  Soybean 18 kD late embryogenesis abundant (Lea) protein
NCBI Description
                  mRNA, complete cds
                   38404
Seq. No.
Seq. ID
                   LIB3094-039-Q1-K1-B4
Method
                   BLASTN
NCBI GI
                   g2920665
BLAST score
                   40
                   2.0e-13
E value
Match length
                   100
% identity
                   85
                   Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                   (GSTa) mRNA, complete cds
                   38405
Seq. No.
                   LIB3094-039-Q1-K1-D2
Seq. ID
                   BLASTN
Method
                   g18764
NCBI GI
BLAST score
                   237
                   1.0e-130
E value
                   309
Match length
                   94
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
                   38406
Seq. No.
Seq. ID
                   LIB3094-039-Q1-K1-G2
                   BLASTX
Method
                   g1169384
NCBI GI
BLAST score
                   159
                   6.0e-11
E value
                   95
Match length
                   40
% identity
```

ANJ1 protein - Atriplex nummularia

DNAJ PROTEIN HOMOLOG ANJ1 >gi 543510 pir JQ2142 chaperone

Seq. ID

Method



```
Seq. No.
                  38407
                  LIB3094-041-Q1-K1-G8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g19394
                  38
BLAST score
E value
                  5.0e-12
                  98
Match length
                  70
% identity
NCBI Description
                  Tomato U3 small nuclear RNA gene
Seq. No.
                  38408
Seq. ID
                  LIB3094-041-Q1-K1-H5
Method
                  BLASTN
NCBI GI
                  q310575
                  165
BLAST score
                  7.0e-88
E value
Match length
                  267
                  93
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                  38409
Seq. No.
Seq. ID
                  LIB3094-043-Q1-K1-D1
Method
                  BLASTN
                  q1675195
NCBI GI
                  108
BLAST score
                  1.0e-53
E value
                  262
Match length
% identity
                  85
                  Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
NCBI Description
                  complete cds
Seq. No.
                  38410
                  LIB3094-043-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1710546
                  197
BLAST score
                   9.0e-16
E value
Match length
                   59
                   71
% identity
                  60S RIBOSOMAL PROTEIN L36 >gi 1276967 (U47095) putative
NCBI Description
                  ribosomal protein [Daucus carota]
Seq. No.
                   38411
Seq. ID
                  LIB3094-043-Q1-K1-G11
                   BLASTN
Method
                   g1675195
NCBI GI
BLAST score
                   46
E value
                   5.0e-17
                   94
Match length
                   88
% identity
                  Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
NCBI Description
                   complete cds
                   38412
Seq. No.
```

5940

LIB3094-044-Q1-K1-E4

BLASTX



```
q1708313
NCBI GI
                  257
BLAST score
                  1.0e-22
E value
                  86
Match length
% identity
                  65
                  HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi 999396_bbs_163637
NCBI Description
                   (S77849) heat-shock Protein=HSP81-3 [Arabidopsis
                  thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis
                  thaliana]
                  38413
Seq. No.
Seq. ID
                  LIB3094-045-Q1-K1-A11
Method
                  BLASTN
                  q857392
NCBI GI
BLAST score
                  85
                   4.0e-40
E value
Match length
                  137
% identity
                   91
NCBI Description Glycine max mRNA for mitotic cyclin al-type, complete cds
Seq. No.
                   38414
Seq. ID
                   LIB3094-045-Q1-K1-F8
Method
                   BLASTX
NCBI GI
                   q3386615
BLAST score
                   293
                   2.0e-26
E value
Match length
                   85
                                                    X 33
                   68
% identity
                   (AC004665) putative phosphomannomutase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   38415
                   LIB3094-047-Q1-K1-A9
Seq. ID
                   BLASTN
Method
                   q1234899
NCBI GI
BLAST score
                   133
                   1.0e-68
E value
                   209
Match length
% identity
                   91
NCBI Description G.max mRNA for homeobox-leucine zipper protein
                   38416
Seq. No.
Seq. ID
                   LIB3094-047-Q1-K1-D2
                   BLASTN
Method
                   g19394
NCBI GI
BLAST score
                   42
                   2.0e-14
E value
Match length
                   98
                   71
% identity
                  Tomato U3 small nuclear RNA gene
NCBI Description
                   38417
Seq. No.
                   LIB3094-047-Q1-K1-F9
```

Seq. ID

Method BLASTX NCBI GI g2511541 BLAST score 220 3.0e-18 E value



```
Match length
% identity
                  49
                  (AF020787) DNA-binding protein GBP16 [Oryza sativa]
NCBI Description
                  38418
Seq. No.
                  LIB3094-048-Q1-K1-A2
Seq. ID
Method
                  BLASTN
                  q169980
NCBI GI
                                                        194
BLAST score
                  1.0e-105
E value
Match length
                  278
% identity
                  92
```

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

38419 Seq. No. LIB3094-048-Q1-K1-B2 Seq. ID Method BLASTX NCBI GI g4469020 BLAST score 165

E value 2.0e-11 Match length 67 48 % identity

(AL035602) putative protein (fragment) [Arabidopsis NCBI Description

thaliana]

38420 Seq. No.

LIB3094-048-Q1-K1-D3 Seq. ID

Method BLASTX g2244934 NCBI GI 141 BLAST score 3.0e-09 E value 48 Match length 60 % identity

(Z97339) similarity to SYNAPTOBREVIN-RELATED PROTEIN NCBI Description

[Arabidopsis thaliana]

Seq. No. 38421

LIB3094-049-Q1-K1-A6 Seq. ID

Method BLASTN NCBI GI g2270989 BLAST score 33 E value 6.0e-09 Match length 45 93 % identity

NCBI Description Glycine max dehydrin (GmPM12) mRNA, complete cds

Seq. No.

38422

38423

LIB3094-049-Q1-K1-B9 Seq. ID

Method BLASTN NCBI GI q2463568 BLAST score 103 5.0e-51 E value 231 Match length 86 % identity

NCBI Description Glycine max mRNA for squalene synthase, complete cds

Seq. No.

NCBI GI

BLAST score

q310575



```
LIB3094-049-Q1-K1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1336081
                   92
BLAST score
                   3.0e-44
E value
                   344
Match length
% identity
                   82
                  Glycine max var. Century ascorbate peroxidase 2 (APx2)
NCBI Description
                  mRNA, complete cds
                   38424
Seq. No.
Seq. ID
                  LIB3094-049-Q1-K1-D12
                  BLASTX
Method
                   q1495251
NCBI GI
BLAST score
                   100
                   3.0e-09
E value
Match length
                   82
                   44
% identity
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   38425
Seq. No.
Seq. ID
                   LIB3094-049-Q1-K1-E3
Method
                  BLASTX
                   g3810598
NCBI GI
BLAST score
                   151
                   8.0e-10
E value
                   96
Match length
% identity
                   36
                   (AC005398) putative endo-xyloglucan transferase
NCBI Description
                   [Arabidopsis thaliana]
                   38426
Seq. No.
Seq. ID
                   LIB3094-049-Q1-K1-F11
Method
                   BLASTN
NCBI GI
                   g1321821
BLAST score
                   42
E value
                   2.0e-14
                   273
Match length
                   81
% identity
                  G.max mRNA for glycinamide ribonucleotide transformylase
NCBI Description
Seq. No.
                   38427
Seq. ID
                   LIB3094-049-Q1-K1-G11
Method
                   BLASTX
NCBI GI
                   g4217999
BLAST score
                   141
                   7.0e-09
E value
Match length
                   40
% identity
                   (AC006135) putative ubiquitin--protein ligase
NCBI Description
                   (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]
                   38428
Seq. No.
Seq. ID
                   LIB3094-049-Q1-K1-G6
Method
                   BLASTN
```



E value 2.0e-54
Match length 209
% identity 88

NCBI Description Glycine max nodulin-26 mRNA, complete cds

Seq. No. 38429

Seq. ID LIB3094-050-Q1-K1-E12

Method BLASTX
NCBI GI g464444
BLAST score 150
E value 3.0e-10
Match length 65
% identity 48

NCBI Description PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE

COMPLEX 30 KD SUBUNIT) >gi\_541889\_pir\_\_S39900 proteasome -

100 m

Arabidopsis thaliana  $>gi_1\overline{16}6830 \pmod{M98495}$  proteasome

[Arabidopsis thaliana]

Seq. No. 38430

Seq. ID LIB3094-051-Q1-K1-A12

Method BLASTN
NCBI GI g2920665
BLAST score 184
E value 3.0e-99
Match length 240
% identity 95

NCBI Description Glycine max 2,4-D inducible glutathione S-transferase

(GSTa) mRNA, complete cds

Seq. No. 38431

Seq. ID LIB3094-052-Q1-K1-A10

Method BLASTX
NCBI GI g462195
BLAST score 173
E value 2.0e-12
Match length 85
% identity 47

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

>gi\_100682\_pir\_\_S21636 GOS2 protein - rice

>gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]

>gi\_3789950 (AF094774) translation initiation factor [Oryza

satīva]

Seq. No. 38432

Seq. ID LIB3094-052-Q1-K1-F3

Method BLASTN
NCBI GI 94193387
BLAST score 71
E value 1.0e-31
Match length 139
% identity 88

NCBI Description Hevea brasiliensis translationally controlled tumor protein

(TCTP) mRNA, complete cds

Seq. No. 38433

Seq. ID LIB3094-053-Q1-K1-B5

Method BLASTX



```
NCBI GI
                   q1706325
BLAST score
                  139
                  5.0e-09
E value
Match length
                   42
                   71
% identity
                  PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi_476286 (U07339)
NCBI Description
                  pyruvate decarboxylase 1 [Oryza sativa] >gi 1098559
                   (U26660) pyruvate decarboxylase [Oryza sativa]
Seq. No.
                   38434
                  LIB3094-053-Q1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2262155
                   48
BLAST score
                   7.0e-18
E value
                   76
Match length
% identity
                   DNA sequence of Arabidopsis thaliana BAC F5J6 from
NCBI Description
                   chromosome IV, complete sequence [Arabidopsis thaliana]
                   38435
Seq. No.
                   LIB3094-054-Q1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2578823
                   296
BLAST score
                   9.0e-27
E value
                   130
Match length
                   50
% identity
NCBI Description (AB000835) similar to YGR200c [Arabidopsis thaliana]
                   38436
Seq. No.
Seq. ID
                   LIB3094-054-Q1-K1-G8
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   34
E value
                   1.0e-09
Match length
                   34
                   59
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   38437
                   LIB3094-055-Q1-K1-F3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g18529
BLAST score
                   236
                   1.0e-130
E value
Match length
                   465
% identity
                   100
NCBI Description G.max Gmachs2 gene for chalcone synthase
                   38438
Seq. No.
Seq. ID
                   LIB3094-056-Q1-K1-C11
                   BLASTX
Method
NCBI GI
                   g1706329
                   336
BLAST score
```

5945

2.0e-31

104

E value Match length



% identity PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) NCBI Description >gi\_2146788\_pir\_\_S65471 pyruvate decarboxylase (EC 4.1.1.1) (clone PDC2) - Garden pea (fragment) >gi 1177605 emb CAA91445 (Z66544) pyruvate decarboxylase [Pisum sativum] Seq. No. 38439 Seq. ID LIB3094-056-Q1-K1-D3 Method BLASTX NCBI GI g2914706 BLAST score 185 E value 6.0e-14 Match length 65 51 % identity NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana] Seq. No. 38440 Seq. ID LIB3094-056-Q1-K1-F5 Method BLASTX NCBI GI g4567220 BLAST score 260 E value 1.0e-22 Match length 91 59 % identity (AC007119) hypothetical protein, 3' partial [Arabidopsis NCBI Description thaliana Seq. No. 38441 Seq. ID LIB3094-058-Q1-K1-E6 Method BLASTX NCBI GI g951449 BLAST score 153 3.0e-13 E value Match length 49 % identity 73 (L46681) aspartic protease precursor [Lycopersicon NCBI Description esculentum] 38442 Seq. No. Seq. ID LIB3094-058-Q1-K1-G11 BLASTN Method NCBI GI g457569 BLAST score 95 5.0e-46 E value Match length 267 % identity 84 NCBI Description Soybean mRNA for endo-xyloglucan transferase, partial cds Seq. No. 38443 续。 Seq. ID LIB3094-058-Q1-K1-G9 Method BLASTX

NCBI GI g3236242 BLAST score 176 E value 1.0e-12 Match length 98 % identity 47



```
(AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                  thaliana]
                  38444
Seq. No.
                  LIB3094-059-Q1-K1-C4
Seq. ID
Method
                  BLASTX
                  g2959767
NCBI GI
                  209
BLAST score
                  5.0e-17
E value
Match length
                  81
% identity
                  49
                   (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292
NCBI Description
                   (AC005309) glutathione-conjugate transporter AtMRP4
                   [Arabidopsis thaliana]
                  38445
Seq. No.
                  LIB3094-060-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g531829
BLAST score
                   191
                   2.0e-14
E value
                   72
Match length
% identity
                   57
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
                   38446
Seq. No.
                  LIB3094-060-Q1-K1-D11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2642237
BLAST score
                   41
                   1.0e-13
E value
Match length
                   150
% identity
                   86
                  Glycine max endoplasmic reticulum HSC70-cognate binding
NCBI Description
                   protein precursor (BIP) mRNA, complete cds
                   38447
Seq. No.
Seq. ID
                   LIB3094-060-Q1-K1-D12
Method
                   BLASTN
                   g2780193
NCBI GI
                   85
BLAST score
                   4.0e-40
E value
Match length
                   145
                   90
% identity
                  Lupinus albus mRNA for adenine nucleotide translocator
NCBI Description
Seq. No.
                   38448
                   LIB3094-060-Q1-K1-D9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2921511
BLAST score
                   35
                   3.0e-10
E value
Match length
                   55
```

NCBI Description Fritillaria agrestis GF14 protein (GRF) mRNA, complete cds

91

% identity



```
38449
Seq. No.
Seq. ID
                  LIB3094-060-Q1-K1-E2
                  BLASTN
Method
                  g2921511
NCBI GI
BLAST score
                  104
E value
                  2.0e-51
Match length
                  216
% identity
                  87
NCBI Description Fritillaria agrestis GF14 protein (GRF) mRNA, complete cds
Seq. No.
                  38450
Seq. ID
                  LIB3094-060-Q1-K1-H2
Method
                  BLASTN
NCBI GI
                  q1675195
BLAST score
                  70
E value
                  5.0e-31
Match length
                  226
% identity
                  83
                  Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
NCBI Description
                  complete cds
Seq. No.
                  38451
Seq. ID
                  LIB3094-062-Q1-K1-A1
Method
                  BLASTN
NCBI GI
                  q2920665
BLAST score
                  207
E value
                  1.0e-113
Match length
                  247
% identity
                  96
                  Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                   (GSTa) mRNA, complete cds
Seq. No.
                  38452
Seq. ID
                  LIB3094-062-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g119167
BLAST score
                  195
E value
                  1.0e-15
                  59
Match length
                   64
% identity
                  ELONGATION FACTOR 2 (EF-2) >gi 421771_pir__S32819
NCBI Description
                  translation elongation factor eEF-2 - Chlorella kessleri
                  >gi 167245 (M68064) elongation factor 2 [Chlorella
                   kessleri] >gi_228693_prf__1808323A elongation factor 2
                   [Chlorella kessleri]
                  38453
Seq. No.
Seq. ID
                  LIB3094-062-Q1-K1-C3
                  BLASTX
Method
                  g1173198
NCBI GI
BLAST score
                  177
E value
                   3.0e-13
Match length
                   52
                   71
% identity
                  40S RIBOSOMAL PROTEIN S13 >gi 480095 pir S36423 ribosomal
NCBI Description
```

protein S13.e - garden pea >gl 396639\_emb\_CAA80974\_ (Z25509) ribosomal protein S13 [Pisum sativum]



```
Seq. No.
                  38454
                  LIB3094-062-Q1-K1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1675195
BLAST score
                  41
                  5.0e-14
E value
Match length
                  93
% identity
NCBI Description
                  Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
                  complete cds
Seq. No.
                  38455
Seq. ID
                  LIB3094-062-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q2507443
BLAST score
                  236
E value
                   4.0e-20
Match length
                   68
                  71
% identity
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) (23
NCBI Description
                  KD CALLUS PROTEIN) (P23) >gi 1675196 (L47968) callus
                  protein P23 [Pisum sativum]
Seq. No.
                   38456
Seq. ID
                  LIB3094-062-Q1-K1-H9
Method
                   BLASTX
NCBI GI
                   a1518540
BLAST score
                   143
E value
                   4.0e-09
Match length
                   67
                   46
% identity
NCBI Description
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                   38457
                   LIB3094-063-Q1-K1-B12
Seq. ID
Method
                   BLASTX
                   g1495251
NCBI GI
BLAST score
                   217
                   4.0e-18
E value
                   73
Match length
% identity
                   58
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   38458
Seq. ID
                   LIB3094-063-Q1-K1-B9
Method
                   BLASTX
NCBI GI
                   q1169384
BLAST score
                   213
                   1.0e-17
E value
                   59
Match length
                   66
% identity
                   DNAJ PROTEIN HOMOLOG ANJ1 >gi_543510_pir JQ2142 chaperone
NCBI Description
                   ANJ1 protein - Atriplex nummularia
```

38459

LIB3094-064-Q1-K1-B10

Seq. No. Seq. ID

E value Match length



```
BLASTN
Method
                  g2463568
NCBI GI
                  57
BLAST score
                  1.0e-23
E value
                  110
Match length
                  93
% identity
                  Glycine max mRNA for squalene synthase, complete cds
NCBI Description
                  38460
Seq. No.
Seq. ID
                  LIB3094-064-Q1-K1-B8
Method
                  BLASTN
NCBI GI
                  g310575
BLAST score
                  32
                  8.0e-09
E value
Match length
                  60
% identity
                  88
                  Glycine max nodulin-26 mRNA, complete cds
NCBI Description
Seq. No.
                  38461
                  LIB3094-064-Q1-K1-D8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1666233
BLAST score
                  113
                   6.0e-57
E value
Match length
                  153
% identity
                   94
                  Pisum sativum actin (PEAc14) mRNA, complete cds
NCBI Description
                  >gi_1724142_gb_U81049_PSU81049 Pisum sativum actin (PEAc14)
                  mRNA, complete cds
                   38462
Seq. No.
Seq. ID
                  LIB3094-065-Q1-K1-C7
Method
                  BLASTX
                   g4454457
NCBI GI
                   299
BLAST score
                   3.0e-27
E value
                   77
Match length
                   74
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   38463
Seq. No.
Seq. ID
                   LIB3094-065-Q1-K1-F10
                  BLASTN
Method
                   g18764
NCBI GI
BLAST score
                   190
                   1.0e-103
E value
                   254
Match length
                   94
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-la
                   38464
Seq. No.
Seq. ID
                   LIB3094-066-Q1-K1-E7
                   BLASTX
Method
                   g4469020
NCBI GI
BLAST score
                   156
                   2.0e-10
```

% identity

NCBI Description



```
% identity
                  (AL035602) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                  38465
Seq. No.
Seq. ID
                  LIB3094-067-Q1-K1-B2
                  BLASTX
Method
NCBI GI
                  g3108209
                  527
BLAST score
                  7.0e-54
E value
Match length
                  123
                  80
% identity
                  (AF028809) eukaryotic cap-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                   38466
Seq. No.
Seq. ID
                  LIB3094-067-Q1-K1-E4
                  BLASTN
Method
                   g458339
NCBI GI
BLAST score
                   85
                   4.0e-40
E value
Match length
                   205
% identity
                   85
                  Vigna radiata clone pVR-ACO2
NCBI Description
                   1-aminocyclopropane-1-carboxylate oxidase homolog mRNA,
                  partial cds
                   38467
Seq. No.
                  LIB3094-068-Q1-K1-C1
Seq. ID
                  BLASTN
Method
                   g310575
NCBI GI
BLAST score
                   54
                   6.0e-22
E value
Match length
                   120
                   93
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
Seq. No.
                   38468
                   LIB3094-068-Q1-K1-F9
Seq. ID
                   BLASTN
Method
                   g19701
NCBI GI
                   75
BLAST score
                   3.0e-34
E value
Match length
                   155
                   87
% identity
                  N.plumbaginifolia mRNA NeIF-5A2 for initiation factor 5A(2)
NCBI Description
Seq. No.
                   38469
Seq. ID
                   LIB3094-069-Q1-K1-F7
Method
                   BLASTN
                   q170007
NCBI GI
BLAST score
                   41
                   1.0e-13
E value
                   132
Match length
```

5951

mRNA, complete cds

Soybean 18 kD late embryogenesis abundant (Lea) protein

Seq. No.

Seq. ID

Method

38475

BLASTX

LIB3094-072-Q1-K1-D9



```
38470
Seq. No.
                  LIB3094-069-Q1-K1-G12
Seq. ID
                  BLASTN
Method
                  g18644
NCBI GI
                  126
BLAST score
                  1.0e-64
E value
                  154
Match length
                  95
% identity
NCBI Description Soybean mRNA for HMG-1 like protein
Seq. No.
                  38471
                  LIB3094-071-Q1-K1-C3
Seq. ID
                  BLASTX
Method
                  g3915826
NCBI GI
                   268
BLAST score
E value
                   1.0e-23
                   99
Match length
                   53
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                   38472
Seq. ID
                   LIB3094-071-Q1-K1-D10
Method
                   BLASTX
                   g1658197
NCBI GI
                   172
BLAST score
                   2.0e-12
E value
                   100
Match length
                   37
% identity
                   (U74630) calreticulin [Ricinus communis] >gi_1763297
NCBI Description
                   (U74631) calreticulin [Ricinus communis]
                   38473
Seq. No.
Seq. ID
                   LIB3094-072-Q1-K1-C6
                   BLASTX
Method
NCBI GI
                   g1168196
BLAST score
                   220
                   5.0e-18
E value
                   80
Match length
                   62
% identity
                   14-3-3-LIKE PROTEIN >gi 555974 (U15036) 14-3-3-like protein
NCBI Description
                   [Pisum sativum]
Seq. No.
                   38474
                   LIB3094-072-Q1-K1-D10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2129583
BLAST score
                   245
                   3.0e-26
E value
                   122
Match length
                   55
% identity
                   ferritin - Arabidopsis thaliana >gi 1246401 emb CAA63932_
NCBI Description
                   (X94248) ferritin [Arabidopsis thaliana]
```

E value

Match length

1.0e-08



```
NCBI GI
                   g4558672
BLAST score
                  143
                  3.0e-09 ^
E value
                   66
Match length
% identity
                   42
NCBI Description
                   (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis
                  thaliana]
                  38476
Seq. No.
Seq. ID
                  LIB3094-072-Q1-K1-H1
                  BLASTN
Method
                  q310575
NCBI GI
BLAST score
                  75
                   4.0e-34
E value
Match length
                  243
                  83
% identity
                  Glycine max nodulin-26 mRNA, complete cds
NCBI Description
                  38477
Seq. No.
Seq. ID
                  LIB3094-072-Q1-K1-H5
Method
                  BLASTN
NCBI GI
                  g310575
BLAST score
                  245
                  1.0e-135
E value
                  398
Match length
                   93
% identity
                  Glycine max nodulin-26 mRNA, complete cds
NCBI Description
                  38478
Seq. No.
Seq. ID
                  LIB3094-073-Q1-K1-A8
                  BLASTX
Method
NCBI GI
                   g2982303
BLAST score
                   294
                   2.0e-26
E value
                  86
Match length
                   63
% identity
NCBI Description
                  (AF051236) hypothetical protein [Picea mariana]
Seq. No.
                   38479
                  LIB3094-073-Q1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4206209
BLAST score
                   161
                   2.0e-11
E value
                   77
Match length
                   45
% identity
NCBI Description
                   (AF071527) putative glucan synthase component [Arabidopsis
                  thaliana] >gi 4263042 gb AAD15311 (AC005142) putative
                   glucan synthase component [Arabidopsis thaliana]
                   38480
Seq. No.
Seq. ID
                  LIB3094-073-Q1-K1-C4
                   BLASTX
Method
NCBI GI
                   q1168189
BLAST score
                   139
```

BLAST score

Match length

E value

69

141

2.0e-30



```
% identity
                  14-3-3-LIKE PROTEIN A (VFA-1433A) >gi 1076542 pir S52899
NCBI Description
                  14-3-3 brain protein homolog - fava bean
                  >gi_695765_emb_CAA88415_ (Z48504) 14-3-3 brain protein
                  homolog [Vicia faba]
                  38481
Seq. No.
                  LIB3094-073-Q1-K1-D1
Seq. ID
                  BLASTX
Method
                  g548746
NCBI GI
BLAST score
                  268
                  1.0e-23
E value
                  82
Match length
                  67
% identity
                  50S RIBOSOMAL PROTEIN L12, CHLOROPLAST PRECURSOR (CL12)
NCBI Description
                  >gi_478604_pir__S21111 ribosomal protein L12 precursor,
                  chloroplast - wood tobacco >gi_248303_bbs_93167 (S93166)
                  ribosomal protein L12, CL12 [Nicotiana sylvestris=tobacco,
                  leaf, Peptide Chloroplast, 186 aa] [Nicotiana sylvestris]
                  38482
Seq. No.
Seq. ID
                  LIB3094-073-Q1-K1-F5
Method
                  BLASTX
                  g4454457
NCBI GI
                  206
BLAST score
                  2.0e-16
E value
                  75
Match length
                  57
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                  38483
Seq. No.
Seq. ID
                  LIB3094-073-Q1-K1-G11
                  BLASTN
Method
                  g1321821
NCBI GI
BLAST score
                  78
                  6.0e-36
E value
Match length
                  198
                  86
% identity
NCBI Description G.max mRNA for glycinamide ribonucleotide transformylase
                   38484
Seq. No.
Seq. ID
                  LIB3094-074-Q1-K1-A1
                  BLASTN
Method
NCBI GI
                  g3452086
BLAST score
                  51
                   9.0e-20
E value
                  67
Match length
                   96
% identity
NCBI Description Glycine max mRNA for 14-3-3 protein, partial
Seq. No.
                   38485
Seq. ID
                  LIB3094-074-Q1-K1-G12
                   BLASTN
Method
NCBI GI
                  q4193387
```



```
% identity
                  Hevea brasiliensis translationally controlled tumor protein
NCBI Description
                  (TCTP) mRNA, complete cds
Seq. No.
                  38486
Seq. ID
                  LIB3094-074-Q1-K1-G6
                  BLASTX
Method
NCBI GI
                  g542157
BLAST score
                  284
E value
                  7.0e-26
                  67
Match length
                  79
% identity
NCBI Description ribosomal 5S RNA-binding protein - Rice
                  38487
Seq. No.
                  LIB3094-075-Q1-K1-A10
Seq. ID
                  BLASTN
Method
                  g2920665
NCBI GI
BLAST score
                  194
                  1.0e-105
E value
Match length
                  245
% identity
                  96
                  Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                  (GSTa) mRNA, complete cds
Seq. No.
                  38488
Seq. ID
                  LIB3094-075-Q1-K1-A7
                  BLASTX
Method
NCBI GI
                  g1170891
BLAST score
                  140
E value
                  8.0e-09
Match length
                  60
% identity
                  53
                  MEMBRANE CHANNEL PROTEIN >gi 558058 (L36881) membrane
NCBI Description
                  channel protein [Medicago sativa]
Seq. No.
                  38489
Seq. ID
                  LIB3094-075-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  q4454457
BLAST score
                  144
E value
                  4.0e-09
Match length
                  69
% identity
                  41
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  38490
Seq. ID
                  LIB3094-077-Q1-K1-A10
                  BLASTX
Method
NCBI GI
                  q266945
BLAST score
                  283
E value
                  1.0e-25
```

Match length 77 75 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9 - garden pea

>gi 20727 emb CAA46273 (X65155) GA [Pisum sativum]



>gi\_1279645\_emb\_CAA65987\_ (X97322) ribosomal protein L9
[Pisum sativum]

Seq. No. 38491

Seq. ID LIB3094-077-Q1-K1-A11

Method BLASTX
NCBI GI g266945
BLAST score 183
E value 5.0e-14
Match length 81
% identity 54

% identity 54

NCBI Description 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)

>gi\_100065\_pir\_\_S19978 ribosomal protein L9 - garden pea

>gi\_20727\_emb\_CAA46273\_ (X65155) GA [Pisum sativum] >gi\_1279645\_emb\_CAA65987\_ (X97322) ribosomal protein L9

[Pisum sativum]

Seq. No. 38492

Seq. ID LIB3094-077-Q1-K1-B11

Method BLASTX
NCBI GI g266945
BLAST score 232
E value 1.0e-19
Match length 82
% identity 62

NCBI Description 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)

>gi 100065 pir S19978 ribosomal protein L9 - garden pea

>gi\_20727\_emb\_CAA46273\_ (X65155) GA [Pisum sativum]
>gi\_1279645\_emb\_CAA65987\_ (X97322) ribosomal protein L9
[Pisum sativum]

Seq. No. 38493

Seq. ID LIB3094-077-Q1-K1-B12

Method BLASTX
NCBI GI g266945
BLAST score 211
E value 4.0e-17
Match length 81
% identity 58

NCBI Description 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)

>gi\_100065\_pir\_\_S19978 ribosomal protein L9 - garden pea

Seq. No. 38494

Seq. ID LIB3094-077-Q1-K1-C9

Method BLASTX
NCBI GI g266945
BLAST score 189
E value 1.0e-16
Match length 81
% identity 62

NCBI Description 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)

>gi\_100065\_pir\_\_S19978 ribosomal protein L9 - garden pea
>gi\_20727\_emb\_CAA46273\_ (X65155) GA [Pisum sativum]
>gi\_1279645 emb\_CAA65987 (X97322) ribosomal protein L9

NCBI GI

E value

BLAST score

g135442

1.0e-19

233



## [Pisum sativum]

```
38495
Seq. No.
Seq. ID
                   LIB3094-078-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   g4115925
BLAST score
                   247
E value
                   3.0e-21
Match length
                   88
% identity
                   32
                   (AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
NCBI Description
                   >gi 4539439 emb CAB40027.1 (AL049523) RNA-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   38496
Seq. ID
                   LIB3094-078-Q1-K1-D9
Method
                   BLASTX
NCBI GI
                   q543868
BLAST score
                   140
E value
                   9.0e-09
Match length
                   63
% identity
                   43
NCBI Description
                   ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL
                   >gi_1076683_pir__B47493 H+-transporting ATP synthase (EC
                   3.6.1.34) epsilon chain - sweet potato
                   >gi_303625_dbj_BAA03527_ (D14700) F1-ATPase epsilon-subunit
                   [Ipomoea batatas]
Seq. No.
                   38497
Seq. ID
                   LIB3094-078-Q1-K1-G1
Method
                   BLASTN
NCBI GI
                   g2739043
BLAST score
                   55
E value
                   3.0e-22
Match length
                   159
% identity
                   Glycine max polyphosphoinositide binding protein Sshlp
NCBI Description
                   (SSH1) mRNA, complete cds
                   38498
Seq. No.
Seq. ID
                   LIB3094-079-Q1-K1-B4
Method
                   BLASTX
NCBI GI
                   g4490732
BLAST score
                   187
E value
                   3.0e-14
Match length
                   104
% identity
                   47
                   (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
NCBI Description
                   protein [Arabidopsis thaliana]
Seq. No.
                   38499
Seq. ID
                   LIB3094-079-Q1-K1-E8
Method
                   BLASTX
```



Match length 60 % identity % TUBULIN BETA-1 CHAIN >gi 71590 pir UBMUBM tubulin beta-1 NCBI Description chain - Arabidopsis thaliana >gi\_166922 (M20405) beta-1 tubulin [Arabidopsis thaliana] 38500 Seq. No. Seq. ID LIB3094-080-Q1-K1-C11 BLASTX Method g3695379 NCBI GI BLAST score 282 E value 4.0e-25 Match length 126 % identity 48 (AF096370) contains similarity to a C. elegans hypothetical NCBI Description protein F44G4.1 (GB:Z49910) and several yeast hypothetical proteins such as 35.1 KD protein in NAM8-GAR1 intergenic region (SP:P38805) [Arabidopsis thaliana] Seq. No. 38501 LIB3094-081-Q1-K1-A4 Seq. ID Method BLASTN NCBI GI g19394 BLAST score 46 8.0e-17 E value Match length 98 % identity 71 NCBI Description Tomato U3 small nuclear RNA gene 38502 Seq. No. LIB3094-081-Q1-K1-C12 Seq. ID Method BLASTX NCBI GI g464720 BLAST score 112 1.0e-08 E value Match length 61 62 % identity 40S RIBOSOMAL PROTEIN S28 >gi 409184 (L09755) ribosomal NCBI Description protein S28 [Arabidopsis thalīana] 38503 Seq. No. Seq. ID LIB3094-081-Q1-K1-D4 Method BLASTN g18764 NCBI GI BLAST score 128 8.0e-66 E value 231 Match length 89 % identity NCBI Description G.max tefS1 gene for elongation factor EF-1a 38504 Seq. No.

Seq. ID LIB3094-081-Q1-K1-F5

Method BLASTN q457569 NCBI GI BLAST score 208 E value 1.0e-113 Match length 284



```
% identity
NCBI Description Soybean mRNA for endo-xyloglucan transferase, partial cds
Seq. No.
                  38505
Seq. ID
                  LIB3094-082-Q1-K1-A3
                  BLASTN
Method
                  g2270989
NCBI GI
BLAST score
                  63
E value
                  5.0e-27
                  122
Match length
                  89
% identity
NCBI Description Glycine max dehydrin (GmPM12) mRNA, complete cds
                  38506
Seq. No.
Seq. ID
                  LIB3094-082-Q1-K1-B6
                  BLASTX
Method
NCBI GI
                  g4138583
BLAST score
                  225
                  1.0e-18
E value
Match length
                  83
% identity
                  61
                  (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
NCBI Description
                  38507
Seq. No.
Seq. ID
                  LIB3094-082-Q1-K1-B8
                  BLASTX
Method
NCBI GI
                  q4138583
                  185
BLAST score
                  2.0e-14
E value
                  55
Match length
                  73
% identity
NCBI Description
                  (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
                  38508
Seq. No.
Seq. ID
                  LIB3094-082-Q1-K1-D9
                  BLASTX
Method
NCBI GI
                  g1169384
BLAST score
                  151
                  2.0e-10
E value
                  50
Match length
                  64
% identity
                  DNAJ PROTEIN HOMOLOG ANJ1 >gi_543510_pir__JQ2142 chaperone
NCBI Description
                  ANJ1 protein - Atriplex nummularia
Seq. No.
                  38509
Seq. ID
                  LIB3094-084-Q1-K1-A7
                  BLASTN
Method
NCBI GI
                  q2920665
BLAST score
                  113
                  7.0e~57
E value
                  197
Match length
% identity
                  90
NCBI Description
                  Glycine max 2,4-D inducible glutathione S-transferase
```

Seq. No. 38510

Seq. ID LIB3094-085-Q1-K1-B5

(GSTa) mRNA, complete cds

BLAST score



```
BLASTX
  Method
                    g4454457
  NCBI GI
                    265
  BLAST score
                    1.0e-23
  E value
                    71

    Match length

                    73
  % identity
                    (AC006234) unknown protein [Arabidopsis thaliana]
  NCBI Description
                    38511
  Seq. No.
                    LIB3094-085-Q1-K1-C11
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q3986110
  BLAST score
                    177
                    2.0e-13
  E value
                     61
  Match length
                     62
  % identity
                    (AB012716) heat shock protein 70 cognate [Salix gilgiana]
  NCBI Description
                     38512
  Seq. No.
                    LIB3094-085-Q1-K1-F2
  Seq. ID
                    BLASTN
  Method
                    g1234899
  NCBI GI
  BLAST score
                     66
  E value
                     7.0e-29
                     175
  Match length
                     83
  % identity
  NCBI Description G.max mRNA for homeobox-leucine zipper protein
  Seq. No.
                     38513
                     LIB3094-085-Q1-K1-G7
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g1706329
  BLAST score
                     263
                     2.0e-23
  E value
  Match length
                     59
  % identity
                     80
                    PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC)
  NCBI Description
                     >gi 2146788 pir S65471 pyruvate decarboxylase (EC 4.1.1.1)
                     (clone PDC2) - Garden pea (fragment)
                     >gi 1177605 emb CAA91445 (Z66544) pyruvate decarboxylase
                     [Pisum sativum]
                     38514
  Seq. No.
                     LIB3094-085-Q1-K1-G8
  Seq. ID
                     BLASTN
  Method
                     g1177604
  NCBI GI
  BLAST score
                     122
                     5.0e-62
  E value
                     270
  Match length
  % identity
                     86
  NCBI Description P.sativum mRNA for pyruvate decarboxylase (PDC2)
                     38515
  Seq. No.
  Seq. ID
                     LIB3094-086-Q1-K1-F1
                     BLASTN
  Method
                     g18644
  NCBI GI
```

NCBI Description



```
4.0e-15
  E value
  Match length
                     51
                     96
  % identity
  NCBI Description Soybean mRNA for HMG-1 like protein
  Seq. No.
                     38516
  Seq. ID
                     LIB3094-087-Q1-K1-A12
Method
                     BLASTX
  NCBI GI
                     g4091806
  BLAST score
                     371
                     5.0e-36
  E value
                     77
  Match length
  % identity
                     83
                    (AF052585) CONSTANS-like protein 2 [Malus domestica]
  NCBI Description
                     38517
  Seq. No.
  Seq. ID
                     LIB3094-087-Q1-K1-A3
  Method
                     BLASTN
  NCBI GI
                     g218188
  BLAST score
                     55
                     4.0e-22
  E value
  Match length
                     123
  % identity
                     36
  NCBI Description Rice mRNA for poly-ubiquitin, partial sequence
                     38518
  Seq. No.
  Seq. ID
                     LIB3094-088-Q1-K1-B12
  Method
                     BLASTX
                     g2895904
  NCBI GI
  BLAST score
                     256
                     5.0e-22
  E value
                     120
  Match length
  % identity
                     44
                     (AF046916) glutamine synthetase type III [Ruminococcus
  NCBI Description
                     flavefaciens]
  Seq. No.
                     38519
  Seq. ID
                     LIB3094-088-Q1-K1-B4
  Method
                     BLASTX
                     g1710546
  NCBI GI
  BLAST score
                     181
                     1.0e-13
  E value
  Match length
                     64
                     59
  % identity
  NCBI Description 60S RIBOSOMAL PROTEIN L36 >gi 1276967 (U47095) putative
                     ribosomal protein [Daucus carota]
  Seq. No.
                     38520
  Seq. ID
                     LIB3094-088-Q1-K1-D10
  Method
                     BLASTX
  NCBI GI
                     g115206
  BLAST score
                     235
  E value
                     6.0e-20
  Match length
                     76
  % identity
                     61
```

C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF

SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE /



METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE /
FORMYLTETRAHYDROFOLATE SYNTHETASE >gi 88152\_pir A31903
C1-tetrahydrofolate synthase - human >gi 307178 (J04031)
MDMCSF (EC 1.5.1.5; EC 3.5.4.9; EC 6.3.4.3) [Homo sapiens]

38521 Seq. No. Seq. ID LIB3094-088-Q1-K1-F10 Method BLASTX NCBI GI g4185892 BLAST score 210 8.0e-17 E value 118 Match length 37 % identity (AL033125) 1-evidence=predicted by content; NCBI Description 1-method=genefinder;084; 1-evidence\_end; 2-evidence=predicted by match; 2-match accession=SWISS-PROT:P38205; 2-match description=HYPOTHETICAL 77.9 KD PROTEIN IN RRN10-MCM2 INTERGENIC 38522 Seq. No. Seq. ID LIB3094-088-Q1-K1-H5 Method BLASTX NCBI GI q543868 175 BLAST score 1.0e-12 E value

% identity 52
NCBI Description ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL

>gi\_1076683\_pir\_\_B47493 H+-transporting ATP synthase (EC

3.6.1.34) epsilon chain - sweet potato

>gi\_303625\_dbj\_BAA03527\_ (D14700) F1-ATPase epsilon-subunit

[Ipomoea batatas]

Seq. No. 38523

Match length

Seq. ID LIB3094-089-Q1-K1-C10

66

Method BLASTX
NCBI GI 9462141
BLAST score 154
E value 1.0e-10
Match length 74
% identity 50

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (GAPDH)

>gi\_1085816\_pir\_\_S38570 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Atriplex nummularia
>gi 409575 (U02886) glyceraldehyde-3-phosphate

dehydrogenase [Atriplex nummularia]
>gi 414607 emb CAA53269 (X75597)

glyceraldehyde-3-phosphate dehydrogenase [Atriplex

nummularia]

Seq. No. 38524

Seq. ID LIB3094-089-Q1-K1-D1

Method BLASTN
NCBI GI g2687439
BLAST score 57
E value 3.0e-23

Match length 84 % identity Peltoboykinia tellimoides large subunit 26S ribosomal RNA NCBI Description gene, partial sequence 38525 Seq. No. Seq. ID LIB3094-089-Q1-K1-D10 Method BLASTX NCBI GI g547683 BLAST score 198 E value 1.0e-15 Match length 51 73 % identity HEAT SHOCK COGNATE PROTEIN 80 >gi 170456 (M96549) heat NCBI Description shock cognate protein 80 [Solanum lycopersicum] >gi\_445601\_prf\_\_1909348A heat shock protein hsp80 [Lycopersicon esculentum] 38526 Seq. No. Seq. ID LIB3094-089-Q1-K1-D6 Method BLASTX NCBI GI q4454457 BLAST score 148 2.0e-09 E value 56 Match length 52 % identity (AC006234) unknown protein [Arabidopsis thaliana] NCBI Description 38527 Seq. No. Seq. ID LIB3094-089-Q1-K1-E10 Method BLASTN NCBI GI g2920665 BLAST score 102 2.0e-50 E value 246 Match length 85 % identity Glycine max 2,4-D inducible glutathione S-transferase NCBI Description (GSTa) mRNA, complete cds Seq. No. 38528 Seq. ID LIB3094-089-Q1-K1-E5 Method BLASTX NCBI GI q548746 BLAST score 214 E value 4.0e-17

Match length 83 % identity 60

NCBI Description 50S RIBOSOMAL PROTEIN L12, CHLOROPLAST PRECURSOR (CL12)

> >gi\_478604\_pir\_S21111 ribosomal protein L12 precursor, chloroplast - wood tobacco >gi 248303 bbs 93167 (S93166) ribosomal protein L12, CL12 [Nicotiana sylvestris=tobacco, leaf, Peptide Chloroplast, 186 aa] [Nicotiana sylvestris]

Seq. No. 38529

Seq. ID LIB3094-089-Q1-K1-F3

Method BLASTN NCBI GI g1680711

E value



```
BLAST score
                  6.0e-21
E value
                  211
Match length
                  84
% identity
                  Glycine max gamma glutamyl hydrolase mRNA, complete cds
NCBI Description
                  38530
Seq. No.
Seq. ID
                  LIB3094-089-Q1-K1-F9
                  BLASTN
Method
                  g2920665
NCBI GI
                  33
BLAST score
E value
                  3.0e-09
                  73
Match length
% identity
                  86
                  Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                  (GSTa) mRNA, complete cds
Seq. No.
                  38531
Seq. ID
                  LIB3094-089-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g4544419
BLAST score
                  222
E value
                  4.0e-18
Match length
                  95
% identity
                  52
                  (AC006955) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  38532
Seq. ID
                 LIB3094-089-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  g464444
BLAST score
                  254
E value
                  4.0e-22
                  79
Match length
                  66
% identity
                  PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                  COMPLEX 30 KD SUBUNIT) >gi 541889 pir S39900 proteasome -
                  Arabidopsis thaliana >gi 166830 (M98495) proteasome
                  [Arabidopsis thaliana]
Seq. No.
                  38533
Seq. ID
                  LIB3094-090-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  g541950
BLAST score
                  164
                  6.0e-12
E value
Match length
                  45
% identity
                  69
NCBI Description
                  SPCP1 protein - soybean >gi 310576 (L12257) nodulin-26
                  [Glycine max]
Seq. No.
                  38534
                  LIB3094-090-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464444
BLAST score
                  242
```

3.0e-21



Match length 64 % identity PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE NCBI Description COMPLEX 30 KD SUBUNIT) >gi\_541889\_pir\_\_S39900 proteasome -Arabidopsis thaliana  $>gi_1\overline{166830}$  ( $\overline{M98495}$ ) proteasome [Arabidopsis thaliana] Seq. No. 38535 Seq. ID LIB3094-091-Q1-K1-D7 BLASTN Method NCBI GI g1234899 75 BLAST score 3.0e - 34E value 195 Match length 85 % identity NCBI Description G.max mRNA for homeobox-leucine zipper protein 38536 Seq. No. LIB3094-091-Q1-K1-E1 Seq. ID BLASTN Method NCBI GI g2780193 BLAST score 54 1.0e-21 E value 70 Match length 94 % identity NCBI Description Lupinus albus mRNA for adenine nucleotide translocator 38537 Seq. No. LIB3094-091-Q1-K1-E6 Seq. ID BLASTX Method g4454457 NCBI GI BLAST score 221 4.0e-18 E value 76 Match length 59 % identity NCBI Description (AC006234) unknown protein [Arabidopsis thaliana] 38538 Seq. No. LIB3094-092-Q1-K1-E12 Seq. ID BLASTN Method g457569 NCBI GI BLAST score 42 3.0e-14 E value Match length 229 87 % identity NCBI Description Soybean mRNA for endo-xyloglucan transferase, partial cds Seq. No. 38539 Seq. ID LIB3094-093-Q1-K1-B12 BLASTN Method

NCBI GI g1234899 BLAST score 217 1.0e-119 E value 289 Match length 94 % identity

NCBI Description G.max mRNA for homeobox-leucine zipper protein



```
38540
Seq. No.
Seq. ID
                  LIB3094-093-Q1-K1-D12
                  BLASTX
Method
                  g3894158
NCBI GI
                  186
BLAST score
                  6.0e-14
E value
                  117
Match length
                  31
% identity
                   (AC005312) similar to phloem-specific lectin [Arabidopsis
NCBI Description
                  thaliana]
                  38541
Seq. No.
Seq. ID
                  LIB3094-094-Q1-K1-A12
Method
                  BLASTX
                  g547683
NCBI GI
                  145
BLAST score
                  3.0e-09
E value
                  51
Match length
                  61
% identity
                  HEAT SHOCK COGNATÉ PROTEIN 80 >gi 170456 (M96549) heat
NCBI Description
                  shock cognate protein 80 [Solanum lycopersicum]
                  >gi_445601_prf__1909348A heat shock protein hsp80
                   [Lycopersicon esculentum]
                  38542
Seq. No.
Seq. ID
                  LIB3094-094-Q1-K1-A4
                  BLASTX
Method
                  g2827637
NCBI GI
BLAST score
                  165
                  2.0e-11
E value
                  87
Match length
                   39
% identity
                  (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
                  38543
Seq. No.
                  LIB3094-094-Q1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                   45
                   2.0e-16
E value
Match length
                  149
% identity
                  83
NCBI Description
                  Cloning vector pSport1, complete cds
Seq. No.
                   38544
                  LIB3094-094-Q1-K1-E3
Seq. ID
Method
                   BLASTN
                   g1732555
NCBI GI
BLAST score
                   60
                   2.0e-25
E value
Match length
                   167
% identity
                   85
```

Glycine max desiccation protective protein LEA5 (Lea5) NCBI Description

mRNA, complete cds

Seq. No. 38545

Seq. ID LIB3094-095-Q1-K1-C7

Match length

% identity

241

82



```
BLASTX
Method
                  g120675
NCBI GI
                  178
BLAST score
                  3.0e-13
E value
                  58
Match length
                  57
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 66011 pir__DEIS3C glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                  >gi 21143 emb CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis
                  alba]
                  38546
Seq. No.
                  LIB3094-095-Q1-K1-D10
Seq. ID
Method
                  BLASTX
                  g549063
NCBI GI
BLAST score
                  333
                  4.0e-31
E value
Match length
                  126
                  56
% identity
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                  >gi 1072464 pir A38958 IgE-dependent histamine-releasing
                  factor homolog - rice >gi 303835 dbj BAA02151 (D12626)
                  21kd polypeptide [Oryza sativa]
                  38547
Seq. No.
Seq. ID
                  LIB3094-095-Q1-K1-D8
Method
                  BLASTX
                  g132944
NCBI GI
                  149
BLAST score
                  4.0e-10
E value
Match length
                  39
% identity
                  72
                  60S RIBOSOMAL PROTEIN L3 >gi 81658 pir JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >gi 806279
                  (M32655) ribosomal protein [Arabidopsis thaliana]
                  38548
Seq. No.
Seq. ID
                  LIB3094-095-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g4263707
BLAST score
                  233
                  9.0e-20
E value
Match length
                  91
% identity
                  (AC006223) putative 70kD heat shock protein [Arabidopsis
NCBI Description
                  thaliana]
                  38549
Seq. No.
                  LIB3094-095-Q1-K1-E6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2642237
BLAST score
                  66
                  1.0e-28
E value
```

5967

NCBI Description Glycine max endoplasmic reticulum HSC70-cognate binding

Seq. ID



protein precursor (BIP) mRNA, complete cds

```
38550
Seq. No.
Seq. ID
                  LIB3094-095-Q1-K1-F4
                  BLASTX
Method
                  g2894592
NCBI GI
                  157
BLAST score
                  1.0e-10
E value
                  69
Match length
                  46
% identity
                  (AL021889) predicted protein [Arabidopsis thaliana]
NCBI Description
                  38551
Seq. No.
                  LIB3094-096-Q1-K1-B9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g441457
                  198
BLAST score
                  1.0e-15
E value
                  70
Match length
                  61
% identity
                   (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
                  38552
Seq. No.
                  LIB3094-096-Q1-K1-E1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3860272
                   366
BLAST score
                   3.0e-35
E value
                   107
Match length
                   71
% identity
                   (AC005824) putative suppressor protein [Arabidopsis
NCBI Description
                   thaliana] >gi 4314399 gb AAD15609 (AC006232) putative skd1
                  protein [Arabidopsis thaliana]
Seq. No.
                   38553
                   LIB3094-097-Q1-K1-C6
Seq. ID
Method
                   BLASTX
                   q4455359
NCBI GI
                   150
BLAST score
E value
                   7.0e-10
                   89
Match length
                   35
% identity
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   38554
Seq. No.
Seq. ID
                   LIB3094-097-Q1-K1-C9
                   BLASTX
Method
NCBI GI
                   g2780194
BLAST score
                   164
                   1.0e-11
E value
Match length
                   81
% identity
                   (AJ003197) adenine nucleotide translocator [Lupinus albus]
NCBI Description
                   38555
Seq. No.
```

LIB3094-097-Q1-K1-D7



```
BLASTX
Method
NCBI GI
                  g2764941
                  155
BLAST score
                  2.0e-10
E value
Match length
                  75
                  39
% identity
                   (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
                  38556
Seq. No.
                  LIB3094-097-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                  q1706329
NCBI GI
BLAST score
                  138
                  7.0e-09
E value
                  53
Match length
                  58
% identity
                  PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC)
NCBI Description
                  >gi_2146788_pir__S65471 pyruvate decarboxylase (EC 4.1.1.1)
                   (clone PDC2) - Garden pea (fragment)
                   >gi_1177605_emb_CAA91445_ (Z66544) pyruvate decarboxylase
                   [Pisum sativum]
                   38557
Seq. No.
Seq. ID
                  LIB3094-098-Q1-K1-F4
                  BLASTX
Method
                  g3935170
NCBI GI
BLAST score
                   163
                   1.0e-11
E value
                   87
Match length
% identity
                   43
NCBI Description
                  (AC004557) F17L21.13 [Arabidopsis thaliana]
Seq. No.
                   38558
Seq. ID
                  LIB3094-099-Q1-K1-C5
                  BLASTN
Method
NCBI GI
                   g18658
BLAST score
                   48
                   2.0e-18
E value
                   107
Match length
                   87
% identity
NCBI Description
                  Soybean hsp22 mRNA
Seq. No.
                   38559
Seq. ID
                  LIB3094-099-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                   q4539350
BLAST score
                   259
                   1.0e-22
E value
                   60
Match length
                   75
% identity
NCBI Description
                  (AL035539) putative pectinesterase [Arabidopsis thaliana]
```

5969

38560

BLASTX

LIB3094-099-Q1-K1-F1

Seq. No. Seq. ID

Method



NCBI GI g548746 BLAST score 161 E value 4.0e-11 Match length 64 % identity 52

NCBI Description 50S RIBOSOMAL PROTEIN L12, CHLOROPLAST PRECURSOR (CL12)

>gi\_478604\_pir\_\_S21111 ribosomal protein L12 precursor,
chloroplast - wood tobacco >gi\_248303\_bbs\_93167 (S93166)
ribosomal protein L12, CL12 [Nicotiana sylvestris=tobacco,
leaf, Peptide Chloroplast, 186 aa] [Nicotiana sylvestris]

Seq. No. 38561

Seq. ID LIB3094-100-Q1-K1-B12

Method BLASTX
NCBI GI g124224
BLAST score 351
E value 3.0e-33
Match length 120
% identity 57

NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)

>gi\_100345 pir S21060 translation initiation factor eIF-5A

- common tobacco >gi\_19887\_emb\_CAA45105\_ (X63543)

eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No. 38562

Seq. ID LIB3094-100-Q1-K1-C12

Method BLASTX
NCBI GI g3024020
BLAST score 363
E value 1.0e-34
Match length 112
% identity 65

NCBI Description INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)

>gi\_2225881 dbj BAA20877 (AB004824) eukaryotic initiation

factor 5A3 [Solanum tuberosum]

Seq. No. 38563

Seq. ID LIB3094-100-Q1-K1-C3

Method BLASTN
NCBI GI g457569
BLAST score 43
E value 6.0e-15
Match length 79
% identity 89

NCBI Description Soybean mRNA for endo-xyloglucan transferase, partial cds

Seq. No.

38564

Seq. ID LIB3094-100-Q1-K1-D8

Method BLASTX
NCBI GI g541939
BLAST score 160
E value 6.0e-11
Match length 59
% identity 56

NCBI Description endoxyloglucan transferase - soybean

Seq. No. 38565



```
LIB3094-100-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2920666
BLAST score
                  154
E value
                  2.0e-10
Match length
                  80
% identity
                  (AF048978) 2,4-D inducible glutathione S-transferase
NCBI Description
                  [Glycine max]
Seq. No.
                  38566
Seq. ID
                  LIB3094-101-Q1-K1-A1
Method
                  BLASTN
                  q1675195
NCBI GI
BLAST score
                  109
E value
                  3.0e-54
Match length
                  233
% identity
                  87
                  Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
NCBI Description
                  complete cds
Seq. No.
                  38567
                  LIB3094-101-Q1-K1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4454457
                  98
BLAST score
E value
                  9.0e-09
                  72
Match length
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                  38568
Seq. No.
Seq. ID
                  LIB3094-101-Q1-K1-E4
Method
                  BLASTN
NCBI GI
                  g2606080
BLAST score
                  51
E value
                  8.0e-20
Match length
                  107
% identity
                  87
NCBI Description Glycine max sucrose synthase (SS) mRNA, complete cds
                  38569
Seq. No.
Seq. ID
                  LIB3094-101-Q1-K1-E5
Method
                  BLASTX
                  q120675
NCBI GI
BLAST score
                  177
                   5.0e-13
E value
Match length
                  79
                  56
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                  >gi 21143 emb CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis
                   alba]
```

5971

38570

LIB3094-101-Q1-K1-F1

Seq. No. Seq. ID



```
Method
                   BLASTN
NCBI GI
                  q1518539
BLAST score
                  155
E value
                  8.0e-82
Match length
                  275
% identity
                  89
NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds
Seq. No.
                  38571
Seq. ID
                  LIB3094-101-Q1-K1-G1
Method
                  BLASTN
NCBI GI
                  q1518539
BLAST score
                  147
                  5.0e-77
E value
Match length
                  311
                  87
% identity
NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds
                  38572
Seq. No.
Seq. ID
                  LIB3094-101-Q1-K1-G6
Method
                  BLASTN
NCBI GI
                  g1518539
BLAST score
                  81
E value
                  8.0e-38
Match length
                  173
                  87
% identity
NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds
Seq. No.
                  38573
Seq. ID
                  LIB3094-103-Q1-K1-C5
Method
                  BLASTN
NCBI GI
                  g1234899
BLAST score
                  215
E value
                  1.0e-117
Match length
                  227
                  99
% identity
NCBI Description G.max mRNA for homeobox-leucine zipper protein
Seq. No.
                  38574
Seq. ID
                  LIB3094-103-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g417494
BLAST score
                  162
E value
                  3.0e-11
Match length
                  84
% identity
                  46
NCBI Description
                  18 KD SEED MATURATION PROTEIN >gi 170008 (M80666)
                  maturation polypeptide [Glycine max]
                  >gi_444332_prf_1906381A 18kD late embryogenesis abundant
                  protein [Glycine max]
Seq. No.
                  38575
Seq. ID
                  LIB3094-103-Q1-K1-D1
```

Method BLASTX
NCBI GI g464444
BLAST score 119
E value 1.0e-12



```
Match length
                   47
% identity
NCBI Description PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
                   COMPLEX 30 KD SUBUNIT) >gi_541889_pir__S39900 proteasome -
                   Arabidopsis thaliana >gi_1\overline{6}6830 \ (\overline{M}984\overline{95}) proteasome
                   [Arabidopsis thaliana]
                   38576
Seq. No.
                   LIB3094-103-Q1-K1-F1
Seq. ID
                   BLASTN
Method
                   q2920665
NCBI GI
BLAST score
                   163
                   1.0e-86
E value
                   199
Match length
                   95
% identity
                   Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                   (GSTa) mRNA, complete cds
                   38577
Seq. No.
                   LIB3094-103-Q1-K1-F4
Seq. ID
                   BLASTX
Method
                   g4191782
NCBI GI
                   141
BLAST score
                   3.0e-09
E value
                   69
Match length
                    49
% identity
                   (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
NCBI Description
                    38578
Seq. No.
Seq. ID
                    LIB3094-104-Q1-K1-G8
                    BLASTN
Method
                    g169980
NCBI GI
BLAST score
                    177
                    6.0e-95
E value
                    277
Match length
                    91
 % identity
                   Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
NCBI Description
                    38579
 Seq. No.
                    LIB3106-003-Q1-K1-A9
 Seq. ID
                    BLASTN
 Method
 NCBI GI
                    g18775
 BLAST score
                    106
 E value
                    1.0e-52
                    249
 Match length
 % identity
                    91
                    G.max tufA gene for chloroplast translation elongation
 NCBI Description
                    factor EF-Tu
                    38580
 Seq. No.
                    LIB3106-003-Q1-K1-B3
 Seq. ID
                    BLASTX
```

Method BLASTX
NCBI GI g3482917
BLAST score 163
E value 8.0e-12
Match length 70
% identity 54

NCBI Description

38586

Seq. No.



```
(AC003970) Similar to Glucose-6-phosphate dehydrogenases,
NCBI Description
                   gi 2276344, gi 2829880, gi 2352919 and others. [Arabidopsis
                   thaliana]
Seq. No.
                   38581
Seq. ID
                   LIB3106-003-Q1-K1-C2
Method
                   BLASTX
NCBI GI
                   g3367,582
BLAST score
                   235
                   1.0e-19
E value
Match length
                   68
                   71
% identity
                   (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Seq. ID
                   LIB3106-003-Q1-K1-D3
                   BLASTX
Method
NCBI GI
                   q541943
BLAST score
                   188
                   2.0e-14
E value
                   56
Match length
% identity
                  metallothionein - soybean >gi 228682 prf 1808316A
NCBI Description
                   metallothionein-like protein [Glycine max]
Seq. No.
Seq. ID
                   LIB3106-004-Q1-K1-A9
                   BLASTN
Method
                   g170089
NCBI GI
BLAST score
                   67
                   2.0e-29
E value
                   303
Match length
% identity
                   G.max vegetative storage protien mRNA (VSP27), complete cds
NCBI Description
Seq. No.
                   38584
Seq. ID
                   LIB3106-004-Q1-K1-B10
Method
                   BLASTX
                   g541943
NCBI GI
BLAST score
                   202
E value
                   9.0e-16
Match length
                   53
% identity
                   68
                   metallothionein - soybean >gi_228682_prf 1808316A
NCBI Description
                   metallothionein-like protein [Glycine max]
                   38585
Seq. No.
                   LIB3106-004-Q1-K1-B4
Seq. ID
Method
                   BLASTX
                   g1495366
NCBI GI
BLAST score
                   180
E value
                   2.0e-13
Match length
                   83
% identity
                   46
                   (Z69370) nitrite transporter [Cucumis sativus]
```



```
LIB3106-004-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   g1848214
NCBI GI
BLAST score
                   346
                   2.0e-39
E value .
                   135
Match length
% identity
                   (Y11210) uracil phosphoribosyltransferase [Nicotiana
NCBI Description
                   tabacum]
                   38587
Seq. No.
                   LIB3106-004-Q1-K1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3122572
BLAST score
                   222
E value
                   2.0e-18
Match length
                   92
                   53
% identity
                   NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I
                   SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato
                   >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial
                   complex I subunit [Solanum tuberosum]
Seq. No.
                   38588
                   LIB3106-004-Q1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2911071
BLAST score
                   193
                   7.0e-15
E value
Match length
                   84
                   49
% identity
                   (AL021960) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   38589
Seq. No.
                   LIB3106-004-Q1-K1-E5
Seq. ID
Method
                   BLASTN
                   g22219
NCBI GI
                   63
BLAST score
                   5.0e-27
E value
                   179
Match length
                   84
% identity
                   Z.mays ZSF4C2 gene for 22 kD zein
NCBI Description
                   38590
Seq. No.
                   LIB3106-005-Q1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4115925
BLAST score
                   168
E value
                   1.0e-19
Match length
                   93
% identity
                   56
                   (AF118222) contains similarity to RNA recognition motifs
NCBI Description
                   (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
```

[Arabidopsis thaliana]

>gi 4539439\_emb\_CAB40027.1\_ (AL049523) RNA-binding protein



52

58

Match length

NCBI Description

% identity

```
38591
Seq. No.
                  LIB3106-006-Q1-K1-A6
Seq. ID
Method
                  BLASTN
                  g1055367
NCBI GI
                  364
BLAST score
                  0.0e+00
E value
Match length
                  4.3.2
                  96
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
                  38592
Seq. No.
                  LIB3106-006-Q1-K1-B8
Seq. ID
                  BLASTN
Method
                  g1055367
NCBI GI
                   375
BLAST score
                  0.0e+00
E value
                   387
Match length
                   99
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   38593
Seq. No.
                   LIB3106-006-Q1-K1-E11
Seq. ID
Method
                  BLASTN
                   g1055367
NCBI GI
                   326
BLAST score
                   0.0e + 00
E value
Match length
                   425
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   38594
Seq. No.
                   LIB3106-006-Q1-K1-E12
Seq. ID
Method
                   BLASTN
                   q297877
NCBI GI
                   60
BLAST score
E value
                   4.0e-25
                   152
Match length
% identity
                   A.thaliana UBC10 mRNA for ubiquitin conjugating enzyme
NCBI Description
                   homolog >gi_349212_gb_L00640_ATHUBCC Arabidopsis thaliana
                   ubiquitin conjugating enzyme mRNA, complete cds
                   38595
Seq. No.
                   LIB3106-006-Q1-K1-E3
Seq. ID
Method
                   BLASTX
                   q1480078
NCBI GI
BLAST score
                   145
                   2.0e-09
E value
```

5976

kinase [Arabidopsis thaliana]

(X99696) shaggy-like protein kinase iota [Arabidopsis

thaliana] >gi 2444277 (AF019927) GSK3/shaggy-like protein



```
- 5
                  38596
Seq. No.
                  LIB3106-006-Q1-K1-F4
Seq. ID
                  BLASTN
Method
                  g18761
NCBI GI
                  275
BLAST score
                  1.0e-153
E value
                  353
Match length
                  96
% identity
NCBI Description Soybean stem mRNA for 31 kD glycoprotein
                  38597
Seq. No.
                  LIB3106-006-Q1-K1-H3
Seq. ID
Method
                  BLASTN
                  g343344
NCBI GI
                  113
BLAST score
                  6.0e-57
E value
                  197
Match length
                  89
% identity
                  Soybean chloroplast 16S rRNA (3' end), 18S rRNA (5' end),
NCBI Description
                  Ile-tRNA, and Ala-tRNA genes
                  38598
Seq. No.
                  LIB3106-006-Q1-K2-A11
Seq. ID
                  BLASTN
Method
                   q1055367
NCBI GI
                   325
BLAST score
                   0.0e+00
E value
                   405
Match length
                   95
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   38599
Seq. No.
                   LIB3106-006-Q1-K2-E6
Seq. ID
                   BLASTN
Method
                   g18729
NCBI GI
                   56
BLAST score
                   7.0e-23
E value
                   84
Match length
                   93
% identity
NCBI Description Soybean (Glycine max) 18S ribosomal RNA
                   38600
Seq. No.
                   LIB3106-006-Q1-K2-F6
Seq. ID
                   BLASTN
Method
                   g170087
NCBI GI
                   74
BLAST score
                   1.0e-33
E value
Match length
                   202
% identity
                   85
                  G.max vegetative storage protein mRNA (VSP25 gene)
NCBI Description
```

Seq. ID LIB3106-006-Q1-K2-G6

Method BLASTX NCBI GI g2392021

5977



```
BLAST score
                  4.0e-14
E value
                  110
Match length
                  42
% identity
                  (D63425) phopholipid hydroperoxide glutathione
NCBI Description
                  peroxidase-like protein [Spinacia oleracea]
                  38602
Seq. No.
                  LIB3106-007-Q1-K1-A2
Seq. ID
Method
                  BLASTX
                  ğ1705678
NCBI GI
BLAST score
                  303
                   6.0e-28
E value
                  74
Match length
                   80
% identity
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                   PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
                   valosin-containing protein [Glycine max]
                   38603
Seq. No.
                   LIB3106-007-Q1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1705678
                   258
BLAST score
                   1.0e-22
E value
                   80
Match length
% identity
                   65
                   CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                   PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
                   valosin-containing protein [Glycine max]
Seq. No.
                   38604
                   LIB3106-007-Q1-K1-B12
Seq. ID
                   BLASTN
Method
                   g3021374
NCBI GI
                   306
BLAST score
                   1.0e-172
E value
                   310
Match length
                   100
% identity
NCBI Description Glycine max mRNA for profilin, PRO1
                   38605
Seq. No.
                   LIB3106-007-Q1-K1-C3
Seq. ID
                   BLASTX
Method
                   q3335375
NCBI GI
                   160
BLAST score
                   5.0e-16
E value
Match length
                   61
                   75
 % identity
                   (AC003028) putative amidase [Arabidopsis thaliana]
 NCBI Description
                   38606
```

LIB3106-007-Q1-K1-C6 Seq. ID

BLASTX Method g130271 NCBI GI 147 BLAST score 2.0e-09 E value



```
Match length
                  40
% identity
                  PLASTOCYANIN PRECURSOR >gi 100238 pir_S05303 plastocyanin
NCBI Description
                  precursor - tomato >gi_19300_emb_CAA32121_ (X13934)
                  pre-plastocyanin (AA -64 to 106) [Lycopersicon esculentum]
                  38607
Seq. No.
                  LIB3106-007-Q1-K1-C9
Seq. ID
                  BLASTX
Method
                  g3935169
NCBI GI
BLAST score
                  299
                  4.0e-27
E value
                  68
Match length
% identity
NCBI Description (AC004557) F17L21.12 [Arabidopsis thaliana]
Seq. No.
                  38608
                  LIB3106-007-Q1-K1-E8
Seq. ID
                  BLASTN
Method
                  q439856
NCBI GI
                   60
BLAST score
                   4.0e-25
E value
                   259
Match length
% identity
NCBI Description Glycine max Williams 82 lipoxygenase mRNA, complete cds
                   38609
Seq. No.
                   LIB3106-007-Q1-K1-F3
Seq. ID
                   BLASTN
Method
NCBI GI
                   q170091
BLAST score
                   306
                   1.0e-172
E value
Match length
                   406
% identity
                   94
                   Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
                   38610
 Seq. No.
                   LIB3106-007-Q1-K1-H10
 Seq. ID
                   BLASTN
 Method
                   g169056
 NCBI GI
 BLAST score
                   75
                   5.0e - 34
 E value
                   233
 Match length
                   84
 % identity
 NCBI Description P.sativum carbonic anhydrase mRNA, complete cds
                   38611
 Seq. No.
                   LIB3106-008-Q1-K1-A1
 Seq. ID
                   BLASTN
 Method
                   g438216
 NCBI GI
                   108
 BLAST score
                   9.0e-54
 E value
```

251 Match length 86 % identity

P.sativum mRNA for T subunit of glycine decarboxylase NCBI Description

multi-enzyme complex



```
38612
Seq. No.
                  LIB3106-008-Q1-K1-D4
Seq. ID
Method
                  BLASTX
                  g2497906
NCBI GI
                   170
BLAST score
                   1.0e-12
E value
Match length
                   61
                   54
% identity
                  METALLOTHIONEIN-LIKE PROTEIN TYPE 3
NCBI Description
                   >gi_1566700_emb_CAA69624_ (Y08322) metallothionein-like
                   protein [Carica papaya]
                   38613
Seq. No.
                   LIB3106-008-Q1-K1-D5
Seq. ID
Method
                   BLASTX
                   g3355465
NCBI GI
BLAST score
                   340 .
                   2.0e-32
E value
                   77
Match length
% identity
                   (AC004218) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   38614
Seq. No.
                   LIB3106-008-Q1-K1-E6
Seq. ID
                   BLASTN
Method
NCBI GI
                   g531832
BLAST score
                   33
                   3.0e-09
E value
                   73
Match length
                   86
% identity
NCBI Description Cloning vector pSport2, complete sequence
                   38615
Seq. No.
                   LIB3106-008-Q1-K1-H5
Seq. ID
                   BLASTX
Method
                   g3914435
NCBI GI
                   138
BLAST score
                    7.0e-09
 E value
                    59
Match length
                    51
 % identity
                   PROFILIN 1 >gi_3021375_emb_CAA11756_ (AJ223982) profilin
 NCBI Description
                    [Glycine max]
                    38616
 Seq. No.
                    LIB3106-009-Q1-K1-A11
 Seq. ID
                    BLASTX
 Method
                    g2842478
 NCBI GI
                    158
 BLAST score
                    1.0e-10
 E value
 Match length
                    97
                    38
 % identity
                    (AL021749) receptor protein kinase like protein
 NCBI Description
                    [Arabidopsis thaliana]
```

BLAST score

E value

339 6.0e-32



```
LIB3106-009-Q1-K1-B11
Seq. ID
                  BLASTN
Method
                  g169897
NCBI GI
                  175
BLAST score
                  1.0e-93
E value
                  351
Match length
                  87
% identity
NCBI Description G.max 28 kDa protein, complete cds
                  38618
Seq. No.
                  LIB3106-009-Q1-K1-C11
Seq. ID
                  BLASTX
Method
                  g3618320
NCBI GI
                  239
BLAST score
                   3.0e-20
E value
                  74
Match length
                   54
% identity
                  (AB001888) zinc finger protein [Oryza sativa]
NCBI Description
                   38619
Seq. No.
                   LIB3106-009-Q1-K1-C6
Seq. ID
                   BLASTX
Method
                   g1922964
NCBI GI
                   153
BLAST score
                   4.0e-10
E value
Match length
                   38
                   79
% identity
                   (AC000106) Similar to Schizosaccharomyces CCAAT-binding
NCBI Description
                   factor (gb_U88525). EST gb_T04310 comes from this gene.
                   [Arabidops\overline{i}s thaliana]
                   38620
Seq. No.
                   LIB3106-009-Q1-K1-D8
Seq. ID
                   BLASTX
Method
                   g4406384
NCBI GI
                   355
BLAST score
                   1.0e-33
E value
                   115
Match length
                   59
% identity
                   (AF112303) serine acetyltransferase [Arabidopsis thaliana]
NCBI Description
                   38621
Seq. No.
                   LIB3106-009-Q1-K1-F3
Seq. ID
                   BLASTN
Method
                   q531832
NCBI GI
                   38
BLAST score
                   4.0e-12
E value
                   142
Match length
 % identity
NCBI Description Cloning vector pSport2, complete sequence
                   38622
 Seq. No.
                   LIB3106-009-Q1-K1-H5
 Seq. ID
                   BLASTX
 Method
                   g4185511
 NCBI GI
```

5981



```
Match length
% identity
NCBI Description
                   (AF102822) actin depolymerizing factor 4 [Arabidopsis
                  thaliana]
Seq. No.
                  38623
                  LIB3106-010-Q1-K1-C4
Seq. ID
Method
                  BLASTX
                  q4432836
NCBI GI
BLAST score
                  170
                   4.0e-12
E value
Match length
                  53
% identity
                  58
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  38624
                  LIB3106-010-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g531829
BLAST score
                  155
                  2.0e-10
E value
Match length
                  55
                   64
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
Seq. No.
                   38625
                  LIB3106-010-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3176874
BLAST score
                  153
E value
                   6.0e-10
Match length
                   43
% identity
                   60
                   (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                   thaliana]
                   38626
Seq. No.
                   LIB3106-010-Q1-K1-F11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2130559
BLAST score
                   80
E value
                   4.0e-37
Match length
                   254
% identity
                   88
NCBI Description
                  Glycine max elongation factor-1 alpha (TefS1) gene, partial
                   cds
                   38627
Seq. No.
                  LIB3106-010-Q1-K1-F8
Seq. ID
```

Method BLASTX NCBI GI g114975 BLAST score 156 E value 1.0e-10 Match length 85 45 % identity

NCBI Description CYANOGENIC BETA-GLUCOSIDASE PRECURSOR (LINAMARASE)



>gi 67490 pir GLJY14 beta-glucosidase (EC 3.2.1.21) precursor (clone TRE104) - white clover (fragment) >gi\_21953\_emb\_CAA40057.1\_ (X56733) beta-glucosidase [Trifolium repens]

Seq. No. 38628 Seq. ID LIB3106-010-Q1-K1-G5 Method BLASTX q4455365 NCBI GI BLAST score 190 E value 8.0e-15 Match length 69 % identity 59 NCBI Description

(AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 38629 Seq. ID LIB3106-011-Q1-K1-A1

Method BLASTN NCBI GI g1055367 BLAST score 121 2.0e-61 E value 294 Match length % identity 92

Glycine max ribulose-1,5-bisphosphate carboxylase small NCBI Description

subunit mRNA, complete cds

Seq. No. 38630

LIB3106-011-Q1-K1-C5 Seq. ID

Method BLASTX NCBI GI q541943 BLAST score 248 E value 4.0e-21 Match length 62 73 % identity

NCBI Description metallothionein - soybean >gi 228682 prf 1808316A

metallothionein-like protein [Glycine max]

38631 Seq. No.

Seq. ID LIB3106-011-Q1-K1-C7

Method BLASTX NCBI GI g2833383 BLAST score 413 E value 4.0e-55 Match length 145 % identity 68

NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR (GBSSI)

>gi 2129897 pir S61504 UDPglucose--starch

glucosyltransferase (EC 2.4.1.11) isoform I precursor garden pea >gi 385411 bbs 131618 granule-bound starch synthase isoform I, GBSSI [Pisum sativum=peas, BC1/9RR, Peptide, 603 aa] >gi\_887571 emb CAA61268 (X88789) glycogen

(starch) synthase [Pisum sativum]

38632 Seq. No.

Seq. ID LIB3106-011-Q1-K1-D7

Method BLASTX NCBI GI g3402705

```
BLAST score
E value
                   7.0e-13
Match length
                   41
                   80
% identity
NCBI Description
                   (AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   38633
Seq. ID
                   LIB3106-011-Q1-K1-G3
Method
                   BLASTN
NCBI GI
                   q169980
BLAST score
                   275
E value
                   1.0e-153
Match length
                   363
                   94
% identity
NCBI Description
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.
                   38634
                   LIB3106-011-Q1-K1-H12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1079735
BLAST score
                   113
                   5.0e-57
E value
Match length
                   201
                   89
% identity
                  Glycine soja ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit precursor (rbcS) gene, nuclear gene encoding
                   chloroplast protein, complete cds
Seq. No.
                   38635
                   LIB3106-011-Q1-K1-H7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g169974
BLAST score
                   55
                   2.0e-22
E value
Match length
                   123
                   86
% identity
                  Glycine max vspA gene, complete cds
NCBI Description
                   38636
Seq. No.
Seq. ID
                   LIB3106-013-Q1-K1-A5
Method
                   BLASTX
NCBI GI
                   g3786009
BLAST score
                   185
E value
                   8.0e-14
                   37
Match length
                   92
% identity
NCBI Description
                   (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.
                   38637
Seq. ID
                   LIB3106-013-Q1-K1-E1
Method
                   BLASTX
NCBI GI
                   g2511576
```

Method BLASTX
NCBI GI g2511576
BLAST score 375
E value 4.0e-36
Match length 132
% identity 63

NCBI Description (Y13177) multicatalytic endopeptidase [Arabidopsis



## thaliana]

```
38638
Seq. No.
                  LIB3106-013-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  q3421104
NCBI GI
                  164
BLAST score
                  1.0e-11
E value
                  80
Match length
                  46
% identity
                  (AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis
NCBI Description
                  thaliana]
                  38639
Seq. No.
                  LIB3106-013-Q1-K1-F2
Seq. ID
Method
                  BLASTN
                  q1055367
NCBI GI
                  104
BLAST score
                   2.0e-51
E value
                   248
Match length
                   86
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   38640
Seq. No.
                   LIB3106-013-Q1-K1-F8
Seq. ID
                   BLASTN
Method
                   g20015
NCBI GI
BLAST score
                   53
                   7.0e-21
E value
                   125
Match length
                   86
% identity
NCBI Description N.tabacum mRNA for chloroplast ribosomal protein CL28
                   38641
Seq. No.
                   LIB3106-013-Q1-K1-F9
Seq. ID
                   BLASTX
Method
                   g2677830
NCBI GI
                   252
BLAST score
                   1.0e-21
E value
                   98
Match length
                   56
 % identity
                   (U93168) ribosomal protein L12 [Prunus armeniaca]
NCBI Description
                   38642
 Seq. No.
                   LIB3106-013-Q1-K1-H10
 Seq. ID
                   BLASTX
 Method
                   g3063445
 NCBI GI
                   201
 BLAST score
                   8.0e-16
 E value
 Match length
                   88
 % identity
                   (AC003981) F22013.7 [Arabidopsis thaliana]
 NCBI Description
                   38643
 Seq. No.
                   LIB3106-014-Q1-K1-A4
 Seq. ID
```

BLASTN

Method



```
g170089
NCBI GI
                  227
BLAST score
                  1.0e-125
E value
Match length
                  291
% identity
                  95
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
                  38644
Seq. No.
                  LIB3106-014-Q1-K1-C11
Seq. ID
                  BLASTX
Method
                   g2347088
NCBI GI
                   257
BLAST score
                   2.0e-22
E value
                   80
Match length
% identity
                  (U72765) non-specific lipid transfer protein PvLTP-24
NCBI Description
                   [Phaseolus vulgaris]
                   38645
Seq. No.
                   LIB3106-014-Q1-K1-C7
Seq. ID
Method
                   BLASTX
                   g4415912
NCBI GI
                   297
BLAST score
                   5.0e-30
E value
                   113
Match length
                   60
% identity
                   (AC006282) putative protease [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   38646
                   LIB3106-014-Q1-K1-D12
Seq. ID
                   BLASTX
Method
                   g267079
NCBI GI
                   190
BLAST score
                   1.0e-14
E value
                   72
Match length
                   60
 % identity
                   TUBULIN BETA-6 CHAIN >gi_320187_pir__JQ1590 tubulin beta-6
 NCBI Description
                   chain - Arabidopsis thaliana >gi 166904 (M84703) beta-6
                   tubulin [Arabidopsis thaliana]
                   38647
 Seq. No.
                   LIB3106-014-Q1-K1-G6
 Seq. ID
                   BLASTX
 Method
                   g4432839
 NCBI GI
                    158
 BLAST score
                    1.0e-10
 E value
                    90
 Match length
                    52
 % identity
                   (AC006283) unknown protein [Arabidopsis thaliana]
 NCBI Description
                    38648
 Seq. No.
                    LIB3106-015-Q1-K1-B6
 Seq. ID
                    BLASTX
 Method
                    q2245140
 NCBI GI
                    221
 BLAST score
                    5.0e-18
 E value
```

59

Match length

NCBI Description



```
% identity
NCBI Description
                  (Z97344) In finger protein homolog [Arabidopsis thaliana]
                  38649
Seq. No.
Seq. ID
                  LIB3106-015-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  q4263712
BLAST score
                  283
E value
                  2.0e-25
Match length
                  108
% identity
                  58
                  (ACO06223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  38650
Seq. ID
                  LIB3106-015-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  g595768
BLAST score
                  137
                  1.0e-08
E value
Match length
                  45
                  62
% identity
NCBI Description
                  (U13866) non-functional lacZ alpha peptide [Cloning vector]
Seq. No.
                  38651
                  LIB3106-015-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2149640
BLAST score
                  397
E value
                  1.0e-38
Match length
                  113
                  72
% identity
NCBI Description
                  (U91995) Argonaute protein [Arabidopsis thaliana]
                  38652
Seq. No.
Seq. ID
                  LIB3106-015-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g548852
BLAST score
                  318
E value
                  2.0e-29
Match length
                  81
% identity
                  69
                  40S RIBOSOMAL PROTEIN S21 >qi 481227 pir S38357 ribosomal
NCBI Description
                  protein S21 - rice >gi 303839 dbj BAA02158 (D12633) 40S
                  subunit ribosomal protein [Oryza sativa]
                  38653
Seq. No.
                  LIB3106-015-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g541943
BLAST score
                  257
                  4.0e-22
E value
Match length
                  71
% identity
                  70
```

metallothionein-like protein [Glycine max]

metallothionein - soybean >qi 228682 prf 1808316A



```
Seq. ID
                  LIB3106-015-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  q1854386
BLAST score
                   169
E value
                   5.0e-12
Match length
                  52
% identity
                   60
                   (AB001375) similar to soluble NSF attachment protein [Vitis
NCBI Description
                  vinifera]
Seq. No.
                   38655
                  LIB3106-015-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1353352
BLAST score
                  211
                   6.0e-17
E value
Match length
                   105
                   39
% identity
                   (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
Seq. No.
                   38656
Seq. ID
                  LIB3106-015-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                   g2369714
BLAST score
                   312
E value
                   4.0e-29
Match length
                   82
                   73
% identity
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
Seq. No.
                   38657
Seq. ID
                  LIB3106-016-Q1-K1-A1
                  BLASTN
Method
NCBI GI
                   g3176073
BLAST score
                   32
                   1.0e-08
E value
Match length
                   81
                   87
% identity
NCBI Description
                  Medicago sativa mRNA for protein phosphatase 1, gamma
                   subunit
                   38658
Seq. No.
                  LIB3106-016-Q1-K1-A2
Seq. ID
Method
                  BLASTN
NCBI GI
                   g516853
BLAST score
                   76
E value
                   1.0e-34
Match length
                   259
% identity
                   43
NCBI Description
                  Soybean SUBI-2 gene for ubiquitin, complete cds
Seq. No.
                   38659
Seq. ID
                  LIB3106-018-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                   g4098517
```



```
BLAST score
                  315
E value
                  5.0e-29
                  108
Match length
                  56
% identity
NCBI Description (U79114) auxin-binding protein ABP19 [Prunus persica]
Seq. No.
                  38660
Seq. ID
                  LIB3106-018-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  q4325342
BLAST score
                  279
                  4.0e-25
E value
                  78
Match length
                  67
% identity
NCBI Description (AF128393) No definition line found [Arabidopsis thaliana]
Seq. No.
                  38661
Seq. ID
                  LIB3106-018-Q1-K1-D7
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
                  6.0e-11
E value
Match length
                  38
% identity
                  61
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  38662
Seq. No.
                  LIB3106-018-Q1-K1-E1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q836895
BLAST score
                  32
                  1.0e-08
E value
Match length
                  68
% identity
                  87
NCBI Description Saccharomyces cerevisiae CSP2 gene, complete cds
                  38663
Seq. No.
Seq. ID
                  LIB3106-019-Q1-K1-A1
                  BLASTX
Method
NCBI GI
                  g595768
BLAST score
                  156
                  2.0e-10
E value
Match length
                  47
% identity
                  62
NCBI Description (U13866) non-functional lacZ alpha peptide [Cloning vector]
Seq. No.
                  38664
                  LIB3106-019-Q1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170089
BLAST score
                  390
E value
                  0.0e+00
```

Match length 424 % identity 98

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds



```
LIB3106-019-Q1-K1-B7
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2580440
                   299
BLAST score
                   3.0e-27
E value
                   61
Match length
% identity
                  (D87261) PCF2 [Oryza sativa]
NCBI Description
                   38666
Seq. No.
                   LIB3106-019-Q1-K1-D12
Seq. ID
                   BLASTN
Method
                   g1658196
NCBI GI
                   157
BLAST score
                   6.0e-83
E value
                   302
Match length
                   79
% identity
NCBI Description Ricinus communis calreticulin mRNA, complete cds
                   38667
Seq. No.
                   LIB3106-019-Q1-K1-D7
Seq. ID
                   BLASTN
Method
                   g1055367
NCBI GI
                   63
BLAST score
                                                                           37.1
                   6.0e-27
E value
                   145
Match length
                   92
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   38668
Seq. No.
                   LIB3106-019-Q1-K1-D8
Seq. ID
                   BLASTN
Method
                   g18775
NCBI GI
                   75
BLAST score
                   5.0e-34
E value
                   332
Match length
% identity
                   G.max tufA gene for chloroplast translation elongation
NCBI Description
                   factor EF-Tu
                   38669
Seq. No.
Seq. ID
                   LIB3106-019-Q1-K1-F4
                   BLASTN
Method
                   q170089
NCBI GI
BLAST score
                   91
                   1.0e-43
E value
                   284
Match length
                   86
 % identity
                   G.max vegetative storage protien mRNA (VSP27), complete cds
NCBI Description
                    38670
 Seq. No.
                   LIB3106-019-Q1-K1-G1
Seq. ID
                    BLASTN
Method
 NCBI GI
                    g169899
 BLAST score
                    173
                    2.0e-92
 E value
```



```
Match length 321
% identity 88
NCBI Description G.max 31 kDa protein mRNA, 3' end
Seq. No. 38671
Seq. ID LIB3106-019-Q1-K1-G4
```

Method BLASTX
NCBI GI 9452593
BLAST score 137
E value 1.0e-08
Match length 53
% identity 53

NCBI Description (D21814) ORF [Lilium longiflorum]

38672

Seq. ID LIB3106-019-Q1-K1-H8 Method BLASTN NCBI GI g533691 BLAST score 107 E value 4.0e-53

Match length 292 % identity 89

Seq. No.

NCBI Description Glycine max Essex protease inhibitor mRNA, complete cds

Seq. No. 38673

Seq. ID LIB3106-020-Q1-K1-A1

Method BLASTX
NCBI GI g2982303
BLAST score 414
E value 1.0e-40
Match length 91
% identity 86

NCBI Description (AF051236) hypothetical protein [Picea mariana]

Seq. No.

Seq. ID LIB3106-020-Q1-K1-A8

38674

Method BLASTX
NCBI GI g3914667
BLAST score 193
E value 7.0e-15
Match length 64
% identity 62

NCBI Description 50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSOR

>gi\_2459427 (AC002332) putative chloroplast 50S ribosomal

protein L28 [Arabidopsis thaliana]

Seq. No. 38675

Seq. ID LIB3106-020-Q1-K1-C10

Method BLASTX
NCBI GI g4580575
BLAST score 181
E value 2.0e-13
Match length 47
% identity 68

NCBI Description (AF082176) auxin response factor 9 [Arabidopsis thaliana]

BLAST score

Match length

E value

137

5.0e-71 373

```
LIB3106-020-Q1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3785983
BLAST score
                  205
E value
                  2.0e-16
                  67
Match length
% identity
                  54
                  (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  38677
Seq. No.
Seq. ID
                  LIB3106-020-Q1-K1-D8
                  BLASTX
Method
NCBI GI
                  g2642433
BLAST score
                  186
E value
                  7.0e-14
Match length
                  115
% identity
                   (AC002391) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  38678
                  LIB3106-020-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3702327
BLAST score
                  150
E value
                  1.0e-09
Match length
                  68
% identity
                  46
NCBI Description
                  (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                  38679
Seq. ID
                  LIB3106-020-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g3033389
BLAST score
                  226
E value
                  2.0e-18
Match length
                  126
                  5
% identity
                  (AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  38680
Seq. ID
                  LIB3106-020-Q1-K1-F6
Method
                  BLASTN
NCBI GI
                  g18761
BLAST score
                  247
E value
                  1.0e-137
Match length
                  323
                  94
% identity
NCBI Description
                  Soybean stem mRNA for 31 kD glycoprotein
Seq. No.
                  38681
Seq. ID
                  LIB3106-020-Q1-K1-G7
Method
                  BLASTN
NCBI GI
                  q169897
```

5992

æ.



% identity 84
NCBI Description G.max 28 kDa protein, complete cds

Seq. No. 38682

Seq. ID LIB3106-021-Q1-K1-A3

Method BLASTX
NCBI GI g629858
BLAST score 197
E value 2.0e-26
Match length 103
% identity 60

NCBI Description protein kinase C inhibitor - maize

Seq. No. 38683

Seq. ID LIB3106-021-Q1-K1-B3

Method BLASTN
NCBI GI g1055367
BLAST score 431
E value 0.0e+00
Match length 450
% identity 99

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 38684

Seq. ID LIB3106-021-Q1-K1-B7

Method BLASTN
NCBI GI g170087
BLAST score 143
E value 1.0e-74
Match length 279
% identity 88

NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)

Seq. No. 38685

Seq. ID LIB3106-021-Q1-K1-C10

Method BLASTN
NCBI GI g2905777
BLAST score 47
E value 2.0e-17
Match length 79
% identity 90

NCBI Description Glycine max ribosomal protein L41 mRNA, partial cds

Seq. No. 38686

Seq. ID LIB3106-021-Q1-K1-D1

Method BLASTN
NCBI GI g1055367
BLAST score 96
E value 1.0e-46
Match length 320
% identity 82

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 38687

Seq. ID LIB3106-021-Q1-K1-D10



Method BLASTX
NCBI GI g3367536
BLAST score 299
E value 4.0e-27
Match length 70
% identity 89

NCBI Description (AC004392) Contains similarity to symbiosis-related like

protein F1N20.80 gi\_2961343 from A. thaliana BAC gb\_AL022140. EST gb\_T04695 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 38688

Seq. ID LIB3106-021-Q1-K1-D2

Method BLASTX
NCBI GI g118926
BLAST score 314
E value 8.0e-29
Match length 116
% identity 55

NCBI Description DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR

>gi\_320600\_pir\_\_E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi\_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi\_227781\_prf\_\_1710351E abscisic acid responsive protein E

[Craterostigma plantagineum]

Seq. No. 38689

Seq. ID LIB3106-021-Q1-K1-D5

Method BLASTX
NCBI GI g537313
BLAST score 104
E value 4.0e-10
Match length 104
% identity 46

NCBI Description (L36159) unknown protein [Medicago sativa]

Seq. No. 38690

Seq. ID LIB3106-021-Q1-K1-E4

Method BLASTN
NCBI GI g340697
BLAST score 139
E value 3.0e-72
Match length 351
% identity 86

NCBI Description Soybean chloroplast 16S/23S ribosomal intergenic spacer DNA

Seq. No. 38691

Seq. ID LIB3106-021-Q1-K1-F2

Method BLASTN
NCBI GI g169897
BLAST score 204
E value 1.0e-111
Match length 328
% identity 91

NCBI Description G.max 28 kDa protein, complete cds



```
LIB3106-021-Q1-K1-F4
Seq. ID
                  BLASTN
Method
NCBI GI
                  g169897
BLAST score
                  429
E value
                  0.0e+00
Match length
                  465
% identity
                  98
NCBI Description
                  G.max 28 kDa protein, complete cds
                  38693
Seq. No.
Seq. ID
                  LIB3106-021-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g4335750
BLAST score
                  230
E value
                  5.0e-19
Match length
                  96
% identity
                   (AC006284) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  38694
                  LIB3106-021-Q1-K1-G12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1076509
BLAST score
                  173
E value
                  2.0e-12
Match length
                  79
% identity
                  56
NCBI Description
                  chloroplast RNA binding protein - kidney bean
                  >gi 558629 emb CAA57551 (X82030) chloroplast RNA binding
                  protein [Phaseolus vulgaris]
Seq. No.
                  38695
Seq. ID
                  LIB3106-022-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g1888357
BLAST score
                  364
                   4.0e-35
E value
                  77
Match length
% identity
                  79
NCBI Description
                   (X98130) alpha-mannosidase [Arabidopsis thaliana]
                  >gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
Seq. No.
                   38696
Seq. ID
                  LIB3106-022-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g1076250
BLAST score
                  309
                  2.0e-28
E value
Match length
                  91
                   65
% identity
                  chitinase (EC 3.2.1.14) B - Virginian pokeweed
NCBI Description
                  >gi 998516 bbs 168133 chitinase-B, PLC-B [Phytolacca
```

americana=pokeweed, leaves, Peptide, 274 aa]

38702

Seq. ID



LIB3106-022-Q1-K1-D12

```
BLASTX
Method
NCBI GI
                  g3319884
BLÄST score
                  103
                  1.0e-09
E value
Match length
                  56
% identity
                  57
                  (AJ224306) PRT1 [Arabidopsis thaliana]
NCBI Description
                  >gi 3319886 emb CAA11892 (AJ224307) PRT1 [Arabidopsis
                  thaliana]
                  38698
Seq. No.
                  LIB3106-022-Q1-K1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4262232
BLAST score
                  163
                  4.0e-11
E value
Match length
                  63
% identity
NCBI Description
                  (AC006200) putative ribosomal protein L7 [Arabidopsis
                  thaliana]
                  38699
Seq. No.
Seq. ID
                  LIB3106-022-Q1-K1-F7
Method
                  BLASTX
                  g121631
NCBI GI
                  312
BLAST score
                  8.0e-29
E value
Match length
                  78
% identity
                  74
                  GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR
NCBI Description
                  >gi 72323 pir KNNT2S glycine-rich protein 2 - wood tobacco
                  >gi 19743_emb_CAA42622 (X60007) nsGRP-2 [Nicotiana
                  sylvestris]
                  38700
Seq. No.
                  LIB3106-022-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2880049
BLAST score
                  141
E value
                  1.0e-08
Match length
                  91
% identity
                  (AC002340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  38701
Seq. No.
                  LIB3106-022-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455155
BLAST score
                  407
                  8.0e-40
E value
Match length
                  108
% identity
                   (AL022023) EF-1 alpha - like protein (fragment)
NCBI Description
                   [Arabidopsis thaliana]
```